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(54) Title: BAX RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN YEAST AND FUNGI

(57) Abstract: The invention describes the use of nucleic acids and polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi, for the preparation of a medicament for treating diseases associated with yeast or fungi or for the treatment of proliferative disorders or for preventing apoptosis in certain diseases. Methods are provided to identify compounds which selectively modulate the expression or functionality of said polypeptides in the same or a parallel pathway. Also provided are compounds as well as pharmaceutical compositions, medicaments and vaccines. The invention also comprises new nucleic acid sequences, probes and primers derived thereof, expression vectors and host cells transformed with said vectors, polypeptides and antibodies raised against said polypeptides.

BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN YEAST AND FUNGI**Field of the invention**

5 The present invention relates to the identification of genes and proteins encoded thereof from yeast and fungi whose expression is modulated upon programmed cell death and which genes, proteins or functional fragments and equivalents thereof may be used as selective targets for drugs to treat infections caused by or associated with yeast and fungi or for the treatment of proliferative disorders or for the prevention of apoptosis in certain diseases.

10

Background to the invention

Invasive fungal infections (e.g. *Candida* spp., *Aspergillus* spp., *Fusarium* spp., *Zygomycetes* spp.) (Walsh, 1992) have emerged during the past two decades as important pathogens causing formidable morbidity and mortality in an increasingly diverse and progressively
15 expanding population of immunocompromised patients. Those with the acquired immune deficiency syndrome (AIDS) constitute the most rapidly growing group of patients at risk for life-threatening mycosis. But fungal infections have also increased in frequency in several populations of other susceptible hosts, including very-low-birth-weight infants, cancer patients receiving chemotherapy, organ transplant recipients, burn patients and surgical patients with
20 complications.

These fungal infections are not limited to humans and other mammals, but are also important in plants where they can cause diseases or cause the production of unwanted compounds (e.g. *Fusarium* spp., *Aspergillus* spp., *Botrytis* spp., *Cladosporium* spp.).

Although recent advances in antifungal chemotherapy have had an impact on these mycoses,
25 expanding populations of immunocompromised patients will require newer approaches to antifungal therapy. The discovery of novel antifungal agents is thus an essential element of any new antifungal therapy.

Classical approaches for identifying antifungal compounds have relied almost exclusively on inhibition of fungal or yeast growth as an endpoint. Libraries of natural products, semi-synthetic,
30 or synthetic chemicals are screened for their ability to kill or arrest growth of the target pathogen or a related nonpathogenic model organism. These tests are cumbersome and provide no information about a compound's mechanism of action. The promising lead compounds that emerge from such screens must then be tested for possible host-toxicity and detailed mechanism of action studies must subsequently be conducted to identify the affected molecular
35 target.

Cells from multicellular organisms can commit suicide in response to specific signals or injury by an intrinsic program of cell death. Apoptosis is a form of programmed cell death which leads to elimination of unnecessary or damaged cells. Cells that are either unwanted or potentially harmful to the organism undergo the apoptotic process and show events like cell shrinkage, chromatin condensation, cytoplasmic condensation, digestion of nuclear DNA, loss of mitochondrial membrane potential, plasma membrane blebbing and phagocytosis of the cell debris (Schwartz, *et al.* 1993). The Bcl-2 family of proteins is centrally involved in the control of the programmed cell death process (PCD). Proteins of this group belong either to the inhibitors of cell death (Bcl-2, Bcl-X_L) or to the group of proteins promoting apoptosis (Bax, Bak) (Oltvai and Korsmeyer 1994; Knudson and Korsmeyer 1997; Reed *et al.* 1998). The ability of the Bcl-2 family of proteins to regulate life and death of a cell is conserved across evolution. Finding of homologues of PCD regulatory genes in plants and animals suggests the possibility that some functions involved in this process may originally have evolved in unicellular organisms, before a divergent development between the plant and the animal kingdom had happened (Apte *et al.* 1995).

Expression of the pro-apoptotic human or mouse Bax protein in *Saccharomyces cerevisiae* did induce cell death in this budding yeast (Sato *et al.* 1994; Greenhalf *et al.* 1996; Zha *et al.* 1996). It was initially described as a process that resembled autophagy with dissolution of the internal organelles and vacuolisation. The apoptotic features characteristic for multicellular eucaryotic cells like morphological changes in nuclear shape and chromatin condensation, were not observed in this yeast (Zha *et al.* 1996). It was therefore suggested that Bax-induced cell death in *S. cerevisiae* is due to the toxicity of the Bax protein itself, mediated by a hypothetical pore-formation without any involvement of a death program (Muchmore *et al.* 1996).

Bax expression in the fission yeast *Schizosaccharomyces pombe* did in contrast show some of the typical apoptotic changes like DNA fragmentation, chromatin condensation, dissolution of the nuclear envelope and cytosolic vacuolisation, suggesting the presence of the evolutionary conserved PCD pathway in this unicellular eucaryote (Ink *et al.* 1997; Jurgensmeier *et al.* 1997). Since it is very unlikely that species dependent differences in the toxicity of the Bax protein are the reason for this observed difference between the two yeasts, a bona fide cell death pathway may well be present in *S. cerevisiae*.

Recent findings of a yeast mutant in the cell division cycle gene *CDC48* show a number of morphological and molecular features that are considered typical indicators of apoptosis markers in metazoan cells: exposure of phosphatidylserine on the outer leaflet of the cytoplasmic membrane, DNA breakage as well as chromatin condensation and fragmentation, supporting the existence of a basic PCD machinery in this unicellular yeast. This theory was

supported by the analysis of a wild type yeast cell expressing the human Bax protein. Comprehensive tests for morphological markers of apoptosis did show a series of changes, identical to morphological markers defining apoptosis (Ligr, Madeo *et al.* 1998). Recent findings from the same group (Madeo *et al.*, 1999) implicate oxygen stress as a general regulator of apoptosis in yeast but the actual mechanism of Bax lethality in *S. cerevisiae* remains unclear.

It is an aim of the present invention to provide new *bax* sequences for expression in yeast and fungi and tools for identifying yeast and candida functions in the pathways leading to programmed cell death.

It is an aim of the present invention to provide nucleic acids as well as polypeptides which represent potential molecular targets for the identification of new compounds which can be used in alleviating diseases or conditions associated with yeast or fungal infections.

It is a further aim of the present invention to provide uses of these nucleic acid and polypeptide molecules for treating diseases associated with yeast or fungi or for the preparation of (a) medicament(s) for treating said diseases.

It is also an aim of the invention to provide pharmaceutical compositions and vaccines comprising these nucleic acids or polypeptides.

It is also an aim of the present invention to provide vectors comprising these nucleic acids, as well as host cells transfected or transformed with said vectors.

It is also an aim of the invention to provide antibodies against these polypeptides, which can be used as such, or in a composition as a medicament for treating diseases associated with yeast and fungi.

It is another aim of the invention to provide methods to selectively identify compounds or polypeptides capable of inhibiting or activating expression of the polypeptides of the invention or capable of selectively modulating expression or functionality of such polypeptides. The nucleic acid and polypeptide molecules alternatively can be incorporated into an assay or kit to identify these compounds or polypeptides.

It is also an aim of the invention to provide methods for preventing infection with yeast or fungi.

It is a further aim of the invention to provide human homologues for the nucleic acids and polypeptides of the invention for use in treating proliferative disorders, such as cancer, or for the prevention of apoptosis in certain diseases, or for the preparation of a medicament for treating such disorders or diseases.

All the aims of the present invention have been met by the embodiments as set out below.

Summary of the invention

Since it has been discovered that the mammalian *bax* gene triggers apoptotic changes in yeast (Ligr *et al.*, 1998), this can be an indication that the molecular pathways eventually leading to programmed cell death may also be partially present in yeast cells and other unicellular eukaryotes. Identification of genes involved in this process could be important for the development of new antifungal therapeutics.

The present inventors overexpressed the Bax protein in the pathogenic yeast *Candida albicans* and found that this leads to a similar phenotype. However these results could only be received after having constructed a new synthetic *BAX* gene which could be adequately expressed in this pathogenic organism.

Furthermore, the present inventors identified a range of specific nucleic acids which are involved in the molecular pathways eventually leading to programmed cell death. The present inventors were able to identify via macro array screening a range of genes involved in a pathway eventually leading to programmed cell death in the yeast *Saccharomyces cerevisiae*.

Genes which were differentially expressed (analysed using the Pathways™ software) at different time points after Bax expression are envisaged as candidate genes in the present invention.

Additionally, the invention also relates to *Candida spp.* homologues of the *S. cerevisiae* candidate genes and their uses in stimulating or preventing cell death in yeast and fungi, especially pathogenic yeast and fungi are herewith envisaged.

Furthermore, also part of the invention are the human homologues of these apoptosis-associated *S. cerevisiae* nucleic acids and polypeptides and their potential use in treating proliferative disorders in human and other mammals.

Detailed description of the invention

The present invention relates to the use of a nucleic acid molecule encoding a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi and which nucleic acid sequence is selected from:

(a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of

SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248,

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662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710,
712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a functional
15 equivalent, derivative or bioprecursor of said protein,
(b) a nucleic acid encoding a protein having an amino acid sequence which is more than 70%
similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or
95% similar and most preferably more than 97% similar to any of the amino acid sequences
as represented by any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44,
20 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92,
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(c) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 292, 294, 296, 298, 299, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732,

(d) a nucleic acid comprising a sequence as represented in any of SEQ ID NOs 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295,

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- (e) a nucleic acid which is more than 70% identical, preferably more than 75 or 80% identical, more preferably more than 85%, or 90% or 95% identical and most preferably more than 97% identical to any of the nucleic acid sequences as represented by any of SEQ ID NOs 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 691, 693, 695, 697, 699, 701, 703, 705, 707, 709, 711, 713, 715, 717, 719, 721, 723, 725, 727, 729 and 731,

(f) a nucleic acid encoding a functional fragment of any of the nucleic acids as specified in a) to e); and

(g) the complement of any of the nucleic acids as specified in a) to f),

for the preparation of a medicament for treating diseases associated with yeast or fungi.

5 Sequence similarity searches were performed using the BLAST software package version 2. Identity and similarity percentages were calculated using BLOSUM62 as a scoring matrix.

As known in the art, "similarity" between two polypeptides is determined by comparing the amino acid sequence and its conserved amino acid substitutes of one polypeptide to the sequence of a second polypeptide. Moreover, also known in the art is "identity" which means
10 the degree of sequence relatedness between two polypeptide or two polynucleotide sequences as determined by the identity of the match between two strings of such sequences. Both identity and similarity can be readily calculated. While there exist a number of methods to measure identity and similarity between two polynucleotide or polypeptide sequences, the terms "identity" and "similarity" are well known to skilled artisans (Carillo and Lipton, 1988). Methods commonly
15 employed to determine identity or similarity between two sequences include, but are not limited to, those disclosed in "Guide to Hype Computers (Bishop, 1994) and Carillo and Lipton (1988). Preferred methods to determine identity are designed to give the largest match between the two sequences tested. Methods to determine identity and similarity are codified in computer programs. Preferred computer program methods to determine identity and similarity between
20 two sequences include, but are not limited to, GCG program package (Devereux *et al.*, 1984), BLASTP, BLASTN and FASTA (Altschul *et al.*, 1990).

The expression "functional fragment of a nucleic acid" as used herein means the minimal nucleic acid which is necessary to encode a functional protein (or polypeptide). For instance, in situations where a nucleic acid is provided comprising at the 5' end and at the 3' end more
25 nucleotides than the actual open reading frame, the invention also relates to fragments of the nucleic acid which are smaller but which still contain the workable open reading frame. Also meant are parts of the open reading frame encoding a polypeptide having the same properties as the polypeptide encoded by the complete open reading frame.

The expression "a pathway eventually leading to programmed cell death" refers to a sequence
30 of steps ultimately leading to cell death and which can be triggered at various steps in this pathway by various agents, such as Bax, Bak, CED4, hydrogen peroxide, diamide and farnesol. The nucleic acid sequences to be used according to this aspect of the invention from *Saccharomyces cerevisiae* are defined in SEQ ID NOs 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85,
35 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125,

The expression "treating diseases associated with yeast and fungi" not only refers to diseases or infections caused by said organisms but also refers to allergic reactions caused by said organisms, such as the so-called "professional diseases" in, for instance, bakery and brewery and that are caused by yeast or fungi which are commonly known as "non-pathogenic". Some examples of specific diseases associated with yeast or fungi are further exemplified.

The invention further relates to the use of nucleic acid sequence homologues of SEQ ID NOS 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377,

379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415,
417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453,
455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491,
493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529,
5 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567,
569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605,
607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643,
645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 691, 693, 695,
697, 699, 701, 703, 705, 707, 709, 711, 713, 715, 717, 719, 721, 723, 725, 727, 729 and 731
10 but isolated from other yeast and fungi strains which are also involved in a pathway eventually
leading to programmed cell death. According to a more specific embodiment, these nucleic acid
sequences are derived from *Aspergillus fumigatus*.

In a more specific embodiment the invention relates to a nucleic acid encoding a polypeptide
which is involved in a pathway eventually leading to programmed cell death of yeast or fungi
15 selected from:

- (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of
SEQ ID NOs 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426,
428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462,
464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498,
20 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534,
536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560,
562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596,
598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632,
634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668,
25 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a functional
equivalent, derivative or bioprecursor of said protein;
- (b) a nucleic acid encoding a protein having an amino acid sequence which is more than 70%
similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or
95% similar and most preferably more than 97% similar to any of the amino acid sequences
30 as represented by any of SEQ ID NOs 398, 400, 402, 404, 406, 408, 410, 412, 414, 416,
418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452,
454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488,
490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524,
526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560,
35 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586,

588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732,

(c) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 569, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732,

(d) a nucleic acid comprising a sequence as represented in any of SEQ ID NOs 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 717, 719, 721, 723, 725, 727, 729 and 731;

(e) a nucleic acid which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the nucleic acid sequences as represented by any of SEQ ID NO 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613,

815, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649,
651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 717, 719, 721, 723, 725,
727, 729 and 731,

(f) a nucleic acid encoding a functional fragment of any of the nucleic acid sequences as
5 specified in a) to e), and,

(g) the complement of any of the nucleic acids as specified in a) to f).

In a preferred embodiment the invention relates to nucleic acids from *Candida albicans*, as
represented by the SEQ ID NOs 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419,
421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457,
10 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495,
497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533,
535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571,
573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609,
611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647,
15 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 717, 719, 721, 723, 725,
727, 729 and 731.

In an even more preferred embodiment the invention relates to an isolated nucleic acid from
mammal or human origin which nucleic acid corresponds to a mammal or human homologue of
at least one of the sequences represented in SEQ ID NOs 17, 19, 21, 23, 25, 27, 29, 31, 33, 35,
20 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85,
87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125,
127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163,
165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201,
203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239,
25 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277,
279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315,
317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353,
355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391,
393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429,
30 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467,
469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505,
507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543,
545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581,
583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619,
35 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657,

659, 661, 663, 665, 667, 669, 671, 673, 687, 681, 693, 695, 697, 699, 701, 703, 705, 707, 709, 711, 713, 715, 717, 719, 721, 723, 725, 727, 729 and 731.

Therefore, according to a further preferred embodiment, the invention relates to an isolated nucleic acid from mammal or human origin which nucleic acid sequence is selected from:

- 5 (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 676, 678, 680, 682, 684 and 686, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or
10 95% similar and most preferably more than 97% similar to any of the amino acid sequences as represented by any of SEQ ID NOs 676, 678, 680, 682, 684 and 686;
- (c) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid
15 sequences as represented by any of SEQ ID NOs 676, 678, 680, 682, 684 and 686;
- (d) a nucleic acid comprising a sequence as represented in any of SEQ ID NOs 675, 677, 679, 681, 683 and 685;
- (e) a nucleic acid which is more than 70% identical, preferably more than 75 or 80% identical, more preferably more than 85%, or 90% or 95% identical and most preferably more than
20 97% identical to any of the nucleic acid sequences as represented by any of SEQ ID NOs 675, 677, 679, 681, 683 and 685;
- (f) a nucleic acid encoding a functional fragment of any of the nucleic acids as specified in a) to e); and
- (g) the complement of any of the nucleic acids as specified in a) to f),

- 25 for the preparation of a medicament for treating diseases associated with yeast or fungi.

The invention also relates to the use of said nucleic acids for treating and/or preventing and/or alleviating proliferative disorders or for the prevention of apoptosis in certain disorders or diseases.

- 30 The expression "proliferative disorders" or "proliferative diseases" refers to an abnormality within a patient or animal such as cancer. Normal cells start to proliferate due to a change in the coding or non-coding sequence of the DNA resulting in a swollen or distended tissue. Mutation may arise without obvious cause. An abnormal benign or malignant mass of tissue is formed that is not inflammatory. Cells of pre-existent tissue start to divide unexpectedly and resulting cell mass possesses no physiologic function.

The expression "apoptosis" or "apoptosis-related diseases" includes diseases such as autoimmunity diseases, ischemia, diseases related with viral infections or neurodegenerations.

It should be clear that the invention also relates to all nucleic acids according to the invention and which are specifically described above, and which can be DNA, cDNA, genomic DNA, synthetic DNA, or RNA wherein T is replaced by U. A nucleic acid according to the invention may also comprise any modified nucleotide known in the art.

The term "nucleic acid sequence" also includes the complementary sequence to any single stranded sequence given.

According to the invention, these sequences and their homologues in other yeast and fungi or in human or other mammals as well as the polypeptides which they encode represent novel molecular targets which can be incorporated into an assay to selectively identify compounds capable of inhibiting or activating expression of such polypeptides. Furthermore, the invention also relates to the potential use of said sequences in alleviating diseases or conditions associated with yeast or fungi infections, such as diseases caused by *Candida* spp., *Aspergillus* spp., *Microsporium* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis* spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*, and *Sporothrix schenckii*, such as, but not limited to:

- Candidiasis, caused by *C. albicans* and other members of the genus *Candida*, which are primary or secondary mycotic infections, also named candidosis, moniliasis and thrush;
- Aspergilliosis, caused by members of the genus *Aspergillus*, form a spectrum of diseases;
- Histoplasmosis, caused by *Histoplasma capsulatum*, which is a pulmonary disease always seen in HIV positive or other immunocompromised individuals;
- Paracoccidioidomycosis, caused by *Paracoccidioides brasiliensis*, which is a granulomatous disease that originates as a pulmonary disease;
- Blastomycosis, caused by *Blastomyces dermatitidis*, which may be a benign and self-limiting infection or a chronic granulomatous and suppurative mycosis, also named Chicago disease or Gilchrist's disease;
- Coccidioidomycosis, caused by *Coccidioides immitis*, and which is a respiratory infection that typically resolves rapidly, but the mycosis can become acute, chronic, severe or fatal; also named San Joaquin Valley fever or Valley fever;
- Cryptococcosis, caused by *Cryptococcus neoformans*, which is a chronic, subacute to acute pulmonary, systemic or meningitic disease, also named Torulosis;

- Sporotrichosis, caused by *Sporothrix schenckii*, which is a chronic infection characterized by nodular lesions of cutaneous or subcutaneous tissues and adjacent lymphatics that suppurate, ulcerate and drain.

Some of the pathways leading to apoptosis are conserved between mammalian cells and yeast or fungi. Therefore the invention also relates to the potential use of homologous sequences from human or mammalian origin for preventing and/or alleviating diseases or conditions where apoptosis or non-apoptosis of cells is impaired, for instance in proliferative disorders. In this respect also cancer can be seen as a proliferative disorder. Furthermore, targets which are part of such a conserved pathway may be used to stimulate or inhibit the apoptosis in mammalian cells. E.g. stimulation of apoptosis is desirable in the treatment of tumor cells/tissues.

Human homologues according to the invention can be obtained by selective hybridisation of the yeast and candida nucleic acid molecules of the invention against human genome or cDNA libraries according to methods well known in the art (Sambrook *et al.*, 1989). Human polypeptide homologues are obtained from the corresponding human nucleic acid homologous nucleotide sequences.

The present invention further relates to a nucleic acid capable of selectively hybridising to at least one of the nucleic acid molecules according to the invention, or the complement thereof.

The term "selectively hybridising" or "specifically hybridising" means hybridising under conditions wherein sequences can be detected which are homologues of the sequences of the invention, but which are for instance derived from heterologous cells or organisms, and wherein said sequences do not hybridize with known sequences. In a preferred embodiment, mammalian homologues can be detected. It is well known to the person skilled in the art which methods for hybridisation can be used and which conditions are necessary for selectively or specifically hybridising. Preferably, hybridization under high stringency conditions can be applied (Sambrook *et al.*, 1989).

As such, the present invention also relates to the use of the nucleic acid sequences of the invention for detecting homologues in heterologous organisms including but not limited to mammalian organisms.

The invention also relates to an isolated nucleic acid comprising a human homologue of at least one of the yeast or candida nucleic acids described earlier. The invention also relates to a polypeptide encodable by said human homologue of said nucleic acid.

In a further embodiment the invention also relates to an expression vector comprising a human homologue of at least one of the yeast or candida nucleic acids described herein. Said expression vector according can be an expression vector wherein said nucleic acid sequence is operably linked to one or more control sequences allowing the expression in prokaryotic and/or

eukaryotic host cells. According to a further embodiment, the expression vector comprises an inducible promoter and/or a reporter molecule.

The invention also relates to a host cell transformed, transfected or infected with any of the above described vectors.

- 5 According to a preferred embodiment, the invention relates to an antisense version of any of the nucleic acids of the invention and described above.

The present invention more particularly relates to an antisense molecule comprising a nucleic acid capable of selectively hybridising to at least one of the nucleic acids of the invention. In an interesting embodiment the invention relates to a nucleic acid capable of selectively hybridising
10 to a human homologue of at least one yeast or candida nucleic acid described herein.

Polynucleotides according to the invention may be inserted into vectors in an antisense orientation in order to provide for the production of antisense RNA. Antisense RNA or other antisense nucleic acids may also be produced by synthetic means.

- The present invention also advantageously provides nucleic acid molecules of at least
15 approximately 10 contiguous nucleotides of a nucleic acid according to the invention and preferably from 10 to 50 nucleotides. These sequences may, advantageously be used as probes or primers to initiate replication, or the like. Such nucleic acid sequences may be produced according to techniques well known in the art, such as by recombinant or synthetic means. The probes will hybridise specifically with any of the nucleic acid molecules of the
20 invention. The primers will specifically amplify any of the nucleic acid molecules of the invention. The probes or primers according to the invention may also be used in diagnostic kits or the like for detecting the presence of a nucleic acid according to the invention. These tests generally comprise contacting the probe with the sample under hybridising conditions and detecting the presence of any duplex or triplex formation between the probe and any nucleic acid in the
25 sample.

- According to the present invention these probes may be anchored to a solid support. Preferably, they are present on an array so that multiple probes can simultaneously hybridize to a single biological sample. The probes can be spotted onto the array or synthesized *in situ* on the array. (Lockhart *et al.*, 1996). A single array can contain more than 100, 500 or even 1,000 different
30 probes in discrete locations. Such arrays can be used to screen for compounds interacting with said probes.

- Advantageously, the nucleic acid sequences, according to the invention may be produced using recombinant or synthetic means, such as for example using PCR cloning mechanisms which generally involve making a pair of primers, which may be from approximately 10 to 50
35 nucleotides to a region of the gene which is desired to be cloned, bringing the primers into

contact with mRNA, cDNA, or genomic DNA from the yeast or fungal cell, performing a polymerase chain reaction under conditions which bring about amplification of the desired region, isolating the amplified region or fragment and recovering the amplified DNA. Generally, such techniques as defined herein are well known in the art, such as described in Sambrook *et al.* (1989). These techniques can be used to clone homologues of the nucleic acid sequences of the invention in other organisms.

The nucleic acids or oligonucleotides according to the invention may carry a revealing label. Suitable labels include radioisotopes such as ^{32}P , ^{33}P or ^{35}S , enzyme labels or other protein labels such as biotin or fluorescent markers. Such labels may be added to the nucleic acids or oligonucleotides of the invention and may be detected using techniques known in the art.

According to another embodiment of the invention, the nucleic acid sequences according to the invention as defined above may, advantageously, be included in a suitable vector, preferably an expression vector which may be transformed, transfected or infected into a host cell. In such an expression vector the nucleic acid is operably linked to one or more control sequences allowing the expression in host cells, such as a suitable promoter, or the like, to ensure expression of the proteins according to the invention in a suitable prokaryotic or eukaryotic host cell. Said promoter may be either constitutive, inducible or cell- or tissue- or organ-specific. The expression vector may advantageously be a plasmid, cosmid, virus or other suitable vector which is known to those skilled in the art. The expression vector and the host cell defined herein also form part of the present invention. Said host cell can be from bacterial, yeast, fungal, insect, mammal or human origin, or any other host wherein said vector can be introduced by at least one of the methods known in the art. However, preferred host cells are lower eukaryotic cells such as a yeast cell or a fungal cell. Yeast and fungal cells are particularly advantageous because they provide the necessary post-translational modifications to the expressed proteins of the invention, similar to those of the natural proteins from which they are derived. These modifications confer optimal conformation of said proteins, which when isolated may advantageously be used in kits, methods or the like.

In a further embodiment, the expression vector may further comprise an inducible promoter, and/or further a reporter molecule.

The invention further relates to any one of the nucleic acids as defined above for use as a medicament.

Nucleotide sequences according to the invention are particularly advantageous for providing selective therapeutic targets for treating yeast or fungi-associated infections. For example, an antisense nucleic acid capable of binding to the nucleic acid sequences according to the invention may be used to selectively inhibit expression of the corresponding polypeptides,

leading to impaired growth or death of yeast and fungi with reductions of associated illnesses or diseases.

Also envisaged in the present invention are promoter or other control sequences that are comprised within the nucleic acids of the invention, said nucleic acid control sequences can also serve as a target for the identification of compounds or proteins which interfere with the control of expression of downstream encoded polypeptides.

Furthermore, also the human homologues of the yeast and candida nucleic acids may be useful in diseases where apoptosis of cells plays a substantial role, both in situations where apoptosis of (particular) cells is wanted or unwanted.

The invention thus also relates to the use of any of the nucleic acids of the invention or to a human homologue thereof for treating proliferative disorders or for the prevention of apoptosis in certain disorders or diseases. As described above, the invention also relates to the use of antisense molecules of the nucleic acids of the invention or to an antisense of any of the human homologues for treating proliferative disorders or for the prevention of apoptosis in certain disorders or diseases.

Said nucleic acids, human homologues and antisense molecules can also be used for the preparation of a medicament for treating or preventing the above-mentioned diseases.

According to yet another embodiment, the invention relates to at least one polypeptide encodable by a nucleic acid of the invention.

The invention also relates to the use of a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi, said polypeptide being selected from:

- (a) a protein having an amino acid sequence as represented in any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498,

- 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 682, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences as represented by any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732,
- (c) a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54,

56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732, and,

(d) a functional fragment of any of said proteins as defined in a) to c),

for the preparation of a medicament for treating diseases associated with yeast or fungi.

The term "functional fragment" of a protein means a truncated version of the original protein or polypeptide referred to. The truncated protein sequence can vary widely in length; the minimum size being a sequence of sufficient size to provide a sequence with at least a comparable function and/or activity of the original sequence referred to, while the maximum size is not critical. In some applications, the maximum size usually is not substantially greater than that required to provide the desired activity and/or function(s) of the original sequence. A functional fragment can also relate to a subunit with similar function as said protein. Typically, the truncated amino acid sequence will range from about 5 to about 60 amino acids in length. More typically, however, the sequence will be a maximum of about 50 amino acids in length, preferably a maximum of about 60 amino acids. It is usually desirable to select sequences of at least about 10, 12 or 15 amino acids.

Functional fragments include those comprising an epitope which is specific or unique for the proteins according to the invention. Epitopes may be determined using, for example, peptide

scanning techniques as described in Geysen *et al.* (1988). Preferred functional fragments have a length of at least, for example, 5, 10, 25, 50, 75, 100, 125, 150, 175 or 200 amino acids.

The polypeptides to be used according to the invention from *Saccharomyces cerevisiae*, are represented by SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50,
 5 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100,
 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138,
 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176,
 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214,
 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252,
 10 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290,
 292, 294, 296, 298, 299, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318,
 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356,
 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394,
 396, 392, 394, 396, 398, 700, 702, 704, 706, 708, 710, 712, 714 and 716. Also according to the
 15 invention is the use of the polypeptides from *Candida albicans* as represented by the SEQ ID
 NOs 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432,
 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470,
 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508,
 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546,
 20 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574,
 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612,
 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650,
 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728,
 730 and 732, and the use of human polypeptides as represented by SEQ ID NOs 676, 678,
 25 680, 682, 684 and 686.

Thus, according to a preferred embodiment, the present invention relates to an isolated polypeptide which is involved in a pathway for programmed cell death of yeast or fungi, for instance a *Candida* spp., selected from:

(a) a polypeptide having an amino acid sequence as represented in any of SEQ ID NOs
 30 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430,
 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464,
 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498,
 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532,
 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566,
 35 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590,

592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a functional equivalent, derivative or bioprecursor of said protein;

- 5 (b) a polypeptide having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences as represented by any of SEQ ID NOs 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 10 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 15 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732,
- (c) a polypeptide having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 20 95% identical and most preferably more than 97% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 25 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 30 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732, and

(d) a functional fragment of any of said polypeptides as defined in a) to c).

According to a further preferred embodiment, the present invention relates to an isolated polypeptide which is involved in a pathway for programmed cell death of mammalian cells selected from:

- (a) a polypeptide having an amino acid sequence as represented in any of SEQ ID NOs 676, 678, 680, 682, 684 and 686, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- 5 (b) a polypeptide having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences as represented by any of SEQ ID NOs human 676, 678, 680, 682, 684 and 686;
- 10 (c) a polypeptide having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 676, 678, 680, 682, 684 and 686; and,
- (d) a functional fragment of any of said polypeptides as defined in a) to c).

15 The invention also relates to the polypeptides of the invention and described above for use as a medicament.

Pharmaceutical or fungicidal compositions comprising at least one of the nucleic acids, antisense molecules, polypeptides of the invention optionally together with a pharmaceutically acceptable carrier, diluent or excipient therefor, are also part of the invention.

20 The polypeptides described above or the human or mammal homologues thereof can also be used for treating proliferative disorders or for the prevention of apoptosis in certain diseases.

The invention furthermore relates to a pharmaceutical composition for use as a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases comprising a nucleic acid molecule of the invention or a human homologue thereof, an antisense molecule to at least one of the nucleic acids of the invention or an antisense molecule to a mammalian
25 homologue of said nucleic acid or a polypeptide of the invention or a human homologue thereof together with a pharmaceutically acceptable carrier, diluent or excipient therefor.

The polypeptide or protein according to the invention may also include variants of any of the polypeptides of the invention as specified above having conservative amino acid changes.

30 The present invention also relates to a vaccine for immunizing a mammal comprising at least one (recombinant) nucleic acid molecule or at least one (recombinant) polypeptide of the invention in a pharmaceutically acceptable carrier. Preferred vaccines are those that can be used for immunization against infections caused by yeast and fungi. Other preferred vaccines can be used for immunizing mammals against proliferative disorders or for preventing apoptosis in certain diseases.

Pharmaceutically acceptable carriers include any carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition. Suitable carriers are typically large, slowly metabolizing macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers; and inactive virus particles. Such carriers are well known to those of ordinary skill in the art.

A "vaccine" is an immunogenic composition capable of eliciting protection against infections caused by yeast or fungi, whether partial or complete.

Said vaccine compositions may include prophylactic as well as therapeutic vaccine compositions. When a vaccine is used for protecting individuals against certain infections or diseases, it is called a prophylactic vaccine. A vaccine may also be useful for treatment of an individual, in which case it is called a therapeutic vaccine.

The term "therapeutic" refers to a composition capable of treating infections caused by yeast or fungi or capable of treating proliferative disorders.

Also encompassed within the present invention are antibodies, monoclonal or polyclonal, capable of specifically binding to one or more epitopes of the polypeptides or proteins of the invention. The polypeptides of the invention are represented in SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 569, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 676, 678, 680, 682, 684, 686, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732.

The term "specific binding" implies that there is substantially no cross-reaction of the antibody with other proteins.

The antibodies according to the invention may be produced according to techniques which are known to those skilled in the art. Monoclonal antibodies may be prepared using conventional hybridoma technology as described by Kohler and Milstein (1979). Polyclonal antibodies may also be prepared using conventional technology well known to those skilled in the art, and which comprises inoculating a host animal, such as a mouse, with a protein or epitope according to the invention and recovering the immune serum. The present invention also includes fragments of whole antibodies which maintain their binding activity, such as for example, Fv, F(ab') and F(ab')₂ fragments as well as single chain antibodies.

The antibodies of the invention are capable of specifically binding to at least one of the yeast or candida polypeptides as defined earlier or to a human homologue thereof or to a specific epitope of said polypeptide or said human homologue. The invention also relates to the use of said antibodies in treating and/or preventing and/or alleviating proliferative disorders or for the prevention of apoptosis in certain diseases. Said antibodies may also be used for the preparation of a medicament for and/or preventing and/or alleviating proliferative disorders or for the prevention of apoptosis in certain diseases.

Antibodies according to the invention may also be used in a method of detecting the presence of a polypeptide according to the invention, which method comprises reacting the antibody with a sample and identifying any protein bound to said antibody. A kit may also be provided for performing said method which comprises an antibody according to the invention and means for reacting the antibody with said sample.

The antibodies according to the invention may be used as a medicament or may be comprised in a pharmaceutical composition. According to a more specific embodiment, the antibodies may be used in the preparation of a medicament for treating diseases associated with yeast and fungi where the yeast or fungus is chosen from, but not restricted to *Candida* spp., *Aspergillus* spp., *Microsporum* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis*, spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*, and *Sporothrix schenckii*.

The invention also relates to a method of preventing infection with yeast or fungi, comprising administering a composition containing at least one polypeptide of the invention to a mammal in effective amount to stimulate the production of protective antibody or protective T-cell response. According to another embodiment, the present invention provides a method of identifying compounds or polypeptides which selectively inhibit, induce or interfere with the

expression/production of the polypeptides encoded by the nucleotide sequences of the invention, or compounds which selectively inhibit, activate or interfere with the functionality of polypeptides expressed from the nucleotide sequences according to the invention, or which selectively inhibit, induce or interfere with the metabolic pathways in which these polypeptides are involved. Compounds (or polypeptides) may carry agonistic or antagonistic properties. The compounds (and polypeptides) to be screened may be of extracellular, intracellular, biologic or chemical origin.

Different alternative methods for identification of said compounds or polypeptides form part of the present invention.

- 10 According to a specific embodiment the invention relates to a method of identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast and fungi or in metabolic pathways in which said polypeptides are involved, which method comprises (a) contacting a compound to be tested with yeast or fungal cells transformed, transfected or infected with an expression vector
- 15 comprising an antisense sequence of at least one of the nucleic acid sequences of the invention, which expression results in underexpression of said polypeptide, in addition to contacting one or more wild type cells with said compound, (b) monitoring the growth and/or death rate or activity of said transformed, transfected or infected cells compared to said wild type cells; wherein differential growth or activity of said transformed, transfected or infected
- 20 yeast or fungal cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway, (c) alternatively monitoring the growth and/or death rate and/or activity of said transformed, transfected or infected cells compared to transformed, transfected or infected cells which were not contacted with the compound to be tested, wherein differential growth or activity of said mutated yeast or fungi cells is indicative of selective action of said
- 25 compound on a polypeptide in the same or a parallel pathway, (d) alternatively monitoring changes in morphologic and/or functional properties of components in said transformed, transfected or infected cells caused by the addition of the compound to be tested, and (e) optionally identifying the compound.

- Alternative methods for identifying compounds which selectively modulate expression or
- 30 functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast or fungi or in metabolic pathways in which said compounds are involved, may comprise the use of any other method known in the art resulting in gene activation, gene inactivation, gene modulation or gene silencing.

- Another alternative to the above described method comprises (a) contacting a compound to be
- 35 tested with a genetically modified yeast or fungus in which modification results in the

- overexpression or underexpression of at least one of the nucleic acids or the polypeptides of the invention, which overexpression or underexpression of said nucleic acid or polypeptide prevents, delays or sensitizes for apoptosis of said genetically modified yeast or fungus, in addition to contacting wild type cells with said compound, (b) monitoring the growth and/or death rate and/or activity of said genetically modified yeast or fungi cells compared to said wild type cells wherein differential growth or activity of said genetically modified yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway, (c) alternatively monitoring the growth and/or death rate and/or activity of said genetically modified cells compared to genetically modified cells which were not contacted with the compound to be tested, wherein differential growth or activity of said genetically modified yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway, (d) alternatively monitoring changes in morphologic and/or functional properties of components in said genetically modified cells caused by the addition of the compound to be tested, and, (e) optionally identifying the compound.
- 15 The invention also relates to a method of identifying compounds which selectively modulate expression of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi which method comprises (a) contacting host cells transformed, transfected or infected with an expression vector comprising a promoter sequence of a nucleic acid molecule of the invention joined in frame with a reporter gene and (b) monitoring increased or decreased expression of said reporter gene caused by the addition of the compound being tested. This enables to analyse the influence of the compound onto all/most aspects of transcriptional activation. Alternatively additional tests can routinely be performed to test the influence of the compound onto mRNA stability, translation and protein stability. All these aspects influence the concentration of corresponding proteins and consequently influence the effect of these on the metabolism of the cell.
- 25 The invention further relates to a method of identifying compounds or polypeptides which bind to or modulate the properties of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi, which method comprises (a) contacting a compound or polypeptide to be tested with at least one of the polypeptides of the invention, (b) detecting the complex formed between the compound or polypeptide to be tested and said polypeptide, (c) alternatively, examining the diminution/increase of complex formation between said polypeptide and a receptor/binding partner, caused by the addition of the compound or polypeptide being tested, (c) alternatively, examining the alteration in the functional activity of the polypeptide, caused by the addition of the compound or polypeptide being tested, and (d) optionally identifying the compound or polypeptide.

The invention also relates to a method for identifying compounds interacting with a polypeptide involved in a pathway eventually leading to programmed cell death of yeast and fungi comprising the steps of (a) providing a two-hybrid screening system wherein a polypeptide of the invention and a protein interacting with said polypeptide or an interacting polypeptide obtainable by a method as described above, are expressed, (b) interacting said compound with the complex formed by the expressed proteins as defined in a), (c) detecting a second complex, wherein the presence of said second complex identifies a compound which specifically binds to one of said polypeptide or to said second complex, and optionally (d) identifying the compound. According to another embodiment the invention relates to a method for identifying compounds which selectively modulate expression of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi which method comprises: (a) contacting host cells transformed, transfected or infected with an expression vector comprising a promoter sequence of a nucleic acid of the invention joined in frame with a reporter gene, (b) monitoring increased or decreased expression of said reporter gene caused by the addition of the compound being tested, and, optionally (c) identifying the compound.

Yet another embodiment of the invention is a method for identifying polypeptides involved in a pathway eventually leading to programmed cell death comprising the steps of: (a) providing a two hybrid system wherein a polypeptide encoded by a nucleic acid or by any of the vectors of the invention as a bait and a *S. cerevisiae* cDNA library as a prey are used, (b) detecting an interaction between said polypeptide and a *S. cerevisiae* polypeptide encoded by said cDNA library, and, optionally (c) identifying said *S. cerevisiae* polypeptide.

The term "cells" as used in the above methods relates to any type of cells such as, but not limited to bacterial, yeast, fungal, plant or human cells.

Compounds found using this approach may additionally be tested on their efficiency in killing or inhibiting the growth of wild type cells in order to confirm their utility as medicament for treating wild type pathogenic strains/tumor cells.

According to the invention, the term "mutation" includes point mutations, deletions, insertions, duplications or any modification in the nucleic acid encoding said polypeptide, or at a different location in the genome of said cells, influencing the expression of said nucleic acid or polypeptide. In case point mutations occur, the number of nucleotides will be identical compared to the original sequence; only a change in nucleotide sequence can be observed. This stands in contrast with the other listed mutations where the number of the nucleotides will be different from the number observed in the wild type sequence and consequently will also reflect in a change of the nucleotide sequence.

Changes in morphologic and/or functional properties of cell components which can be monitored include for example morphological and molecular changes such as abnormal cell morphology, nuclear fragmentation, DNA breakage or changes in the expression of certain enzymes such as caspases, as well as monitoring changes in membrane potential or activity of mitochondria and release of cytochrome c from mitochondria. All these changes can be monitored on the whole cell which is contacted to the compound to be tested.

Detection of the complex formation can be performed using several approaches. First, binding of a compound onto a polypeptide can be studied using classical binding tests: one of the binding partners, compound or polypeptide is labeled and interaction of both is measured. Most of these tests comprise following steps: incubating both binding partners in conditions where binding is allowed, separation of free label from bound label present in the complex formed between both partners, and measuring the number of labeled complexes formed. Separation of free and bound label can be performed via filtration, centrifugation or other means as known by the person skilled in the art. Other techniques allow visualisation of complex formation without the need of such a separating step. For example, test systems using SPA (scintillation proximity assay) beads are based on the principle that radioactive ^3H can only be measured when present in scintillation fluid. SPA beads contain scintillation fluid and can be coated with one of the binding partners. When this bead is approached and binds the other binding partner which is radioactively labeled, a signal will be detected allowing the complex to be visualised. Binding of the radioactive compound onto the scintillation bead is needed in order to result in a detectable signal; non-bound radioactive partners that stay free into the solution will not result in a detectable signal.

The protein or peptide fragments according to the invention employed in such a method may be for example in solution or coated on suspended beads as described above. Alternatively, these can be affixed to a solid support, borne on a cell or phage surface or located intracellularly.

When protein or peptide fragments are coated on solid supports, they can be tested for their binding affinity for large numbers of compounds. These can be used in different kinds of high throughput screenings in order to identify compounds having suitable binding affinity to the polypeptides according to the invention. Platform technologies or technologies based on SPR (see below) can be applied.

One may measure for example, the formation of complexes between the proteins of the invention and the compound being tested. Alternatively, one may examine the diminution or increase of complex formation between the protein according to the invention and a receptor/binding partner caused by the compound being tested.

Proteins which interact with the polypeptide of the invention may be identified by investigating protein-protein interactions using the two-hybrid vector system first proposed by Chien *et al.* (1991).

This technique is based on functional reconstitution *in vivo* of a transcription factor which
5 activates a reporter gene. More particularly the technique comprises providing an appropriate host cell with a DNA construct comprising a reporter gene under the control of a promoter regulated by a transcription factor having a DNA binding domain and an activating domain, expressing in the host cell a first hybrid DNA sequence encoding a first fusion of a fragment or
10 all of a nucleic acid sequence according to the invention and either said DNA binding domain or said activating domain of the transcription factor, expressing in the host at least one second hybrid DNA sequence, such as a library or the like, encoding putative binding proteins to be investigated together with the DNA binding or activating domain of the transcription factor which is not incorporated in the first fusion; detecting any binding of the proteins to be investigated with a protein according to the invention by detecting for the presence of any reporter gene
15 product in the host cell; optionally isolating second hybrid DNA sequences encoding the binding protein.

An example of such a technique utilizes the GAL4 protein in yeast. Gal4 is a transcriptional activator of galactose metabolism in yeast and has a separate domain for binding to activators
20 upstream of the galactose metabolising genes as well as a protein-binding domain. Nucleotide vectors may be constructed, one of which comprises the nucleotide residues encoding the DNA binding domain of Gal4. These binding domain residues may be fused to a known protein encoding sequence, such as for example the nucleic acids according to the invention. The other vector comprises the residues encoding the protein-binding domain of Gal4. These residues are fused to residues encoding a test protein. Any interaction between polypeptides encoded by the
25 nucleic acid according to the invention and the protein to be tested leads to transcriptional activation of a reporter molecule in a GAL4 transcription deficient yeast cell into which the vectors have been transformed. Preferably, a reporter molecule such as β -galactosidase is activated upon restoration of transcription of the yeast galactose metabolism genes. Alternatively, other reporter proteins can be used such as EGFP (enhanced green fluorescent protein), or hEGFP. This latter has a decreased lifetime enabling the system to screen for
30 compounds improving the interaction of studied binding partners.

The two-hybrid approach was first developed for yeast, and is an ideal screening system when looking for compounds active in killing yeast or fungi. Indeed, proteins expressed in this system will most probably carry the correct modifications as found in the pathogenic yeast strains. In
35 addition, compounds active in this test system allow to screen and select compounds which are

able to enter the cell, this selection is not possible when using *in vitro* test systems. When compounds are needed to target mammalian cells, modification of the studied proteins can be different, changing the structure of corresponding proteins. Moreover working with yeast might block certain compounds to enter the cell, which are normally able to traverse the mammalian cell membrane. Consequently, working with mammalian two-hybrid system for this purpose will give already an immediate selection of the compounds that may enter mammalian cells.

Alternative *in vitro* methods can be used to investigate protein - protein interactions. Protein interaction analysis *in vitro* can shed light on their role in the intact cell by providing valuable information on specificity, affinity, and structure-function relation ship. Significant progress in this respect has become with the advent, in the last few years, of commercially available biosensor technology. This allows to study macromolecular interactions in real-time, providing a wealth of high-quality data that can be used for kinetic analysis, affinity measurements, competition studies, etc. A major advantage of biosensor analysis is that there is no requirement for labeling one of the interacting components and then separating bound from free molecules- a fact that simplifies experimental procedures and provides more accurate measurements. The principle of surface plasmon resonance (SPR) is based on the detection of a change of the refractive index of the medium when a compound or protein binds to an immobilised partner molecule. For the SPR technology, one needs to load one of the interacting partners to the chip surface, followed by the superfusion of the second binding partner or more molecules. The second partner can be available as purified product, but alternatively a complex suspension containing this partner can also be used. Interaction of two or more compounds can be analysed, alternatively, compounds can be identified interfering or increasing this binding affinity towards each other.

SPR is not restricted to protein-protein interactions; any macromolecule with a suitable size will change the refractive index of the medium in contact with the biosensor surface and therefore give a signal. Studies have been done with protein-DNA interactions, as well as protein-lipid interactions. Moreover intact viruses, and even cells, can also be injected over the biosensor surface, in order to analyse their binding to receptors, lectins, and so on.

Alternatively, NMR is also an excellent tool for a detailed study of protein-protein or DNA-protein interactions. Isotope edited or isotope filtered experiments whereby one compound is isotopically labeled with ^{15}N or ^{13}C are an ideal way to study these complexes. This method does not allow high throughput analysis of compounds interfering or enhancing molecular interactions. Nevertheless, medium or low throughput systems can be used to confirm results obtained by the high throughput assays or in cases where none of the binding partners are labeled. Other techniques which can be used to study interactions are: overlay, ligand blotting,

band-shift, co-immuno-precipitation, size exclusion chromatography and microcalorimetry (In. "Protein targeting Protocols" Ed. Clegg R.A. Humana Press, Totowa, New Jersey).

Compounds modulating pathways leading to apoptosis may change the activity of the polypeptide of the invention. Therefore screening tests may be setup looking for altered protein activity of the polypeptide of the invention. Based on the amino acid sequence a possible function of the polypeptide might be envisaged; activities can be confirmed and corresponding activity test can be started.

Alternatively additional tests can be performed to test the influence of the compound onto protein stability, post-translational modification, precursor processing and protein translocation.

All these aspects influence the concentration and/or activity of corresponding proteins and consequently influence the effect of these onto the metabolism of the cell. Also here, medium or low throughput systems can be used to confirm results obtained by the high throughput assays.

In cases compounds need to be found to target tumor cells, screening assays will have to be used focused on the stimulation of the apoptotic pathway. This invention therefore also relates

to *in vitro* and *in vivo* model systems comprising tumor tissue or cells expressing the polypeptides according to the invention which can be used to screen for therapeutic agents. *In vivo* model systems allow to test for compound efficacy but also the toxicity of these compounds can be tested. The compounds identified using any of the methods described in the invention not only include compounds which exert their effect in promoting cell death of yeast and fungi, but also include compounds which prevent or delay cell death. The latter compounds can be used to prevent or delay apoptosis of endogenic yeast or fungi in humans and other mammals which may be caused by pathogens or toxic environmental components.

According to a preferred aspect of the invention, the yeast or fungi according to any of the methods described, are chosen from *Candida* spp., *Aspergillus* spp., *Microsporum* spp.,

Trichophyton spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis*, spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*, and *Sporothrix schenckii*.

The invention also relates to a compound identified using any of the methods of the invention.

Compounds identifiable or identified using a method according to the invention, may advantageously be used as a medicament. The invention also relates to a method for treating diseases associated with yeast or fungi comprising admixing a compound obtainable by a method of the invention with a suitable pharmaceutically acceptable carrier.

The invention further relates to a method for preparing pharmaceutical composition for treating diseases associated with yeast or fungi comprising admixing a compound as identified above

with a suitable pharmaceutically acceptable carrier. The invention also relates to said pharmaceutical composition.

The compounds or pharmaceutical compositions of the invention can be used for the preparation of a medicament to treat diseases or conditions associated with yeast and fungi infections, more preferably where the yeast or fungus is chosen from *Candida* spp., *Aspergillus* spp., *Microsporum* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botrytis* spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*, and *Sporothrix schenckii*.

10 These compounds may also advantageously be included in a pharmaceutical composition together with a pharmaceutically acceptable carrier, diluent or excipient therefor.

A medicament according to the invention not only relates to fungicidal and fungistatic compounds for treating humans or mammals but also relates to fungicides for treating plants.

According to yet another embodiment, the invention relates to a genetically modified yeast or
15 fungus in which modification results in the overexpression or underexpression of at least one of the nucleic acids or the polypeptides of the invention, which overexpression or underexpression of said nucleic acid or polypeptide prevents, delays or sensitizes for apoptosis of said genetically modified yeast or fungus. These genetically modified organisms may have a positive effect on the endogenic flora of humans and other mammals. The genetically modified yeast or
20 fungi can be included in a pharmaceutical composition or can be used for the preparation of a medicament for prophylactic or therapeutic use.

Also according to the invention is the use of a compound obtainable by a method of the invention, a pharmaceutical composition or a genetically modified organism as described above for the preparation of a medicament for modifying the endogenic flora of humans and other
25 mammals.

According to another embodiment, the invention relates to a genetically modified mammalian cell or non-human organism in which modification results in the overexpression or underexpression of at least one of the nucleic acids of the invention or a human homologue thereof or at least one of the polypeptides of the invention or a human homologue thereof,
30 which overexpression or underexpression of said nucleic acid or polypeptide prevents or delays apoptosis of said genetically modified mammalian cell or in said genetically modified non-human organism.

According to a preferred embodiment, the invention relates to a genetically modified mammalian cell or non-human organism as described above wherein said modification comprises the

expression of an antisense molecule to at least one of the nucleic acids of the invention or an antisense molecule to a mammalian homologue of said nucleic acid.

The invention also relates to a method for identifying compounds for stimulating or inhibiting apoptosis comprising the use of at least one of the nucleic acid sequences of the invention or a
5 human homologue thereof and/or at least one of the polypeptides of the invention or a human homologue thereof and/or a genetically modified mammalian cell or non-human organism as described in the invention.

Some examples of preferred human homologues of yeast and/or *Candida* spp. sequences which can be used in the above methods are represented in SEQ ID NOs 675 to 686.

10 The invention further relates to the compounds identifiable according to the above-described method and their use as a medicament.

The invention further relates to a method for preparing a pharmaceutical composition for treating proliferative disorders or for preventing apoptosis in certain diseases comprising admixing a compound identifiable according to the above-described methods with a suitable
15 pharmaceutically acceptable carrier.

The invention also relates to the use of compounds obtainable by the above described methods for the preparation of a medicament for treating proliferative disorders or for preventing apoptosis in certain disorders.

Furthermore, the present inventors overexpressed the Bax protein in the pathogenic yeast
20 *Candida albicans* and found that this leads to a similar phenotype. However these results could only be received after having constructed a new synthetic *bax* gene which could be adequately expressed in this pathogenic organism.

Therefore, the present invention relates to an isolated nucleic acid representing a synthetic BAX-gene for expression in *Candida* spp. selected from the group of:

- 25 a) a nucleic acid comprising a sequence as represented by SEQ ID NO 1,
b) a nucleic acid comprising a fragment of a sequence of SEQ ID NO 1 and encoding a functional fragment of the sequence represented by SEQ ID NO 2,
c) a nucleic acid comprising a sequence as represented in any of SEQ ID NOs 3 to 10,
d) a nucleic acid which is more than 75 % identical, preferably more than 80%, 85%, 90%
30 or 95% identical, most preferably more than 97% identical to the nucleic acid as represented by SEQ ID NO 1, or to a nucleic acid according to the nucleic acid as defined in b) or c), and
e) a nucleic acid as defined in any one of (a) to (d) interrupted by intervening DNA sequences,

or a nucleic acid representing the complement of any of said nucleic acids as defined in (a) to (d).

The synthetic *BAX* gene shows 73.7% identity with the gene coding for Bax- α . It should be clear that the present invention also relates to nucleic acids wherein other, also frequently used *Candida* spp. codons, are used instead of the choice made for the sequence represented in SEQ ID NO 1. (Table 8)

It should be clear that all nucleic acids according to the invention and which are specifically described above, can be DNA, cDNA, genomic DNA, synthetic DNA, or RNA wherein T is replaced by U.

According to another embodiment of the invention, the nucleic acid sequences according to the invention as defined above may, advantageously, be included in a suitable vector, preferably an expression vector which may be transformed, transfected or infected into a host cell. In such an expression vector the nucleic acid is operably linked to one or more control sequences allowing the expression in host cells, such as a suitable promoter, or the like, to ensure expression of the proteins according to the invention in a suitable prokaryotic or eukaryotic host cell. In this respect, a constitutive or an inducible promoter can be used.

As described in the examples, the invention also relates to nucleic acids and constructs comprising the synthetic *BAX*, or parts thereof, as a fusion with a carrier gene, such as, but not restricted to the yeast *GFP* gene. It is not necessary to include the complete gene of the fusion partner in the expression construct, so the invention relates to various fusion products which can result from the synthetic *BAX* gene and its fusion partner.

The expression vectors comprising the synthetic construct or fusion protein and the host cell defined herein also form part of the present invention. Said host cell can be from bacterial, yeast, fungal, insect, mammal or human origin. An interesting host cell according to the invention is a *Candida* spp. cell.

In another embodiment, the expression vector may further comprise an inducible promoter, and/or further a reporter molecule.

The invention also relates to a vector as described above for inducing programmed cell death in *Candida* spp.

The invention further also relates a genetically modified yeast or fungal cell as described above wherein said modification results in the onset of at least one pathway eventually leading to programmed cell death.

The invention also relates to a genetically modified *Candida* spp. cell wherein said modification results in the onset of at least one pathway eventually leading to programmed cell death

According to a further embodiment, the invention relates to a method for identifying genes in *Candida* spp. which are differentially expressed in a pathway eventually leading to programmed cell death using a synthetic BAX gene, as described above, or a vector comprising said gene as described herein, or a genetically modified yeast or fungal cell as described above.

- 5 In this respect different model systems are envisaged. It has been shown in the present invention that expression of the synthetic BAX gene as a fusion protein more rapidly kills the host cells than when expressed without a fusion partner. Accordingly there will be a difference in which *Candida* spp. genes will be differentially expressed in each system. The invention thus relates to methods for identifying genes in *Candida* spp. which are differentially expressed in a pathway eventually leading to programmed cell death, wherein in said methods the host cells will need a longer or shorter time period for starving. Said time period is dependent on the expression construct or system used.

The invention further relates to a method for obtaining and identifying *Candida* spp. sequences (genes or polypeptides) involved in a pathway eventually leading to programmed cell death comprising the steps of:

- 15 a) providing a two hybrid system wherein a polypeptide encoded by a nucleic acid as described above or a vector as described above as a bait and a *Candida* spp. cDNA library as a prey are expressed,
b) detecting an interaction between said polypeptide and a *Candida* spp. polypeptide encoded by said cDNA library, and,
20 c) identifying said *Candida* spp. polypeptide.

The invention also relates to a method for identifying inhibitors (or inhibitor sequences) of Bax-induced cell death comprising the steps of:

- 25 a) providing a genetically modified organism as described above,
b) expressing a cDNA library in said genetically modified organism, and,
c) identifying a polypeptide or a cDNA which expression has a beneficial effect on the survival and/or growth of said genetically modified organism.

The invention further relates to a method for identifying Bax-resistant yeast or fungi comprising the steps of:

- 30 a) providing (a) genetically modified yeast or fungi as described above,
b) treating said genetically modified yeast or fungi with a mutagen,
c) isolating resistant yeast or fungal cells, and,
d) optionally identifying and/or characterizing mutated genes in said resistant yeast or fungal cells.

The invention further relates to any of the methods described above wherein said genetically modified organism is a *Candida* spp.

The invention also relates to an isolated *Candida* spp. nucleic acid identifiable by any of the methods described above.

5

The invention, now being generally described, may be more clearly understood by reference to the following examples, which are included merely for purposes of illustration of certain aspects and embodiments of the present invention and are not intended to limit the invention. The contents of all references referred to in this text are hereby incorporated by reference.

FIGURE AND TABLE LEGENDS

Figure 1. *Saccharomyces cerevisiae* sequences based on information obtained from the Saccharomyces Genome Database (SGD) (SEQ ID NOs 17 to 386 and SEQ ID

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Figure 2. *Candida albicans* (SEQ ID NOs 397 to 674, 687, 688 and 717 to 732) and human homologues (SEQ ID NOs 675 to 686).

Human homologues were confirmed via forward and reverse BLAST using BLOSUM62 as a scoring matrix.

10

YGL080W (SEQ ID NO 161) codes for a yeast protein with an unknown cellular role and an unknown biochemical function. The human homologue (330 bp (SEQ ID NO 675), 109 aa (SEQ ID NO 676)) LOC51660/g7706369 has no reported cellular role or biochemical function.

15

YGR243W (SEQ ID NO 189) codes for a yeast protein with an unknown cellular role and an unknown biochemical function. The human homologue (384 bp (SEQ ID NO 677), 127 aa (SEQ ID NO 678)) DKFZP564B167/g5817257 has no reported cellular role or biochemical function.

20

YGR183C (QCR9) (Table 3) codes for a yeast protein with a known cellular role and a known biochemical function. QCR9 codes for subunit 9 of ubiquinol cytochrome-c reductase (7.3 kDa protein) which is a component of the ubiquinol cytochrome-c reductase complex. Cellular role: energy generation. Biochemical function: oxidoreductase and active transporter. The human homologue (132aa (SEQ ID NO 679), 399bp (SEQ ID NO 680)) AF161536 was predicted to have an analogous cellular role and biochemical function.

25

YBR009C (SEQ ID NO 37), **YGR209C** (SEQ ID NO 187) and **YPR028W** (SEQ ID NO 393) correspond to known yeast ORFs. Their human homologues have a reported cellular role or biochemical function.

Figure 3. Yeast genome macroarray containing a total of 6144 gene ORFs spotted on 2 nylon membrane filters (I and II). Each filter contains 2 fields and each field is divided into

30

8 grids, organised in 24 rows and 8 columns. The spots represent the genome wide expression profile without (Minus BAX) and with (Plus BAX) induction of Bax expression for 30 min, 1 hour, 2 hours, 3 hours and 6 hours.

Figure 4 Yeast cells with a disrupted **YGR183C** gene are fully resistant to Bax-induced cell death. Resistance is observed in both the low-copy (A) and the high-copy (B) Bax

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expression system. Clonogenic survival was determined by recovering cells at various times from galactose-containing medium and plating of 1000 cells on glucose-based semisolid medium. Data are representative of three experiments (mean \pm SD, n=3). SD bars are obscured by symbols.

- 5 **Figure 5.** Scheme for the synthesis of the synthetic *BAX* gene using *C. albicans* optimal codons.
- Figure 6.** DNA (SEQ ID NO 1) and protein (SEQ ID NO 2) sequence of the synthetic *C. albicans BAX* gene.
- Figure 7.** Representation of the expression constructs of the synthetic Ca*BAX* gene (A) and the yEGFP-synth Ca*BAX* fusion (B).
- 10 **Figure 8.** Growth of the *Candida Albicans* transformants: the individual transformants of pGAL1P:synthCa*BAX* and pGAL1P:GFP-synthCa*BAX* were streaked onto plates containing either 2% glucose or 2% galactose as sole carbon source. Growth was monitored 4 days later.
- 15 **Figure 9.** Growth kinetics of GAL1P:synthCa*BAX* (A) and GAL1P:GFP-synthCa*BAX* (B) on galactose containing minimal medium.
- Figure 10.** Immunoblot analysis of two independent transformants of GAL1P:synthCa*BAX* after 15 hours Bax induction on minimal galactose containing media. The arrow at 20kDa indicates the position of the Bax protein. The band seen at 50kDa probably represents a cell wall mannan. Not all of the contamination of the polyclonal Bax antibody could be removed by the threatment with *S. cerevisiae* mannan.
- 20 **Figure 11.** Immunoblot analysis of the GAL1P:GFP-synthCa*BAX* strain on galactose containing minimal medium. The band appearing at 45kDa represents the Gfp-Bax fusion protein, while the band at 20kDa represents the Gfp protein alone.
- 25 **Figure 12.** FACS analysis of two independent GAL1P:GFP-synthCa*BAX* transformants grown on galactose containing media: the light grey peak indicates the autofluorescence of the wt strain, the GFP-fluorescence peak is not shaded.
- Figure 13.** Viability test synthCa*BAX* (A) and GFP-synthCa*BAX* transformants (B): Cells were pregrown in minimal dextrose medium and then switched to fresh minimal medium containing galactose. At the time points indicated, samples were taken and equal cell amounts were spread on minimal dextrose plates. The appearing colonies represented the viable fraction of the total pool.
- 30 **Table 1.** Oligonucleotides used for construction of the synthetic Ca*BAXx* gene: start and stop codon are in bold, restriction sites used for cloning are in bold and italic.
- 35

Tables 2- 6. Genes modulated by Bax expression in *S. cerevisiae*.

This list includes the genes for which mRNA levels changed significantly after a 30 min (Table 2), 1 hour (Table 3), 2 hours (Table 4), 3 hours (Table 5) or 6 hours (Table 6) induction of Bax protein expression. The Qt values were calculated using the Pathways™ software (Research Genetics).

Table 7. Genes modulated by *Bax* expression in *S. cerevisiae*. This list includes all the genes for which mRNA levels changed significantly after induction of Bax protein expression. The Qt values were calculated using the Pathways software (Research Genetics). Positive values correspond with upregulated genes. Negative values correspond with downregulated genes. (Comparable with ↑ and ↓ respectively in Tables 2-6).

Table 8. Codon usage for the synthetic *BAX* gene.

Table 9. Regulation of 23 selected "Bax-specific" functions.

EXAMPLES

Example 1. Differential gene expression analysis upon Bax-induced cell death

Materials and media

- 5 Bacterial strain *Escherichia coli* MC1061 (Casadaban and Cohen, 1980) was used for the construction and the amplification of plasmids. Yeast strains were grown under normal conditions on standard media (Sherman *et al.*, 1979). The *Saccharomyces cerevisiae* strain INVSc1 (Invitrogen®, San Diego, CA, USA) was transformed by means of the lithium acetate method (Schieff and Gietz, 1989) with YipUTyL or YipUTyLMuBax, after linearisation in the Ty
10 δ element (Zhu, 1986).

Cloning of mouse BAX cDNA

- Mouse *bax* cDNA, encoding the mouse Bax- α protein, was cloned by Pfu DNA polymerase (Stratagene®, La Jolla, CA, USA) chain reaction amplification (PCR) from an EL4/13.18
15 thymoma cDNA library (BCCM™/LMBP-LIB15) by making use of the primers:

5'-ATGGACGGGTCCGGGAGCAG-3' (SEQ ID NO 689) and

5'-TCAGCCCATCTTCTCCAGATGGTGAG-3' (SEQ ID NO 690).

- The resulting PCR product was cloned in a *HincII*-opened pUC19 according to standard procedures (Sambrook J. *et al.*, 1989).
20

Plasmid constructions

- The 2 μ ori and the *URA3* marker gene were removed from pUT332 (Gatignol *et al.*, 1990) by successive digestions with *ClaI* and *BglII*. A *BamHI-HindIII GALI* promoter fragment was ligated into the *BglII-HindIII*-opened plasmid. A *XbaI-FspI FLP* terminator fragment was inserted into
25 this *XbaI-HindIII*(blunted)-opened plasmid so that the plasmid YipUT was obtained. Insertion of a blunted *EcoRI-BsaAI* Ty δ element in the *KpnI-AatII*-opened and blunted YipUT resulted in the plasmid YipUTy. Subsequent insertion of the *LEU2* marker gene, as a blunted *BsaAI-BsrGI* fragment, in the *BamHI*-opened and blunted YipUTy resulted in the plasmid YipUTyL.
Mouse *bax* cDNA was excised from pUC19 by digestion with *XbaI* and *HindIII* and subcloned
30 into the *XbaI-HindIII*-opened plasmid YipUTyL, obtaining the final expression plasmid YipUTyLMuBax.

The plasmid YipUTyLMuBax has been deposited in the BCCM™/LMBP culture collection as pSCTyGALmBax with accession number 3871 under restricted use.

GeneFilters

The Yeast GeneFilters™ were purchased from Research Genetics Inc. (Huntsville, AL, USA).

The Yeast GeneFilters™ are hybridization ready nylon membranes containing a total of 6144 gene ORFs (Open Reading Frames) individually amplified by PCR and spotted on 2 nylon
5 membrane filters (Filter I and II). The filters are cut in the upper right corner and the DNA is on the labeled side of the filter.

Filter I contains 3072 ORFs organized into two fields (fields 1 and 2). Each field contains 1536 ORFs divided into 8 grids (A, B, C, D, E, F, G and H). The grids are organized in 24 rows and 8
columns.

10 Filter II contains 3072 ORFs organized in two fields (field 3 and 4). Fields 3 and 4 are organized in the same way as fields 1 and 2.

The Yeast ORF target

The yeast filters consist of over 6144 PCR products corresponding to 6144 yeast ORFs derived
15 from the SGD. The PCR reactions used ORF specific primer pairs designed to amplify the entire open reading frame. The primers were generated from unique sequences containing the start codon ATG and termination codon (kindly provided by M. Cherry at Stanford Genome Center). Thus the PCR product contains the complete open reading frame including the start and stop
codons. These products were purified and resuspended at 50 nanograms per microliter in a
20 colored solution to allow the printing to be monitored. A robotic device was used to spot approximately 1/10 of a microliter of the denatured PCR product solution on a positively charged nylon membrane. The DNA was then UV cross-linked to the membrane.

Results**25 Induction of Bax-expression in yeast cells**

A preculture of yeast strain INVSc1 containing YlpUTyLMuBax, wherein 5 Bax cassettes under the control of the *GAL1* promoter are integrated in the genome near Ty δ elements, was grown overnight in minimal glucose-containing medium in parallel with the yeast strain INVSc1 containing YlpUTyL as a control. The precultures were diluted in 100-ml minimal glucose-
30 containing medium and grown until an OD₆₀₀ of 1 was reached. Subsequently, the yeast cells were transferred into 100-ml galactose-containing medium and incubated for an additional period of 30 min, 1 hour, 2 hours, 3 hours or 6 hours.

RNA isolation

Total RNA was isolated using RNeasyTM Reagent (GenHunter Corporation Nashville, TN, USA) according to the GenHunter protocol. $1.5 \cdot 10^8$ cells were concentrated in a microcentrifuge tube and 1 ml RNeasyTM Reagent was added together with 1 g of glass pearls. The yeast cells
5 were broken by thorough mixing during five 2-minutes periods, and placed on ice in-between to avoid RNA degradation. Chloroform (150 μ l) was added to the lysate and centrifuged for 10 min at 4°C and at 15000 rpm. The supernatant was transferred to a new tube and the RNA was precipitated with an equal volume of isopropanol. After 10 min incubation on ice, the RNA was pelleted by centrifugation and the pellet was washed with 70% ice-cold ethanol. The dried RNA
10 pellet was resuspended in 50 μ l RNase free dH₂O.

First strand cDNA synthesis in the presence of α -³²P dCTP

Probes with high specific activity were prepared by first strand cDNA synthesis using total RNA isolated from INVSc1 YlpUTyLMuBax or INVSc1 YlpUTyL yeast cells and incorporation of α -³²P dCTP as follows: 2 μ l (1 μ g/ml) of Oligo dT was added to 20 μ g of total RNA in a maximal
15 volume of 8 μ l RNase-free dH₂O and incubated at 70°C for 10 min. After cooling down on ice for 1 min, the following components were added:

6 μ l 5x concentrated First Strand Buffer (GIBCO-BRL, Paisley, UK)
1 μ l 0,1 M DTT
20 1 μ l RNase Block (40 units/ μ l) (Stratagene)
1,5 μ l 20 mM dXTP-solution (X = A, G and T) (Amersham Pharmacia biotech Uppsala, Sweden)
1,5 μ l SuperScriptTM Reverse Transcriptase (200 units/ μ l) (GIBCO-BRL)
10 μ l α -³²P dCTP (10mCi/ml, 3000 Ci/mmol) (Amersham Pharmacia biotech Uppsala,
25 Sweden),

and incubated for 2 h at 37°C during which first strand cDNA synthesis took place.

Unincorporated label was separated from the probe on a Sephadex G-50 column (Amersham Pharmacia biotech Uppsala, Sweden). The radioactivity incorporated in the probe was measured by liquid scintillation. The specific activity of the probes was $5 \cdot 10^8$ cpm/ μ g for both
30 the INVSc1YlpUTyL and the INVSc1 YlpUTyLMuBax probes.

Additionally, the length of first strand cDNA probes was controlled on an alkaline 2% agarose gel using standard electrophoresis techniques, and resulted in the detection, via stimulated phosphorescence autoradiography, of the bulk of the fragments around 500 bp.

Hybridisation with the *S. cerevisiae* Yeast GeneFilters™ and signal detection

The Yeast GeneFilters™ were successively hybridised with the α -³²P dCTP labelled cDNA probes using the MicroHyb™ solution provided by the manufacturer (Research Genetics Inc., Huntsville, AL, USA). This solution was applied as well in the prehybridisation step as during
5 hybridisation. The MicroHyb™ solution contains formamide to allow hybridisation to occur at lower temperatures.

The hybridisation experiment was performed essentially as follows: during prehybridisation, the Yeast GeneFilters™ were placed in a hybridisation flask (35x250 mm) filled with 5 ml MicroHyb™ solution (42°C) containing 5 μ l polydA (1 μ g/ml) and incubated for 24 hours at 42°C
10 whilst rotating (10 rpm). After disposal of the prehybridisation solution, the denatured (3 min at 100°C) cDNA was added in 5 ml prewarmed MicroHyb solution and again incubated overnight at 42°C whilst rotating. Following two wash steps of 20 min in wash buffer (2x SSC, 1% SDS) at 50°C, a third wash step was performed in a second wash buffer (0.5x SSC, 1% SDS) for an additional 15 min at room temperature. The Yeast GeneFilters™ were placed in a
15 PhosphorImager™ cassette (Molecular Dynamics, Sunnyvale, CA, USA) with storage phosphor screen. After 4 days of development the screen was scanned at a resolution of 50 μ m using the (BioRad, Richmond, CA, USA) Personal FX. The results of these can be seen in Figure 3.

Example 2. Quantification of Hybridisation Signals

20 Quantification of the hybridisation signals was done using the Pathways™ software (Research Genetics, Huntsville, AL, USA) and these signals were normalised against all data points. Comparison of these normalised data revealed differentially expressed candidate genes. Visual inspection of the hybridisation spots confirmed their selection. The genes as well as the factors with which they are up- or down- regulated are listed in the Tables 2 to 6 for each individual time
25 point. An overview of the up and down regulated genes modulated in function of induction of Bax expression for several time points is shown in Table 7. The sequences of these genes and amino acid sequences that they encode are shown in Figure 1.

Example 3. Comparative gene expression analysis upon Bax-induced cell death and H₂O₂-induced cell death***The oxidative H₂O₂-challenge***

A preculture of yeast strain INVSc1 containing YIpUTyL was grown overnight in minimal glucose-containing medium. The preculture was diluted in 100-ml minimal glucose-containing medium and grown until an OD₆₀₀ of 1 was reached. Subsequently, the yeast cells were
35 transferred into 100-ml galactose-containing medium supplemented with 0.1 mM H₂O₂, and

incubated for an additional period of 1 hour. This oxidative challenge resulted in the same final toxicity as a 1-hour induction of Bax expression in the same growth conditions.

First strand cDNA synthesis in the presence of α -³²P dCTP

- 5 RNA was isolated as mentioned in Example 1. Probes with high specific activity were prepared (detailed in Example 1) by first strand cDNA synthesis using total RNA isolated from INVSc1 YlpUTyLMuBax or INVSc1 YlpUTyL (growth conditions as described in Example 1) or oxidatively stressed INVSc1 YlpUTyL yeast cells.
The specific activity of all probes was $5 \cdot 10^8$ cpm/ μ g.

10

Quantification of Hybridisation Signals

- Hybridisation and signal detection as described in Example 1. Conversion of the digital images to a 16 bit TIFF format using the Quantity One program (BioRad, Hercules, CA, USA) preserved image data and was necessary for file import into the Pathways® software (Research Genetics,
15 Huntsville, AL, USA). Pathways® was used for the quantification of hybridisation signals and these signals were normalised against all data points.

Identification of Bax-responsive genes

- Pairwise comparisons of the normalised data obtained from INVSc1 YlpUTyLMuBax (B) and
20 INVSc1 YlpUTyL (C) revealed differentially expressed genes. To determine the -fold induction or repression, the normalised signal intensity after Bax induction (B) was divided by that before the shock (C). Visual inspection of the hybridisation spots confirmed their selection (*replacement*).

25 ***Identification of Bax-specific genes within the Bax-responsive pool***

- Pairwise comparisons of the normalised data obtained from INVSc1 YlpUTyLMuBax (B) and INVSc1 YlpUTyL (C) at the 1-hour time point revealed differentially expressed genes. Linear ratios (B vs C) were estimated significant when changes were at least two-fold and the normalised signal intensity of one spot was at least tenfold above the average background
30 value. The normalised data of the Bax-responsive genes were compared with data obtained from the H₂O₂-stressed INVSc1 YlpUTyL (H). A Bax-responsive (up-regulated/down-regulated) gene was considered to be Bax-specific when the normalised signal intensity after Bax induction was at least twice as high/low as the corresponding intensity after oxidative stress. Visual inspection of the hybridisation spots confirmed their selection. An overview of the Bax-

specific genes for the 1-hour time point is shown in Table 9. The sequences of these genes and amino acid sequences that they encode are shown in Figure 2.

Example 4. Search for homologues in *Candida albicans* and human

- 5 Sequence similarity searches against public and commercial sequence databases were performed with the BLAST software package (Altschul *et al.*, 1990) version 2. Both the original nucleotide sequence and the six-frame conceptual translations were used as query sequences. The used public databases were the EMBL nucleotide sequence database (Stoesser *et al.*, 1998), the SWISS-PROT protein sequence database and its supplement TrEMBL (Bairoch and
- 10 Apweiler, 1998), and the ALCES *Candida albicans* sequence database (Stanford University, University of Minnesota). The commercial sequence database used was the PathoSeq™ microbial genomic database (Incyte Pharmaceuticals Inc., Palo Alto, CA, USA).
- Sequence similarity searches were performed using the BLAST software package version 2. The identity between 2 sequences was calculated as percentage identical residues, the
- 15 similarity percentage between two sequences was calculated using BLOSUM62 as a scoring matrix.
- The sequences of homologues *Candida* spp. and human genes and the corresponding amino acid sequences are shown in Figure 2.

20 **Example 5. Screening for compounds modulating expression of polypeptides involved in induction of cell death of *C. albicans***

- The method proposed is based on observations (Sandbaken *et al.*, 1990; Hinnebusch and Liebman 1991; Ribogene PCT WO 95/11969, 1995) suggesting that underexpression or overexpression of any component of a process (e.g. translation) could lead to altered sensitivity
- 25 to an inhibitor of a relevant step in that process. Such an inhibitor should be more potent against a cell limited by a deficiency in the macromolecule catalyzing that step and/or less potent macromolecule, as compared to the wild type (WT) cell.
- Mutant yeast strains, for example, have shown that some steps of translation are sensitive to the stoichiometry of macromolecules involved. (Sandbaken *et al.*, 1990). Such strains are more
- 30 sensitive to compounds which specifically perturb translation (by acting on a component that participates in translation) but are equally sensitive to compounds with other mechanisms of action.
- This method thus not only provides a means to identify whether a test compound perturbs a certain process but also an indication of the site at which it exerts its effect. The component

which is present in altered form or amount in a cell whose growth is affected by a test compound is potentially the site of action of the test compound.

The assay to be set up involves measurement of growth and/or death rate of an isogenic strain which has been modified only in a certain specific allele, relative to a wild type (WT) *Candida albicans* strain, in the presence of R-compounds. Strains can be ones in which the expression of a specific protein is impaired upon induction of anti-sense or strains which carry disruptions in an essential gene. An *in silico* approach to find novel genes in *Candida albicans* will be performed. A number of essential genes identified in this way will be disrupted (in one allele) and the resulting strains can be used for comparative growth and/or death rate screening.

Example 6. Assay for High Throughput screening for drugs

35 µl minimal medium (S medium + 2% galactose + 2% maltose) is transferred in a transparent flat-bottomed 96 well plate (MW96) using an automated pipetting system (Multidrop, Labsystems, Helsinki, Finland). A 96-channel pipettor transfers 2.5 µl of R-compound at 10^{-3} M in DMSO from a stock plate into the assay plate.

The selected *Candida albicans* strains (mutant and parent (CAI-4) strain) are stored as glycerol stocks (15%) at -70°C . The strains are streaked out on selective plates (SD medium) and incubated for two days at 30°C . For the parent strain, CAI-4, the medium is always supplemented with 20 µg/ml uridine. A single colony is scooped up and resuspended in 1 ml minimal medium (S medium + 2% galactose + 2% maltose). Cells are incubated at 30°C for 8 hours while shaking at 250 rpm. A 10 ml culture is inoculated at 250,000 cells/ml. Cultures are incubated at 30°C for 24 hours while shaking at 250 rpm. Cells are counted in Coulter counter and the final culture (S medium + 2% galactose + 2% maltose) is inoculated at 20,000 to 50,000 cells/ml. Cultures are grown at 30°C while shaking at 250 rpm until a final OD_{600} of 0.24 (± 0.04) is reached.

200 µl of this yeast suspension is added to all wells of MW96 plates containing R-compounds in a 450 µl total volume. MW96 plates are incubated (static) at 30°C for 48 hours.

Optical densities are measured after 48 hours.

Test growth is expressed as a percentage of positive control growth for both mutant (x) and wild type (y) strains. The ratio (x/y) of these derived variables is calculated.

Example 7. Yeast cell viability assay upon induction of Bax expression

Materials and media

Yeast strains were grown under normal conditions on standard media (Sherman *et al.*, 1979). The *Saccharomyces cerevisiae* BY4742 wild type strain and BY4742 with the YGR183C gene disruption (EUROSCARF collection) were transformed by means of the lithium acetate method (Schiestl and Gietz, 1989) with the low-copy centromeric pRS415Bax plasmid or pRS415 as a control, or with the high-copy episomal pRS425Bax plasmid or pRS425 as a control.

Plasmid constructions

The Bax expression cassette, a *BsgI*(blunted)-*SapI*(blunted) fragment excised from YlpUTyLMuBax containing the *GAL1* promoter, the *bax* cDNA and the *FLP* terminator, was ligated into the *EcoI*36II-opened pRS415 (ATCC 87520) and pRS425 (ATCC 77106) plasmids, obtaining the low-copy centromeric pRS415Bax and the high-copy episomal pRS425Bax expression plasmids.

Results

Single colonies of yeast cells transformed with pRS415 or pRS415Bax or pRS425 or pRS425Bax were grown in 10 ml minimal glucose-containing medium with vigorous aeration at 30°C to an optical density of 1 OD₆₀₀. Cells were pelleted by centrifugation and washed two times with sterile dH₂O before resuspending in 10 ml minimal galactose-containing medium. After culturing for various times at 30°C, the total cell density of the cultures was determined, and 1000 cells were spread on minimal glucose-based semisolid medium, followed by incubation at 30°C for 3 days. The number of colonies on plates from the 0 hr cultures was designated as 100% (Fig. 4).

Example 8. Bax Expression In Candida cells

Strains

The *Candida albicans* strain CAI4 (*ura3⁺*) was used to perform the experiments (Fonzi and Irwin 1993).

E. coli transformations were done using the Top10 strain from Invitrogen (San Diego, CA, USA) (F' *morA* Δ (*mirr hsdRMS-morBC*) Δ 80/*lacZ*ΔM15 Δ *lacX74 deoR recA1 araD139* Δ (*ara-leu*)7697 *galU galK rpsL* (Str^R) *endA1 nupG*).

Media

Synthetic cextrose media (SD), containing 2% glucose, 1.34% Yeast Nitrogen Base without amino acids and 0.77g/l CSM-ura (Bio 101, Vista, CA, USA) was used to grow the *Candida albicans* transformants. In case of the wild type (CAI4), the media was supplemented with

50µg/ml uridine. To prepare plates the media was solidified with 2% agar. Expression of the synthetic *BAX* gene was performed using 2% galactose as carbon source.

Construction of the codon-optimised *BAX* gene

- 5 Construction of the synthetic *BAX* gene followed the nomenclature described for *Candida albicans* (Lloyd and Sharp 1992; Brown, *et al.* 1991; <http://alces.med.umn.edu/candida/codons.html>; <http://www.kazusa.or.jp/codon>). To ensure a high expression of the synthetic gene, the subset of 'optimal' codons of highly expressed genes was used to design the synthetic *BAX* gene.
- 10 The synthCa*BAX* gene was constructed in three parts using eight oligonucleotides (Fig. 5). The sequences of the oligonucleotides are given in Table 7. Primer A1 introduced upstream of the ATG codon a *Pst* I site and a *Bgl* II site. The *Pst* I site was used later on for direct cloning into the *Candida albicans* expression vector, while the *Bgl* II site served as a linker for a *yEGFP* fusion. Primer C2 introduced a *Sma* I site, suitable for cloning into the expression vector.
- 15 Fragment A and B were synthesised in two steps: in a first PCR round primer X1 and X2 (X represents A or B, respectively) were used together. The resulting fragment served as a template in a second PCR round together with primers X1 and X3. Fragment C was synthesised in a single PCR round using the primers C1 and C2. Fragment A and B were cloned into the pCR-BluntII-TOPO vector (Stratagene), while fragment C was cloned into the pCR2.1-TOPO vector (Stratagene). All three fragments were sequenced to ensure that no mutation was
- 20 introduced by the PCR.
- Subsequently, fragment A was digested with *Pst* I and *Taq* I, fragment B with *Taq* I and *Bam* HI and fragment C with *Bam* HI and *Sma* I. The three products were cloned in a quadruple ligation into pUC21 digested with *Pst* I and *Sma* I resulting in the plasmid pUC21:synthCandidaBAX.
- 25 The sequence of the synthetic *BAX* gene is shown in Figure 6.

Construction of synthetic *BAX*- and GFP-synthetic *BAX* expression plasmids

- A *Pst* I-*Sma* I fragment containing the ORF of the synthetic *BAX* gene was cloned into the *Pst* I-*Sma* I digested vector pGAL1ACT1LUC (W. Martinet, EP application nr 99204557.5) resulting in
- 30 the expression construct pGAL1P:synthCa*BAX* (Fig. 7A). To facilitate recognition of the AUG codon during formation of initiation complexes a purine base (A) was introduced at position -3 from the AUG codon (Kozak 1981) using the Quick change site directed mutagenesis kit from Stratagene.
- The yeast enhanced GFP gene *yEGFP*, (Cormack *et al.* 1997) was amplified by PCR using
- 35 primer 5'-AACTGCAGATGTCTAAAGGTGAAGAATTATTC-3' (SEQ ID NO 11) as upstream primer and primer 5'-GGAAGATCTTCCTTTGTACAATTCATCC ATACC-3' (SEQ ID NO 12) as

downstream primer. The sense primer introduced a *Pst* I site (shown in bold and italic), while the anti-sense primer contained a *Bgl* II linker (shown in bold and italic) for fusion with the synthetic *BAX* gene. After cloning of the *yEGFP* gene into the pCR2.1-TOPO vector (Stratagene), the gene was sequenced to ensure that no mutation was introduced by PCR.

- 5 The *yEGFP*-synth *Candida BAX* fusion was created by cloning a *Pst*I-*Bgl*II *yEGFP* fragment together with a *Bgl* II-*Sma* I synthetic *Candida BAX* fragment into the *Pst* I-*Stu* I digested expression vector pGAL1ACT1LUC. The obtained pGAL1P:*yEGFP*-synthCa*BAX* fusion construct (Fig.7B) was sequenced to ensure that no frameshift had occurred.

10 **Creation of the synthetic *BAX* expression strains**

- Transformation of the expression plasmids was performed using a modified procedure (Logghe, unpublished) of the spheroblasting protocol (Herreros *et al.* 1992). The plasmids were linearised with *Bpu*1102 I to allow directed integration into the genome at the GAL1 promoter site. Correct integration was analysed by Southern blotting. Therefore genomic DNA from different
- 15 transformants was prepared using the Nucleon[®] extraction and purification kit (Amersham Pharmacia Biotech) and digested with *Xba* I. The *BAX* probe used in the Southern blot was prepared by PCR. The PCR was performed using the pGAL1P:synthCa*BAX* plasmid as template, together with the sense primer 5'-ATGGATGGTTCTGGTGAAC-3' (SEQ ID NO 13) and the anti-sense primer 5'-TTAACCCATTTTTTCCAGATG-3' (SEQ ID NO 14). Standard
- 20 PCR conditions were used. For detection of the *yEGFP* a probe was synthesised by PCR using primer 5'-AGAGATCTCGAGGGATCC-3' (SEQ ID NO 15) as sense primer and primer 5'-GCATTATTTGTACAATTCATCC-3' (SEQ ID NO 16) as anti-sense primer. Southern blot hybridisation and detection were performed using the AlkPhos DIRECT labelling and detection system (Amersham Pharmacia Biotech) following the instructions of the manufacturer.

25

Western blot analysis

- For Western blot analysis cells were pre-grown over night in SD-ura media till late log phase. The cells were harvested by centrifugation, washed twice with water and inoculated in SG-ura to induce *Bax* expression. Induction was performed for 15 hours. Yeast crude extracts were
- 30 prepared as described before (Sambook, Fritsch *et al.* 1989). Detection of the *Bax* protein was performed using a polyclonal rabbit anti-mouse /rat *Bax* antibody (Pharmingen). Due to contamination of this antibody with yeast cell wall mannan antibodies, a very high background occurred. This problem could be avoided by pre-incubation of the antibody with 0.5mg/ml purified yeast mannan (Rossanese *et al.* 1999). Detection of the *Gfp* protein was done using an
- 35 anti-*Gfp* monoclonal antibody (Molecular Probes, Eugene, OR, USA).

Growth curves

For growth curves, yeast cells were grown for 24 h in SD-ura medium (supplemented with uridine for the wild type). These cultures were harvested, washed twice with water and inoculated to an OD₆₀₀ of 0.1 into fresh SD-ura or SG-ura media. Growth was monitored in microtitre plates using the Bioscreen C system (Labsystems).

Viability tests

Cells were pregrown in minimal dextrose medium to an OD₆₀₀ of 1. After washing the cells twice with water they were switched to minimal medium containing galactose as carbon source. At the time points indicated, samples were taken and equal cell amounts were spread on minimal dextrose plates. The appearing colonies represent the viable fraction of the pool.

Results : Conditional expression of the synthetic *BAX* gene in *Candida albicans*

A cDNA encoding the full-length mouse Bax protein was placed under control of the *Candida albicans* GAL1 promoter allowing for conditional expression when cells are grown in galactose containing media. Initial experiments were performed using the wild type mouse *bax* gene. Expression of this gene did not result in any detectable phenotype, no difference in growth compared to the wild type was observed when cells were grown on galactose containing media (data not shown). This could be due to the non-traditional codon strategy adopted by *Candida albicans* and related species. Analysis of the codons used in the mouse *BAX* gene revealed a for *Candida albicans* not optimal codon usage as found for highly expressed genes in this yeast. To ensure a high expression of the *BAX* gene a codon-adapted, synthetic version of the gene was created using the strategy described above. The synthetic *BAX* gene was fused to the yEGFP to allow screening for transformants with a high yEGFP-synthCaBAX expression level using FACS technology. The newly obtained plasmids pGAL1P:synthCaBAX and pGAL1:GFP-synthCaBAX were transformed into the *C. albicans* CAI4 strain. Transformants were selected on uridine-free minimal medium. About 25 transformants of each expression construct were chosen and streaked onto minimal dextrose medium (non-inducing conditions) as well as on minimal galactose medium (inducing conditions). After two days incubation at 30°C all transformants did grow on the glucose containing media. When galactose was used as a sole carbon source, most of the transformants did not grow (Fig. 8). Southern blot analysis of the galactose negative transformants revealed that a copy of the synthCaBAX gene had been integrated into the endogenous copy of the GAL1 promoter. To study differences in growth, the transformants were grown over night in synthetic glucose containing medium. Subsequently, cells were washed with water and switched to fresh medium containing galactose as carbon source. While the wild type strain did grow well on galactose containing media no growth was

observed for the Bax expressing transformants (Fig. 9A and B). Western blot analysis of the synthCaBAX transformants showed accumulation of the Bax protein (15 hours Bax induction, Fig. 10). A similar result was observed when immunoblotting was performed with the GFP-synthCaBAX expressing strains. Here the fusion protein was detected at the expected
5 molecular weight of about 45K under inducing conditions (galactose as carbon source). In addition to the fusion protein a band appeared at the molecular weight of about 20K. This corresponds to the molecular weight of the Gfp protein alone. Addition of a Gfp-expressing strain as a positive control to the western blot did confirm these results. Here the Gfp protein was detected at the same molecular weight as the unexpected band in the GFP-synthCaBAX
10 expressing strain (Fig. 11). This is most probably due to a partly proteolytic degradation of the fusion protein. Analysis of the Gfp-fluorescence using FACS technology showed a high Gfp-fluorescence signal for the transformants expressing the fusion protein (Fig. 12). When cell viability was analysed, different results were obtained for the synthCaBAX strain and the GFP-synthCaBAX strain. The synthCaBAX strain showed quite a rapid decrease in the amount of
15 colony forming units during the first 6 hours of incubation on galactose containing media. Afterwards the process slowed down significantly. This is in contrast to the results obtained for the strain expressing the gfp-synthCabax fusion protein. Here almost all the cells died at a very rapid rate during the first 3 hours of incubation in media containing galactose as sole carbon source. It is possible that the Bax trigger in the synthCabax expressing cells is not strong
20 enough to kill all cells. The cell has enough time to activate a sort of defence mechanism, possibly by proteolytic degradation of the Bax protein. The situation is different for the fusion protein. Gfp is a very stable protein itself. Fusion of the Gfp to another protein could result in a stabilisation of this protein. It would be more resistant to proteolytic degradation. This would explain the situation for the Gfp-Bax fusion. The Gfp-Bax protein is more protected from
25 proteolytic degradation. Like that it is for a longer period present in the cell. The death trigger is herewith stronger, so the cells die faster. The time that the cells have to activate the proteolytic machinery is not sufficient for them to survive.

Table 1:

Oligo	Sequence 5' → 3'
A1	AACTGCAGGAAGATCTTCCATGGATGGTTCCTGGIGAACAATTGGGTTCTGGTGG TCCAACTCTTCTGAACAATCATGAACCGGTGCTTCTTGTTG (SEQ ID NO 3)
A2	TAGAAGCATCTTGTGGTGGTTCCTCAAGGTCAATTCTGGGTTCAACAGCC ATTCTACCAGCTCTATCTTGGATGAACCTTGCAACAAGAACACC (SEQ ID NO 4)
A3	GGAAATCTCGACATCAGCGATCATCTTTGGCAATTCATGTTAGAAATCCAAATC ATCACCGATTCTTCTCAAAACATTCAGACAATTTTGGTAGAAGCATCTTGTG (SEQ ID NO 5)
B1	GGAAATTCGCTGATGTCGATACCGATTCTCCAAGAGAAGTCTTCTCAGAGTCG CTGCTGATATGTTGCTGATGGTAACCTCAACTG (SEQ ID NO 6)
B2	AATCTGGGACTTTGGTACACAAAGCTTCAAGACCAATTTAGAAGCGAAGTA GAACAAAGCGACGACTCTACCCAGTTGAAGTTACCA (SEQ ID NO 7)
B3	CCAACTTGATCTTGGATCCAGACCAACAATCTTCTCTCAAGAAATCCAAAGGTC CAACCCATGATGGTTCGATCAATTCGCGACTTTG (SEQ ID NO 8)
C1	ATTGTTGGTCTGGATCCAAGATCAAGGTGGGTTGGGAAAGTTGTGTTCTTACTT CGGTACCCCAACCTGGCAACCGTCA (SEQ ID NO 9)
C2	TCCCCCGGGGATTAACCCATTTTTCAGATGGTCAAGAAGCGGTCAAGAC ACCAGCGACGAAGATGGTGACGGTTTGCCAGGTTGGG (SEQ ID NO 10)

Table 2: Overview of the differentially expressed genes after 30 min Bax expression**Comparison: INVSc1 YlpUTL versus INVSc1 YlpUTyLB**

YLP	YLB	Normalized expression YLP	Normalized expression YLB	Log2 ratio	P-value
<i>Cellular role : Cell cycle control</i>					
YBR139C	HSL7	18932.54	37877.20	↑	2.00
<i>Cellular role : Polymerase II transcription</i>					
YDR259C	MET32	17681.13	45567.17	↑	2.58
YBR112C	SSN6	26698.87	65315.83	↑	2.45
YDR145W	TAF61	38697.96	79117.62	↑	1.89
YBR269W	SNF5	33111.77	72328.70	↑	2.18
YDR216W	ADR1	30127.45	8815.87	↓	3.42
YEL009C	GCN4	16533.76	3030.44	↓	5.46
YBR089C-A	NHP6B	22698.83	6297.48	↓	3.60
YMR043W	MCM1	39141.64	84180.45	↑	2.15
YKR092C	SRP40	5965.63	16105.62	↑	2.70
YMR279C	ZDS1	14899.61	35508.04	↑	2.42
YPL089C	RLM1	34922.61	67858.88	↑	1.94
YOR372C	NDD1	20285.12	44445.20	↑	2.19
YPL037C	EGD1	30633.33	5250.70	↓	5.63
<i>Cellular role : Cell polarity</i>					
YBL065W	BOI1	7693.29	18614.99	↑	2.42
<i>Cellular role : Chromatine structure</i>					
YBR009C	HHF1	16668.00	4178.80	↓	3.99
YNL030W	HHF2	49878.04	12568.96	↓	3.97
YDR224C	HTB1	67355.40	29155.82	↓	2.91
YBL002W	HTB2	25269.02	5383.97	↓	4.69
<i>Cellular role: RNA processing</i>					
YER112W	USS1	12776.74	31470.70	↑	2.46
YPL190C	NAB3	8381.36	17892.11	↑	2.80
YNL112W	DBP2	9956.84	28036.48	↑	2.82
<i>Cellular role: Energy generation</i>					
YPL078C	ATP4	28902.69	5980.38	↓	4.50
YDL004W	ATP16	36525.08	3004.34	↓	12.16
YDR377W	ATP17	14419.41	756.86	↓	19.05
YDR529C	QCR7	35348.95	5394.85	↓	8.55
YGR008C	STF2	13275.51	2276.27	↓	5.89
YEL039C	CYC7	13604.38	2889.66	↓	5.06
YKL150W	MCR1	105337.67	30743.75	↓	3.43
YLR038C	COX12	52687.73	5455.83	↓	9.66
YLR327C		113,986.77	54,014.65	↓	2.11
<i>Cellular role: Carbohydrate metabolism</i>					
YBR149W	ARA1	15149.55	4095.17	↓	3.70
YMR094C	HXT1	12526.80	785.73	↓	15.94
YDR345C	HXT3	36643.13	1632.48	↓	22.45
YDR343C	HXT6	77064.71	32080.05	↓	2.40
YDR342C	HXT7	76349.13	27615.15	↓	2.76
<i>Cellular role: Signal transduction</i>					
YER177W	BMH1	22856.29	44771.71	↑	1.96
YDR099W	BMH2	40127.38	74572.38	↑	1.86

YGR070W	ROM1	12055.28	28169.57	↑	2.34
YGR023W	MTL1	7354.78	19648.06	↑	2.67
Cellular role: Protein synthesis					
YGR034W	RPL26B	71942.48	74625.22	↑	1.04
Cellular role: Protein folding					
YLA216C	CPR6	9616.80	31126.02	↑	3.24
Cellular role: Protein modification/degradation					
YFR052W	RPN12	5583.57	14855.67	↑	2.66
YDL147W	RPN5	31832.20	52939.11	↑	1.66
YGR132C	PH51	15429.56	5591.19	↓	2.76
YGR135W	PRE9	38921.63	5517.17	↓	7.24
YFR010W	UBP6	1892.76	828.94	↓	2.26
Cellular role: Cell stress					
YIR037W	GPX3	7869.22	21789.00	↑	2.77
YDR513W	TTR1	55986.32	33263.12	↓	1.68
YCL035C	GRX1	70248.30	10069.97	↓	6.40
YFL014W	HSP12	41689.29	18658.48	↓	2.23
YHR053C	CUP1A	72852.07	43488.52	↓	1.68
YHR055C	CUP1B	71934.03	56799.80	↓	2.77
YMR173W	DDR18	16670.70	5022.40	↓	3.32
YMR251W-A	HOR7	26878.85	417.36	↓	64.41
YLR043C	TRX1	58251.39	4435.79	↓	13.13
YBL084C	PRX1	21525.00	40969.00	↑	1.30
YOL151W	GRE2	2024.55	24152.03	↑	9.20
Cellular role: Unknown					
YBL081W		73834.11	74612.35	↑	1.31
YDR368C		39398.46	57428.80	↑	1.44
YCR004C	YCP4	6869.08	28115.73	↑	4.09
YCR013C		3988.55	15144.34	↑	3.80
YBR050C	REG2	4687.91	14408.20	↑	3.07
YBL108W		18744.60	35440.24	↑	1.80
YDR154C		19565.23	69428.03	↑	3.55
YEL071W	DLD3	22235.73	68790.83	↑	3.09
YHR095W		14426.76	34896.68	↑	2.42
YGR069W		43413.57	72420.39	↑	1.67
YDR544C		13567.00	27004.37	↑	1.99
YGR236C		24927.59	8032.35	↓	3.10
YIL057C		24248.39	773.56	↓	31.34
YGL080W		23425.00	3217.81	↓	7.28
YGL072C		16437.52	2652.80	↓	6.20
YHR056C	RSC30	72072.88	57446.85	↓	1.25
YKL054C	VID31	17990.49	38258.80	↑	2.13
YLR311C		7982.40	24164.87	↑	3.02
YJR115W		64690.69	102086.34	↑	1.58
YJL188C	BUD19	7580.28	23325.70	↑	2.95
YKR040C		50934.76	100733.41	↑	1.98
YLR053C		8117.68	20317.34	↑	2.50
YOR121C		59950.94	92470.43	↑	1.54
YNL143C		98811.28	110534.34	↑	1.12
YOR131C		7941.55	22353.72	↑	2.81
YNL338W		21800.45	38777.28	↑	1.78
YNL179C		13729.36	39513.53	↑	2.88
YOL150C		3408.74	60298.39	↑	17.89

YMR107W		65118.70	10042.46	↓	6.48
YKL065C	YET1	69556.19	12804.88	↓	5.43
YJR096W		21780.37	10655.13	↓	2.04
YJL161W		16468.73	2618.26	↓	6.29
YML128C	MSC1	80130.20	13795.84	↓	5.81
YMR251W		26879.95	417.36	↓	64.41
YMR173W-A		110104.98	61951.29	↓	1.78
YPL201C		17913.32	5018.97	↓	3.57
YOR285W		64074.73	29749.43	↓	2.15
YOR286W		13458.08	733.06	↓	18.36
<i>Cellular role: Cell wall maintenance</i>					
YKR078W	ECM4	2674.15	13040.04	↑	4.89
YLR300W	ECM19	5472.05	15145.35	↑	2.77
<i>Cellular role: Membrane fusion</i>					
YHR138C		19921.35	3707.57	↓	6.37
<i>Cellular role: Vesicular transport</i>					
YHR161C	YAP180A	13086.35	30160.90	↑	2.30
YPL085W	SEC16	6668.57	15206.49	↑	2.28
YKL196C	YKT6	18933.84	2890.07	↓	6.55
YPR028W	YIP2	25434.34	2049.47	↓	12.41
<i>Cellular role: DNA repair/recombination</i>					
YDL059C	RAD59	1948.81	19089.13	↑	6.72
<i>Cellular role: DNA synthesis</i>					
YEL082W	MCM9	23422.85	44327.48	↑	1.89
<i>Cellular role: Amino acid metabolism</i>					
YIL074C	SER33	3978.42	16702.88	↑	4.20
YGF155W	CYS4	4184.59	19270.89	↑	4.61
<i>Cellular role: Fatty acid metabolism</i>					
YHR179W	OYE2	2291.38	40274.02	↑	17.58
<i>Cellular role: Protein translocation</i>					
YNL131W	TOM22	16287.21	1679.78	↓	9.70
<i>Cellular role: Small molecule transport</i>					
YDR276C	SNA1	21140.46	1580.68	↓	13.98
YOR267C	HRK1	82689.30	110516.24	↑	1.76
YHR039-C	VMA10	60107.90	8490.93	↓	7.08
YOR382W	FIT2	6780.82	27298.15	↑	4.02

Table 3: Overview of the differentially expressed genes after 1h Bax expression**Comparison: INVSc1 YlpUTL versus INVSc1 YlpUTyL8**

Gene	Gene	YlpUTL	YlpUTyL8	YlpUTL	YlpUTyL8
Cellular role: Polymerase II transcription					
YDR145W	TAF61	20729.58	57376.27	↑	2.77
YDR216W	ADR1	5925.91	18459.00	↑	3.11
YBR112C	CYC8	50186.77	84511.50	↑	1.29
YMR043W	MCM1	21011.54	53700.49	↑	2.58
YPL089C	RLM1	23440.54	64284.32	↑	2.74
YOR072C	NDN1	26412.58	50804.99	↑	1.92
Cellular role: Cell cycle control					
YBR133C	HSL7	18761.64	53238.86	↑	2.84
Cellular role: Cell polarity					
YBL085W	BOI1	37895.40	57781.52	↑	1.52
Cellular role: Chromatin structure					
YDR224C	HTB1	13661.40	55656.34	↑	4.07
Cellular role: Energy generation					
YGR183C	QCR9	23181.54	81865.40	↑	3.53
YLR294C		5054.57	28994.72	↑	5.74
YKL150W	MCR1	43663.07	60593.16	↑	1.39
YMR256C	COX7	7606.58	29801.54	↑	3.79
YOL126C	MDH2	34144.61	65326.97	↑	1.91
YLR327C		97416.84	101651.17	↑	1.04
Cellular role: Vesicular transport					
YHR181C	YAP180A	11602.81	34695.20	↑	2.99
YLR206W	ENT2	14439.24	34621.70	↑	2.40
Cellular role: Carbohydrate metabolism					
YDR342C	HXT7	65273.58	22231.06	↓	2.94
YDR343C	HXT6	43572.28	6075.38	↓	7.17
YDR346C	HXT3	76352.52	40296.00	↓	1.89
YGR192C	TDH3	38472.30	14145.84	↓	2.72
YKR097W	PCK1	22919.81	38225.98	↑	1.67
YOR374W	ALD4	33711.37	2607.43	↓	12.93
Cellular role: Signal transduction					
YER177W	BMH1	16298.14	31748.91	↑	1.95
YDR099W	BMH2	50572.45	65123.58	↑	1.29
Cellular role: Cell wall maintenance					
YLR110C	CCW12	102525.29	11230.41	↓	9.13
Cellular role: Protein modification/degradation					
YOR261C	APN8	12575.49	32568.47	↑	2.59
Cellular role: Cell stress					
YHR053C	CUP1A	32531.53	63579.94	↑	1.95
YHR055C	CUP1B	27939.92	65142.82	↑	2.33
YMR173W	DDR48	38338.83	60514.70	↑	1.58
YOR031W	CAS5	2922.32	23848.60	↑	8.16

YLR109W	AMP1	43067.08	6302.46	↓	6.83
Cellular role: Unknown					
YBL081W		82476.13	44279.86	↑	1.86
YBL109W		22998.63	63428.23	↑	2.76
YDR366C		14599.17	46494.73	↑	3.18
YDR154C		21288.57	56534.93	↑	2.65
YGR236C	SPG1	17717.80	64439.98	↑	3.64
YHR056C	RSC30	27020.16	65110.42	↑	2.41
YGR182C		8171.02	34669.96	↑	4.24
YDR544C		14797.70	37704.91	↑	2.55
YHR182W		13836.79	33381.84	↑	2.41
YGR243W		30829.68	59765.39	↑	1.91
YBR050C	REG2	14008.24	29603.16	↑	2.11
YEL071W	DLD3	19487.41	35273.39	↑	1.81
YDR135C		83074.54	62986.96	↓	1.32
YDR134C		83111.03	16839.53	↓	4.94
YHL021C		46028.06	8577.00	↓	5.37
YKL054C	VID31	28018.48	66537.91	↑	2.37
YLR311C		7803.52	31180.73	↑	3.99
YMR107W		13459.16	78850.98	↑	5.86
YKL066W		8751.84	24129.32	↑	2.76
YMR173W-A		38398.83	60514.70	↑	1.58
YML053C		23670.88	66254.48	↑	2.80
YOR121C		17039.58	58010.58	↑	3.40
YOL108W		19917.67	69853.68	↑	3.51
YNL338W		17864.90	49911.08	↑	2.79
YJR115W		84858.02	98161.71	↑	1.16
Cellular role: Small molecule transport					
YOR267C	HRK1	90123.84	98824.51	↑	1.07

Table 4: Overview of the differentially expressed genes after 2h Bax expression**Comparison: INVSc1 YlpUTL versus INVSc1 YlpUTyLB**

Gene	Gene	INVSc1 YlpUTL	INVSc1 YlpUTyLB	Up/Down	FC
<i>Cellular role: Protein modification/degradation</i>					
YCL052C	PBN1	5264.22	8175.70	↑	1.55
YOL147W	RPN5	22386.40	47857.67	↑	2.14
YOR261C	RPN8	27349.25	42198.05	↑	1.54
YGR132C	PHB1	5252.03	8458.53	↑	1.61
YBR139W		9458.26	3611.21	↓	2.62
<i>Cellular role: Unknown</i>					
YDR202C	RAY2	7493.71	10089.19	↑	1.35
YBR062C		4893.97	9894.82	↑	2.02
YDR366C		25468.2	59682.92	↑	2.34
YBL109W		24803.62	37444.64	↑	1.51
YDR154C		21166.26	33434.35	↑	1.58
YEL071W	DLD3	34153.85	41083.39	↑	1.29
YGR238C	SPG1	18878.52	31419.12	↑	1.85
YGR182C		30569.31	58805.05	↑	1.92
YDR544C		15937.14	24421.98	↑	1.53
YHR162W		28610.34	33794.73	↑	1.27
YHR056C	RSC30	33372.66	68425.24	↑	2.05
YDR133C		75520.99	62984.50	↓	1.20
YCR010C	ADY2	17240.59	11835.82	↓	1.46
YDR134C		72723.66	9776.23	↓	7.44
YGR059W		65418.73	53767.35	↓	1.22
YIL057C		16510.16	2198.04	↓	7.51
YGL072C		12209.68	6509.91	↓	1.88
YGL080W		22550.78	11525.24	↓	1.96
YLR311C		11095.31	24060.47	↑	2.22
YJR115W		74757.79	108422.48	↑	1.38
YMR099C		7057.15	11477.42	↑	1.63
YMR173W-A		31901.05	48886.91	↑	1.47
YML132W	COS3	24648.97	34995.33	↑	1.42
YKL066W		13581.94	25433.97	↑	1.87
YIL142C		7205.86	11920.21	↑	1.65
YLR346C		6447.57	11569.63	↑	1.79
YLR053C		41161.10	78636.82	↑	1.91
YMR110C		19410.64	29861.23	↑	1.63
YKR075C		19134.57	29948.72	↑	1.57
YOR121C		36492.56	59452.09	↑	1.63

Cellular role: Unknown					
YOL106W		31382.10	76664.72	↑	2.44
YNL338W		24117.93	38981.22	↑	1.62
YNL134C		9617.33	14613.60	↑	1.52
YKL085C	YET1	52422.65	33794.03	↓	1.55
YMR009W		20666.22	9519.29	↓	2.17
YJL144W		10316.92	3122.77	↓	3.90
YNL128C	MSC1	584128.13	25434.11	↓	2.29
YNL179C		21938.96	10883.98	↓	2.02
YOL109W	ZEO1	22711.98	6581.11	↓	3.45
YNR002C	FUN34	18241.25	9752.25	↓	1.87
Cellular role: Chromatine structure					
YDR224C	HTB1	25356.73	30827.54	↑	1.22
YBL002W	HTB2	9241.68	14261.54	↑	1.54
YBL003C	HTA2	3453.55	6553.49	↑	1.90
YNL031C	HHT2	13376.02	2348.84	↓	5.89
Cellular role: Polymerase II transcription					
YBR289W	SNF5	59542.27	65885.13	↑	1.11
YDR073W	SNF11	12190.01	23088.03	↑	1.89
YMR043W	MCM1	66457.16	77022.05	↑	1.16
YPL089C	RLM1	49844.99	60624.28	↑	1.22
Cellular role: Signal transduction					
YDR099W	BMH2	55902.13	73874.51	↑	1.32
Cellular role: Cell stress					
YBL064C	PRX1	11203.87	14815.42	↑	1.32
YBR101C		25016.21	35781.64	↑	1.43
YLR043C	TRX1	10864.53	3912.33	↓	2.78
YGR209C	TRX2	30492.38	37829.20	↑	1.24
YER103W	SSA4	8763.38	15799.18	↑	1.80
YHR055C	CUP1B	18824.43	77613.05	↑	4.12
YHR053C	CUP1A	32726.62	83536.72	↑	1.94
YDR256C	CTA1	9614.29	4232.17	↓	2.27
YCA021C	HSP30	8090.05	3604.78	↓	2.24
YCL035C	GRX1	28437.57	12843.99	↓	2.21
YGR086C		36796.12	24272.57	↓	1.52
YFL014W	HSP12	61868.64	23288.19	↓	2.66
YOR031W	CRS5	6015.69	14519.12	↑	2.41
YMR251W-A	HOR7	17791.14	4231.30	↓	4.19
YOR120W	GCY1	114252.98	78052.05	↓	1.46
Cellular role: Protein synthesis					
YAL003W	EFB1	3044.80	5772.68	↑	1.90
YOL127W	RPL25	6263.96	12055.41	↑	1.92
YHR010W	RPL27	4057.16	10856.34	↑	2.68
YLR325C	RPL38	5401.85	12955.89	↑	2.40
YJL189W	RPL39	2044.64	8010.57	↑	3.92
YIL148W	RPL40A	6052.35	11595.54	↑	2.30
YKR094C	RPL40B	3994.57	10011.19	↑	2.54
YOL139C	CDC33	4132.18	8956.14	↑	2.17

Cellular role : Protein folding					
YLR216C	CPR6	20353.43	32713.37	↑	1.61
YKL117W	SBA1	11144.25	1500.56	↓	7.43
Cellular role: Vesicular transport					
YCR009C	RVS181	5350.32	9780.92	↑	1.83
YHR161C	YAP180A	25136.63	32481.67	↑	1.29
YBL078C	AUT7	16528.91	9843.25	↓	1.68
Cellular role : Carbohydrate metabolism					
YBL058W	SHP1	4626.50	8178.94	↑	1.77
YBR149W	ARA1	30706.41	9637.76	↓	3.19
YOR178W	SDH4	14880.91	6237.35	↓	2.39
YHR094C	HXT1	30389.99	18383.00	↓	1.65
YMR011W	HXT2	39524.90	21221.96	↓	1.86
YOR345C	HXT3	77025.40	56749.40	↓	1.36
YDR343C	HXT6	73149.70	8676.17	↓	8.43
YDR342C	HXT7	75331.76	27052.43	↓	2.78
YKL060C	FBA1	16273.54	21323.23	↑	1.31
Cellular role : Cell cycle control					
YBR133C	HSL7	32903	41984.32	↑	1.28
Cellular role : Energy generation					
YMR256C	COX7	18558.01	40422.91	↑	2.18
YML129C	COX14	11418.54	21798.88	↑	1.91
YFR033C	QCR6	9159.48	13398.67	↑	1.46
YDR529C	QCR7	24821.75	16558.87	↓	1.50
YIL168W	QCR8	15554.30	24508.28	↑	1.58
YHR001W-A	QCR10	12416.35	23485.31	↑	1.89
YBR039W	ATP3	11709.79	3088.19	↓	3.79
YPL078C	ATP4	11325.64	13769.72	↑	1.22
YPL271W	ATP15	3261.75	7839.05	↑	2.40
YLR327C		51742.90	128511.27	↑	2.48
YLR294C		15832.61	38544.44	↑	2.43
YAL060W	FUN49	11792.72	5778.91	↓	2.04
Cellular role: Small molecule transport					
YDR276C	SNA1	19337.39	12392.20	↓	1.56
YGR197C	SNG1	4756.18	10484.09	↑	2.20
YHR039C-B	VMA10	21190.93	10592.98	↓	2.00
YDR267C	HRK1	111849.17	101339.10	↓	1.10
Cellular role: RNA processing					
YGR250C		8709.92	17358.43	↑	1.99
Cellular role : Cell wall maintenance					
YER150W	SPI1	55592.73	22403.59	↓	2.48
YLR110C	CCW12	35147.41	5786.88	↓	6.07
Cellular role : Cell polarity					
YOR122C	PFY1	14459.45	20178.41	↑	1.40
Cellular role : Amino acid metabolism					
YPR035W	GLN1	20894.14	7522.05	↓	2.78

Table 5: Overview of the differentially expressed genes after 3h Bax expression**Comparison: INVSc1 YlpUTL versus INVSc1 YlpUTyLB**

Gene	Gene	Normalised Intensity	Normalised Intensity	Log2 ratio	P-value
<i>Cellular role: Cell cycle control</i>					
YBR133C	HSL7	63562.10	43191.28	↓	1.47
<i>Cellular role: Cell polarity</i>					
YBL085W	BOI1	32734.79	23497.41	↓	1.39
<i>Cellular role: Chromatine structure</i>					
YDR545W	YRF1-1	20111.51	11479.67	↓	1.75
<i>Cellular role: Energy generation</i>					
YCR005C	CIT2	11882.42	25632.94	↑	2.16
YGR183C	QCR9	74474.20	11510.99	↓	8.47
YOL126C	MDH2	55984.88	17978.10	↓	3.11
<i>Cellular role: Carbohydrate metabolism</i>					
YBR019C	GAL10	3092.50	15697.52	↑	5.08
YDR345C	HXT3	14086.41	25857.66	↑	1.82
YKR097W	PCK1	50736.44	20858.02	↓	2.43
<i>Cellular role: Signal transduction</i>					
YDR089W	BMH2	63285.16	56028.91	↓	1.13
<i>Cellular role: Protein synthesis</i>					
YHR010W	RPL27A	23254.90	7217.14	↓	3.22
YLR325C	RPL38	26725.96	9121.29	↓	2.93
<i>Cellular role: Cell stress</i>					
YFL014W	HSP12	40848.44	89781.91	↑	1.71
YHR053C	CUP1A	20399.10	65037.14	↑	3.19
YHR055C	CUP1B	21763.09	64594.58	↑	2.97
YMR178W	DDR48	75407.16	38354.37	↓	2.07
YOL052C-A	DDR2	20479.72	33702.23	↑	1.65
<i>Cellular role: Unknown</i>					
YIL057C		7602.78	24104.02	↑	3.17
YHR056C	RSC30	41473.41	64809.08	↑	1.56
YDR544C		55075.67	29731.72	↓	1.85
YCR040C		48049.71	59649.47	↑	1.24
YNL338W		86107.91	30045.62	↓	2.87
YJR115W		74889.58	81238.98	↓	1.08
YBL109W		64754.79	57185.99	↓	1.13
YMR173W-A		75407.16	36354.97	↓	2.07

Table 6: Overview of the differentially expressed genes after 6h Bax expression**Comparison: INVSc1 YlpUTL versus INVSc1 YlpUTyLB**

YipUTL	YipUTyLB	Normalised YipUTL	Normalised YipUTyLB	log2(YipUTL/YipUTyLB)	log2(YipUTyLB/YipUTL)
<i>Cellular role: Cell stress</i>					
YDR171W	HSP42	13484.04	27183.07	↑	2.02
YFL014W	HSP12	41197.12	25081.08	↓	1.42
YDR513W	TTR1	19985.22	12935.02	↓	1.54
YCL035C	GRX1	31735.39	12930.71	↓	2.45
YGR209C	TRX2	54455.65	47569.21	↓	1.14
YHR053C	CUP1A	81488.64	15289.39	↓	5.39
YHR055C	CUP1B	81278.95	20031.69	↓	4.06
YMR251W-A	HOR7	18824.54	5914.28	↓	3.18
<i>Cellular role: Signal transduction</i>					
YDR099W	BMH2	29412.99	56588.42	↑	1.99
<i>Cellular role: Protein synthesis</i>					
YGL147C	RPL9A	13655.66	1585.97	↓	9.81
YGR085C	RPL11B	27465.15	3791.35	↓	7.24
YDR418W	RPL12B	14417.77	1555.24	↓	9.27
YLR029C	RPL15A	37122.11	9321.81	↓	3.98
YOR312C	RPL20B	50334.94	5706.59	↓	8.82
YBR191W	RPL21A	21740.90	2571.30	↓	8.40
YPL079W	RPL21B	31059.43	5023.61	↓	6.18
YOL127W	RPL25	75971.72	11749.17	↓	6.47
YHR010W	RPL27A	45716.64	8096.40	↓	5.85
YDR471W	RPL27B	14636.79	2613.40	↓	5.60
YOL075W	RPL31A	11969.47	2811.53	↓	4.56
YBL092W	RPL32	7872.80	857.85	↓	9.18
YOL191W	RPL35A	28582.59	6046.25	↓	4.73
YOL136W	RPL35B	25493.49	5064.51	↓	5.02
YLR325C	RPL38	48051.23	8217.18	↓	5.85
YIL148W	RPL40A	47028.95	9543.65	↓	4.93
YKR094C	RPL40B	38900.50	5957.78	↓	6.70
YHR141C	RPL42B	10163.88	937.21	↓	10.84
YML065W	RPS1B	15916.48	1144.54	↓	13.91
YGL123W	RPS2	12505.56	2243.26	↓	5.57
YOR096W	RPS7A	24164.37	3223.80	↓	7.50
YBL072C	RPS8A	17198.50	3233.30	↓	5.82
YER102W	RPS8B	16234.93	1791.18	↓	9.06
YBR189W	RPS9B	10075.22	2150.89	↓	4.68
YDR293W	RPS10A	51787.23	12110.74	↓	4.28
YDR084W	RPS13	9736.57	1587.67	↓	6.13
YDR450W	RPS18A	37913.71	5674.80	↓	6.68
YML026C	RPS18B	14458.01	2027.28	↓	7.13
YKL156W	RPS27A	20725.18	1117.26	↓	2.13
YLR167W	RPS31	38648.54	2811.97	↓	14.80
YJL138C	TIF2	20154.61	7264.66	↓	2.77
<i>Cellular role: Energy metabolism</i>					
YGR183C	QCR9	57357.59	80447.53	↑	1.40
YDL004W	ATP16	25047.95	10988.85	↓	2.28
YKL150W	MCR1	50931.48	37076.83	↓	1.37

YLR038C	COX12	39506.08	29534.70	↓	1.34
Cellular role: Unknown					
YDR442W		14854.81	2242.42	↓	6.94
YDR134C		17025.59	10681.72	↓	1.61
YHR056C	RSC90	81350.52	31447.10	↓	2.59
YKR040C		48390.21	90126.88	↑	1.86
YLR414C		13463.40	8085.92	↓	1.67
YLR312C		25589.67	16184.57	↓	1.58
YJL188C	BUD19	22074.09	4526.38	↓	4.88
YOR285W		75099.98	61896.00	↓	1.21
YOL109W	ZEO1	66287.15	35502.43	↓	1.87
Cellular role: Chromatine structure					
YBR009C	HHF1	11173.15	5416.74	↓	2.06
YNL030W	HHF2	31366.74	20132.23	↓	1.56
Cellular role: Nucleotide metabolism					
YDR399W	HPT1	13338.03	5383.81	↓	2.50
Cellular role: Polymerase II transcription					
YEL009C	GCM4	34617.98	20798.63	↓	1.86
YPL037C	EGD1	17882.37	8229.01	↓	2.17
Cellular role: Vesicular transport					
YBL078C	AUT7	42661.70	32333.01	↓	1.32
YOR327C	SNC2	22716.58	13704.48	↓	1.68
Cellular role: Small molecule transport					
YHR039C-B	VMA10	44429.30	23826.61	↓	1.86
Cellular role: Cell wall maintenance					
YKL097W-A	CWP2	13529.93	1617.20	↓	8.37
Cellular role: Carbohydrate metabolism					
YKL060C	FBA1	33329.74	10367.82	↓	3.21

Table 7:

Sequence ID NO	ORF	GENE	30 min	1h	2h	3h	6h
SEQ ID NO 17	YAL003W	EFB1			1.90		
SEQ ID NO 19	YAL060W	FUN49			-2.00		
SEQ ID NO 21	YBL002W	HTB2	-4.69		1.54		
SEQ ID NO 23	YBL058W	SHP1			1.77		
SEQ ID NO 25	YBL054C	PRX1	1.90		1.32		
SEQ ID NO 27	YBL072C	RPS8A					-5.32
SEQ ID NO 29	YBL081W		1.01	1.86			
SEQ ID NO 31	YBL085W	BOI1	2.42	1.52		-1.39	
SEQ ID NO 33	YBL092W	RPL32			2.76		-9.18
SEQ ID NO 35	YBL109W		1.89	2.76	1.51	-1.13	
SEQ ID NO 37	YBR009C	HHF1	-3.99				-2.06
SEQ ID NO 39	YBR019C	GAL10				5.08	
SEQ ID NO 41	YBR039W	ATP3			-9.70		
SEQ ID NO 43	YBR050C	REG2	3.07	2.11			
SEQ ID NO 45	YBR062C				2.02		
SEQ ID NO 47	YBR089C-A	NMP6B	-3.60				
SEQ ID NO 49	YBR101C				1.43		
SEQ ID NO 51	YBR112C	SSN6	2.45	1.29			
SEQ ID NO 53	YBR133C	HSL7	2.00	2.84	1.28	-1.47	
SEQ ID NO 55	YBR139W				-2.60		
SEQ ID NO 57	YBR149W	ARA1	-3.70		-3.11		
SEQ ID NO 59	YBR189W	RPS9B					-4.88
SEQ ID NO 61	YBR191W	RPL21A					-8.46
SEQ ID NO 63	YBR289W	SNF5	2.18		1.11		
SEQ ID NO 65	YCL035C	GRX1	-8.40		-2.20		-2.45
SEQ ID NO 67	YCL052C	PBN1			1.55		
SEQ ID NO 69	YCR004C	YCP4	4.09				
SEQ ID NO 71	YCR005C	CIT2				2.16	
SEQ ID NO 73	YCR009C	RVS161			1.83		
SEQ ID NO 75	YCR010C				-1.40		
SEQ ID NO 77	YCR013C		3.80				
SEQ ID NO 79	YCR021C	HSP30			-2.20		
SEQ ID NO 81	YDL004W	ATP16	-12.16				-2.28
SEQ ID NO 83	YDL059C	RAD59	6.72				
SEQ ID NO 85	YDL075W	RPL31A					-4.58
SEQ ID NO 87	YDL147W	RPN5	1.86		2.14		
SEQ ID NO 89	YDR064W	RPS13					-6.13
SEQ ID NO 91	YDR073W	SNF11			1.89		
SEQ ID NO 93	YDR099W	BMH2	1.86	1.29	1.32	-1.13	1.99
SEQ ID NO 95	YDR133C			-1.32	-1.20		
SEQ ID NO 97	YDR134C			-4.84	-7.40		-1.61
SEQ ID NO 99	YDR145W	TAF61	1.89	2.77			
SEQ ID NO 101	YDR154C		3.55	2.65	1.58		
SEQ ID NO 103	YDR171W	HSP42					2.02
SEQ ID NO 105	YDR178W	SDH4			-2.30		
SEQ ID NO 107	YDR202C	RAV2			1.35		
SEQ ID NO 109	YDR216W	ADR1	-3.42	3.11			
SEQ ID NO 111	YDR224C	HTB1	-2.91	4.07	1.22		
SEQ ID NO 113	YDR253C	MET32	2.58				
SEQ ID NO 115	YDR256C	CTA1			-2.20		
SEQ ID NO 117	YDR278C	SNA1	-13.38		-1.50		

Sequence ID NO	ORF	GENE	30 min	1h	2h	3h	6h
SEQ ID NO 119	YDR342C	HXT7	-2.76	-2.94	-2.70		
SEQ ID NO 121	YDR343C	HXT8	-2.40	-7.17	-8.40		
SEQ ID NO 123	YDR345C	HXT3	-22.45	-1.89	-1.30	1.82	
SEQ ID NO 125	YDR366C		1.44	3.18	2.34		
SEQ ID NO 127	YDR377W	ATP17	-19.05				
SEQ ID NO 129	YDR399W	HPT1					-2.50
SEQ ID NO 131	YDR418W	RPL12B					-9.27
SEQ ID NO 133	YDR513W	TTR1	-1.68				-1.54
SEQ ID NO 135	YDR544C		1.99	2.55	1.53	-1.85	
SEQ ID NO 137	YDR545W	YRF1-1				-1.75	
SEQ ID NO 139	YEL009C	GCN4	-5.46				-1.68
SEQ ID NO 897	YEL032W	MCM3	1.89				
SEQ ID NO 141	YEL039C	CYC7	-5.06				
SEQ ID NO 143	YEL071W	DLD3	3.09	1.21	1.29		
SEQ ID NO 145	YER103W	SSA4			1.80		
SEQ ID NO 147	YER112W	USS1	2.46				
SEQ ID NO 149	YER150W	SPH1			-2.40		
SEQ ID NO 151	YER177W	BMH1	1.96	1.95			
SEQ ID NO 153	YFR010W	UBP6	-2.28				
SEQ ID NO 155	YFR033C	QCR6			1.46		
SEQ ID NO 157	YFR052W	RPN12	2.66				
SEQ ID NO 159	YGL072C		-6.20		-1.80		
SEQ ID NO 161	YGL080W		-7.28		-1.90		
SEQ ID NO 163	YGL123W	RPS2					-5.57
SEQ ID NO 165	YGR008C	STF2	-5.83				
SEQ ID NO 167	YGR023W	MTL1	2.67				
SEQ ID NO 169	YGR034W	RPL26B	1.04				
SEQ ID NO 171	YGR069W		1.67		-1.20		
SEQ ID NO 173	YGR070W	ROM1	2.34				
SEQ ID NO 175	YGR086C				-1.50		
SEQ ID NO 177	YGR132C	PHB1	-2.76		1.61		
SEQ ID NO 179	YGR135W	PRE9	-7.24				
SEQ ID NO 181	YGR155W	CYS4	4.61				
SEQ ID NO 183	YGR192C	TDH3		-2.72			
SEQ ID NO 185	YGR197C	SNG1			2.20		
SEQ ID NO 187	YGR209C	TRX2			1.24		-1.14
SEQ ID NO 189	YGR243W			1.94			
SEQ ID NO 191	YGR250C				1.89		
SEQ ID NO 193	YHL021C			-5.37			
SEQ ID NO 195	YHR001W-A	QCR10			1.89		
SEQ ID NO 197	YHR039C-B	VMA10	7.08		-2.00		-1.86
SEQ ID NO 199	YHR053C	CUP1A	-1.68	1.95	1.94	3.19	-5.33
SEQ ID NO 201	YHR055C	CUP1B	-2.77	2.33	4.12	2.97	-4.08
SEQ ID NO 203	YHR056C		-1.25	2.41	2.05	1.56	-2.59
SEQ ID NO 205	YHR094C	HXT1	-15.94		-1.80		
SEQ ID NO 207	YHR095W		2.42				
SEQ ID NO 209	YHR138C		-5.37				
SEQ ID NO 211	YHR161C	YAP180A	2.30	2.99	1.29		
SEQ ID NO 213	YHR162W			2.41	1.27		
SEQ ID NO 215	YHR175W	OYE2	17.58				
SEQ ID NO 217	YIL057C		31.34		-7.50	3.17	
SEQ ID NO 219	YIL074C	SER33	4.20				
SEQ ID NO 221	YIR037W	GPX3	2.77				

Sequence ID NO	ORF	GENE	30 min	1h	2h	3h	6h
SEQ ID NO 223	YJL158C	TIF2					-2.77
SEQ ID NO 225	YJL142C				1.65		
SEQ ID NO 227	YJL144W				-3.30		
SEQ ID NO 229	YJL161W		-6.29				
SEQ ID NO 231	YJL166W	OCR8			1.58		
SEQ ID NO 233	YJR096W		-2.04				
SEQ ID NO 235	YJR115W		1.58	1.16	1.38	-1.08	
SEQ ID NO 237	YKL054C	VID31	2.13	2.37			
SEQ ID NO 239	YKL060C	FBA1			1.31		-3.21
SEQ ID NO 241	YKL065C	YET1	-5.43		-1.55		
SEQ ID NO 243	YKL066W			2.76	1.87		
SEQ ID NO 245	YKL087W-A	CWP2					-8.37
SEQ ID NO 247	YKL117W	SBA1			-7.43		
SEQ ID NO 249	YKL150W	MCR1	-3.43	1.38			-1.37
SEQ ID NO 251	YKL156W	RPS27A					-2.13
SEQ ID NO 253	YKL196C	YKT6	-6.55				
SEQ ID NO 255	YKR040C		1.98			1.24	1.86
SEQ ID NO 257	YKR075C				1.57		
SEQ ID NO 259	YKR076W	ECM4	4.88				
SEQ ID NO 261	YKR092C	SRP46	2.70				
SEQ ID NO 263	YKR097W	PCK1		1.67		-2.43	
SEQ ID NO 265	YLR029C	RPL15A					-3.98
SEQ ID NO 267	YLR038C	COX12	-9.66				-1.34
SEQ ID NO 269	YLR043C	TRX1	-13.13		-2.78		
SEQ ID NO 271	YLR053C		2.50		1.91		
SEQ ID NO 273	YLR109W	AHP1		-6.83			
SEQ ID NO 275	YLR110C			-9.13	-6.07		
SEQ ID NO 277	YLR208W	ENT2		2.40			
SEQ ID NO 279	YLR216C	CPR6	3.24		1.61		
SEQ ID NO 281	YLR294C			5.74	2.43		
SEQ ID NO 283	YLR311C		3.02	3.99	2.22		
SEQ ID NO 285	YLR312C						-1.58
SEQ ID NO 287	YLR327C		-2.10	1.04	2.48		
SEQ ID NO 289	YLR346C				1.79		
SEQ ID NO 291	YLR390W	ECM19	2.77				
SEQ ID NO 293	YLR414C						-1.67
SEQ ID NO 295	YML053C			2.80			
SEQ ID NO 297	YML128C	COX14			1.81		
SEQ ID NO 299	YML132W	COS3			1.42		
SEQ ID NO 301	YMR009W				-2.17		
SEQ ID NO 303	YMR011W	HXT2			-1.86		
SEQ ID NO 305	YMR043W	MCM1	2.15	2.56	1.16		
SEQ ID NO 307	YMR099C				1.63		
SEQ ID NO 309	YMR107W		-6.48	5.88			
SEQ ID NO 311	YMR110C				1.53		
SEQ ID NO 313	YMR173W	DDR48	-3.32	1.58		-2.07	
SEQ ID NO 315	YMR173W-A		-1.78	1.58	1.47	-2.07	
SEQ ID NO 317	YMR251W		-64.41				
SEQ ID NO 319	YMR251W-A	HQR7	-64.41		-4.19		-3.18
SEQ ID NO 321	YMR256C	COX7		3.79	2.18		
SEQ ID NO 323	YMR273C	ZDS1	2.42				
SEQ ID NO 325	YNL030W	HHF2	-3.97				-1.56
SEQ ID NO 325	YNL031C	HHT2			-5.69		

Sequence ID NO	ORF	GENE	30 min	1h	2h	3h	6h
SEQ ID NO 327	YNL112W	DBP2	2.82				
SEQ ID NO 329	YNL131W	TOM22	-9.70				
SEQ ID NO 331	YNL134C				1.52		
SEQ ID NO 333	YNL143C		1.12				
SEQ ID NO 335	YNL179C		2.88		-2.02		
SEQ ID NO 337	YNL338W		1.78	2.79	1.62	-2.87	
SEQ ID NO 339	YNA002C	FUN34			-1.87		
SEQ ID NO 709	YOL052C-A	DDR2				1.65	
SEQ ID NO 341	YOL106W			3.51	2.44		
SEQ ID NO 343	YOL109W	ZEO1			-3.45		-1.87
SEQ ID NO 345	YOL126C	MDH2		1.91		-3.11	
SEQ ID NO 347	YOL139C	COC33			2.17		
SEQ ID NO 349	YOL150C		17.69				
SEQ ID NO 351	YOL151W	GRE2	9.20				
SEQ ID NO 353	YOR120W	GCY1			-1.46		
SEQ ID NO 355	YOR121C		1.54	3.40	1.63		
SEQ ID NO 357	YOR122C	PFY1			1.40		
SEQ ID NO 359	YOR131C		2.81				
SEQ ID NO 361	YOR261C	RPN8		2.59	1.54		
SEQ ID NO 363	YOR267C		1.78	1.07	-1.10		
SEQ ID NO 365	YOR285W		-2.15				-1.21
SEQ ID NO 367	YOR286W		-18.36				
SEQ ID NO 369	YOR327C	SNC2					-1.66
SEQ ID NO 371	YOR373C	NDD1	2.19	1.92			
SEQ ID NO 373	YOR374W	ALD4		-12.93			
SEQ ID NO 375	YOR382W		4.02				
SEQ ID NO 377	YPL037C	EGD1	-5.83				-2.17
SEQ ID NO 379	YPL078C	ATP4	-4.50		1.22		
SEQ ID NO 381	YPL079W	RPL21B					-6.18
SEQ ID NO 383	YPL085W	SEC18	2.28				
SEQ ID NO 385	YPL089C	RLM1	1.94	2.74	1.22		
SEQ ID NO 387	YPL190C	NAB3	2.80				
SEQ ID NO 389	YPL201C		-3.57				
SEQ ID NO 391	YPL271W	ATP15			2.40		
SEQ ID NO 393	YPR028W	YIP2	-12.41				
SEQ ID NO 395	YPR035W	GLN1			-2.78		

TABLE 8

C. albicans 522 CDS's					S. cerevisiae 11645 CDS's		
aa	codons	frequency, per thousand	total number	codon chosen for synthCaiBAX gene	codons used in wt muBAX gene	frequency, per thousand	total number
Ala	GCU	30.7	8686	x	6	21.1	118595
	GCC	12.7	3582		4	12.6	70785
	GCA	15.4	4367		2	18.2	91018
	GCG	2	578		1	6.1	34546
Arg	CGU	5.9	1682	x	1	6.5	36518
	CGC	0.7	204		1	2.6	14571
	CGA	3.5	989		3	3	16957
	CGG	0.8	220		3	1.7	9801
	AGA	23.6	6673		1	21.3	119672
	AGG	2.7	769		2	9.3	52057
Asn	AAU	37.9	10731	x	1	36	202351
	AAC	18.7	5293		2	24.9	140194
Asp	GAU	43.6	12323	x	5	37.3	212658
	GAC	14.7	4152		7	20.4	114451
Cys	UGU	9.7	2757	x	1	8	44797
	UGC	1.7	493		1	4.7	26357
Gln	CAA	35.2	9964	x	1	27.5	154529
	CAG	6.9	1948		8	12.2	89463
Glu	GAA	49.5	14001	x	3	45.9	257930
	GAG	11.5	3252		10	19.1	107568

TABLE 8 - continued

TABLE 6 - continued

C. albicans 522 CDS's					S. cerevisiae 11645 CDS's			
aa	codons	frequency: per thousand	total number	codon chosen for		codons used in		total number
				synthCaBAX gene	wt muBAX gene	frequency: per thousand		
Gly	GGU	33.5	9492	x	2	23.9	134515	
	GGC	4.5	1281		7	9.7	54629	
	GGA	13.7	3874		2	10.9	61481	
His	GGG	7.7	2182		8	6	33627	
	CAU	14	3964			13.7	77260	
	CAC	5.8	1642			7.8	43878	
Ile	AUU	39.9	11281	x	3	30.2	169795	
	AUC	14.2	4005		7	17.1	96126	
	AUA	12.3	3478			17.8	100027	
Leu	UUA	1	295	x		26.3	148133	
	UUG	36.1	10204			2	27.1	152590
	CUU	9.8	2777			2	12.2	68479
	CUC	2.5	694			7	5.4	30218
	CUA	4	1133			1	13.4	75414
Lys	AAA	48.6	13760	x	2	42.1	236746	
	AAG	19.4	5477		6	30.8	173174	
Met	AUG	18.4	5219	x	8	20.9	117410	
Phe	UUU	28.6	8100	x	4	26	146355	
	UUC	15.9	4486		7	18.2	102389	

TABLE 8 - continued

C. albicans 522 CDS's				S. cerevisiae 11645 CDS's		
aa	codons	frequency, per thousand	total number	codon chosen for synthCaBAX gene	codons used in wt muBAX gene	total number
Pro	CCU	13.2	3722		1	76366
	CCC	3.6	1027		5	38247
	CGA	26.6	7531	x		102277
	CCG	2.4	686		1	29758
Ser	CUG	3.1	875		9	58583
	UCU	23.3	6595	x	1	132608
	UCC	10.3	2928		4	79928
	UCA	24.6	6955			105570
	UCG	6.5	1836		1	48186
	AGU	23.6	6673			79648
	AGC	4.5	1269		5	54330
Thr	ACU	30.7	8889		1	113634
	ACC	13.9	3928	x	8	70777
	ACA	17.4	4928		5	99759
	ACG	3.6	1019		1	44817
Trp	UGG	11	3115	x	6	58092
Tyr	UAU	24	6782			105489
	UAC	11.6	3280	x	2	82483
Val	GUU	33.2	9391		1	123726
	GUC	10.3	2927	x	3	65203
	GUA	8	2265			66100
	GUG	10	2842		7	60033

TABLE 9: Regulation of 23 selected "Bax-specific" functions

<i>Cellular role: Amino-acid metabolism</i>					
ORF	Gene	Control	Bax	H2O2	B vs C
YOR302W	YOR302W	11541.92	26806.35	5595.74	2.32
<i>Cellular role: Cell stress</i>					
ORF	Gene	Control	Bax	H2O2	B vs C
YML028W	TSA1	12889.91	2168.45	11327.36	0.17
<i>Cellular role: Chromatin/chromosome structure</i>					
ORF	Gene	Control	Bax	H2O2	B vs C
YBR009C	HHF1	2149.89	8855.43	2909.14	4.03
YDR224C	HTB1	13661.40	55656.34	18829.27	4.07
YNL030W	HHF2	8676.99	19603.93	4732.39	2.26
<i>Cellular role: Energy generation</i>					
ORF	Gene	Control	Bax	H2O2	B vs C
YBL099W	ATP1	2728.21	8786.71	1644.48	3.22
YGR183C	OCR9	23181.54	81865.40	24053.00	3.53
YJL186W	OCR8	5296.71	18093.93	5001.65	3.42
YLR038C	COX12	7336.65	19935.69	5118.43	2.72
<i>Cellular role: Signal transduction</i>					
ORF	Gene	Control	Bax	H2O2	B vs C
YHR135C	YCK1	3939.64	8358.11	3707.17	2.12
YOL100W	PKH2	2218.45	6088.96	2619.31	2.74
<i>Cellular role: Transcription factor</i>					
ORF	Gene	Control	Bax	H2O2	B vs C
YDR216W	ADR1	5925.91	18459.00	6434.43	3.11
<i>Cellular role: Unknown</i>					
ORF	Gene	Control	Bax	H2O2	B vs C
YDR504C	YDR504C	2741.47	6908.49	2839.62	2.52
YGR146C	YGR146C	2099.74	5616.94	1303.89	2.68
YGR236C	SPG1	17717.80	64439.96	24134.29	3.64
YHR138C	YHR138C	6218.30	14817.41	5220.50	2.38
YJL142C	YJL142C	6988.27	16006.02	6740.46	2.29
YKL123W	YKL123W	2826.82	5952.34	2766.04	2.11
YLR414C	YLR414C	4510.80	11867.69	3531.27	2.63
YMR107W	YMR107W	13453.15	78850.98	17417.00	5.86
YOL099C	YOL099C	3690.45	11604.72	5454.15	3.14
YPL201C	YPL201C	15960.14	33633.74	7449.66	2.11
YJL060W	YJL060W	8798.50	2406.38	6356.11	0.27

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CLAIMS

1. An isolated nucleic acid representing a synthetic BAX-gene selected from the group consisting of:
 - 5 a) a nucleic acid comprising a sequence as represented by SEQ ID NO 1,
 - b) a nucleic acid comprising a fragment of a sequence of SEQ ID NO 1 and encoding a functional fragment of the sequence represented by SEQ ID NO 2,
 - c) a nucleic acid comprising a sequence as represented in any of SEQ ID NOs 3 to 10,
 - d) a nucleic acid which is more than 75 % identical to the nucleic acid as represented by
10 SEQ ID NO 1, or to a nucleic acid according to the nucleic acid as defined in b) or c), and,
 - e) a nucleic acid as defined in any one of (a) to (i) interrupted by intervening DNA sequences,
or a nucleic acid representing the complement of any of said nucleic acids as defined in (a)
15 to (d).
2. An isolated nucleic acid according to claim 1 which is DNA, cDNA, genomic DNA, synthetic DNA, or RNA wherein T is replaced by U.
3. A vector comprising a nucleic acid as defined in claim 1 or 2.
4. A vector according to claim 3 which is an expression vector wherein said nucleic acid
20 sequence is operably linked to one or more control sequences allowing the expression in prokaryotic and/or eukaryotic host cells.
5. An expression vector according to claim 4 which comprises an inducible promoter
6. An expression vector according to claim 4 or 5 which comprises a sequence encoding a reporter molecule.
- 25 7. A vector according to any of claims 3 to 6 for inducing programmed cell death in *Candida* spp.
8. A host cell transformed, transfected or infected with a vector according to any of claims 3 to 7.
9. A host cell of claim 8 which is a bacterial, yeast or fungal cell.
- 30 10. A host cell according to claim 8 or 9 wherein said cell is a *Candida* spp. cell.
11. A genetically modified yeast or fungal cell according to claim 9 wherein said modification results in the onset of at least one pathway eventually leading to programmed cell death.

12. A genetically modified *Candida* spp. cell according to claim 10 wherein said modification results in the onset of at least one pathway eventually leading to programmed cell death.
13. A method for identifying Bax-resistant yeast or fungi comprising the steps of:
- a) providing (a) genetically modified yeast or fungi according to claim 11,
 - 5 b) treating said genetically modified yeast or fungi with a mutagen,
 - c) isolating resistant yeast or fungal cells, and,
 - d) optionally identifying and/or characterizing mutated genes in said resistant yeast or fungal cells.
- 10 14. A method for identifying *Candida* spp. sequences which are differentially expressed in a pathway eventually leading to programmed cell death using a nucleic acid as defined in claim 1 or 2, a vector according to any of claims 3 to 7 or a genetically modified host cell according to claim 10.
15. A method for obtaining and identifying *Candida* spp. sequences involved in a pathway eventually leading to programmed cell death comprising the steps of:
- 15 a) providing a two hybrid system wherein a polypeptide encoded by a nucleic acid according to claim 1 or a vector according to any of claims 3 to 7 as a bait and a *Candida* spp. cDNA library as a prey are expressed,
 - b) detecting an interaction between said polypeptide and a *Candida* spp. polypeptide encoded by said cDNA library, and,
 - 20 c) identifying said *Candida* spp. polypeptide or cDNA.
16. A method for identifying inhibitors (or inhibitor sequences) of Bax-induced cell death comprising the steps of:
- a) providing a genetically modified organism according to claim 10,
 - b) expressing a cDNA library in said genetically modified organism, and,
 - 25 c) identifying a polypeptide or a cDNA which expression has a beneficial effect on the survival and/or growth of said genetically modified organism.
17. A method according to claim 16 wherein said genetically modified organism is a *Candida* spp.
- 30 18. An isolated *Candida* spp. nucleic acid identifiable by any of the methods of any of claims 12 to 17.
19. An isolated *Candida* spp. nucleic acid according to claim 18 selected from:

- (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 434, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a functional equivalent, derivative or bioprecursor of said protein,
- b) a nucleic acid encoding a protein having an amino acid sequence which is more than 70 % similar to any of the amino acid sequences represented in SEQ ID NOs 434, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732,
- c) a nucleic acid encoding a protein having an amino acid sequence which is more than 70 % identical to any of the amino acid sequences represented in SEQ ID NOs 434, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732,

- d) a nucleic acid comprising a sequence as represented in any of SEQ ID NOs 433, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 717, 719, 721, 723, 725, 727, 729 and 731,
- e) a nucleic acid which is more than 70 % identical to any of the nucleic acid sequences as represented by any of SEQ ID NOs 433, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 717, 719, 721, 723, 725, 727, 729 and 731, and
- f) a nucleic acid encoding a functional fragment of any of the nucleic acid sequences as specified in any of a) to d),
20. An isolated nucleic acid as defined in according to claim 19 which is DNA, cDNA, genomic DNA, synthetic DNA, or RNA wherein T is replaced by U.
21. An isolated nucleic acid capable of selectively hybridizing to a nucleic acid as defined in any of claims 18 to 20 or the complement thereof.
22. An antisense molecule comprising a nucleic acid capable of selectively hybridizing to a nucleic acid as defined in any of claims 18 to 21.
23. A nucleic acid probe which selectively hybridises with any of the nucleic acid molecules as defined in claim 18 or 19.
24. A nucleic acid primer which selectively amplifies any of the nucleic acid molecules defined in claim 18 or 19.

25. An expression vector comprising a nucleic acid according to any of claims 18 to 22.
26. An expression vector according to claim 25 which is an expression vector wherein said nucleic acid is operably linked to one or more control sequences allowing the expression in prokaryotic and/or eukaryotic host cells.
- 5 27. An expression vector according to claim 25 or 26 which comprises an inducible promoter.
28. An expression vector according to any of claims 25 to 27 which comprises a sequence encoding a reporter molecule.
29. A host cell transformed, transfected or infected with the vector of any of claims 25 to 28.
30. An isolated nucleic acid according to any of claims 18 to 22 for use as a medicament.
- 10 31. An isolated polypeptide which is involved in a pathway for programmed cell death of *Candida* spp. and encoded by a nucleic acid as defined in claim 18 or 19, wherein said polypeptide is selected from:
- (a) a polypeptide having an amino acid sequence as represented in any of SEQ ID NOs 434, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428,
- 15 430, 432, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590,
- 20 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a polypeptide having an amino acid sequence which is more than 70% similar to any of
- 25 the amino acid sequences as represented by any of SEQ ID NOs 434, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540,
- 30 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632,

634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732,

- (c) a polypeptide having an amino acid sequence which is more than 70% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 434, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 569, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732, and
- (d) a functional fragment of any of said polypeptides as defined in a) to c).

32. A polypeptide according to claim 31 for use as a medicament.
33. An antibody capable of specifically binding to a polypeptide of claim 30 or to a specific epitope of said polypeptide.
34. An antibody according to claim 33 for use as a medicament.
35. A pharmaceutical composition comprising an antibody of claim 33 or 34.
36. Use of an isolated nucleic acid encoding a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi and which nucleic acid is selected from:
- (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396,

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- (b) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% similar to any of the amino acid sequences as represented by any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732,

- (c) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 569, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732,
- (d) a nucleic acid comprising a sequence as represented in any of SEQ ID NOs 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415,

- 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 691, 693, 695, 697, 699, 701, 703, 705, 707, 709, 711, 713, 715, 717, 719, 721, 723, 725, 727, 729 and 731,
- 5 (e) a nucleic acid which is more than 70% identical to any of the nucleic acid sequences as represented by any of SEQ ID NOs 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 691, 693, 695, 697, 699, 701, 703, 705, 707, 709, 711, 713, 715, 717, 719, 721, 723, 725, 727, 729 and 731,
- 10 (f) a nucleic acid encoding a functional fragment of any of the nucleic acid sequences as specified in a) to e), and
- 15 (g) the complement of any of the nucleic acid molecule as specified in a) to f),
- 20 for the preparation of a medicament for treating diseases associated with yeast or fungi.
- 25
- 30
- 35

37. Use of an isolated polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi, said polypeptide being selected from:

(a) a polypeptide having an amino acid sequence as represented in any of SEQ ID NOs

18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60,
 5 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102,
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 15 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432,
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 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a
 25 functional equivalent, derivative or bioprecursor of said protein,

(b) a polypeptide having an amino acid sequence which is more than 70% similar o any

of the amino acid sequences as represented by any of SEQ ID NOs 18, 20, 22, 24,
 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68,
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 30 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142,
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 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210,
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 35 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 292, 294, 296, 298, 300, 302,

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- (c) a polypeptide having an amino acid sequence which is more than 70% identical to any of the amino acid sequences as represented by any of SEQ ID 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666,

668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732, and,

(d) a functional fragment of any of said polypeptides as defined in a) to c),

for the preparation of a medicament for treating diseases associated with yeast or fungi.

5 38. A pharmaceutical or fungicidal composition comprising a nucleic acid as defined in claim 36 or a polypeptide as defined in claim 37 together with a pharmaceutically acceptable carrier diluent or excipient therefor.

39. A vaccine for immunizing a mammal against yeast or fungal infections comprising at least one nucleic acid as defined in claim 36 or at least one polypeptide as defined in claim 37 in
10 a pharmaceutically acceptable carrier.

40. A genetically modified yeast or fungus in which modification results in the overexpression or underexpression of at least one of the nucleic acids as defined in claim 36 or the polypeptides as defined in claim 36, which overexpression or underexpression of said nucleic acid or polypeptide prevents, delays or sensitizes for apoptosis of said genetically
15 modified yeast or fungus.

41. A method of identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast or fungi or in metabolic pathways in which said polypeptides are involved, which method comprises:

20 (a) contacting a compound to be tested with a genetically modified yeast or fungus according to claim 40, in addition to contacting wild type cells with said compound,

(b) monitoring the growth and/or death rate and/or activity of said genetically modified cells compared to said wild type cells; wherein differential growth or activity of said genetically modified yeast or fungi cells is indicative of selective action of said
25 compound on a polypeptide in the same or a parallel pathway,

(c) alternatively monitoring the growth and/or death rate and/or activity of said genetically modified cells compared to genetically modified cells which were not contacted with the compound to be tested, wherein differential growth or activity of said genetically modified yeast or fungi cells is indicative of selective action of said
30 compound on a polypeptide in the same or a parallel pathway,

(d) alternatively monitoring changes in morphologic and/or functional properties of components in said genetically modified cells caused by the addition of the compound to be tested, and,

(e) identifying the compound.

42. A method of identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast and fungi or in metabolic pathways in which said polypeptides are involved, which method comprises:

- 5 (a) contacting a compound to be tested with yeast or fungal cells transformed, transfected or infected with an expression vector comprising an antisense sequence of at least one of the nucleic acid as defined in claim 36, which expression results in underexpression of said polypeptide, in addition to contacting one or more wild type cells with said compound,
 - 10 (b) monitoring the growth and/or death rate and/or activity of said transformed, transfected or infected cells compared to said wild type cells; wherein differential growth or activity of said transformed, transfected or infected yeast or fungal cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway,
 - 15 (c) alternatively monitoring the growth and/or death rate and/or activity of said transformed, transfected or infected cells compared to transformed, transfected or infected cells which were not contacted with the compound to be tested, wherein differential growth or activity of said mutated yeast or fungal cells is indicative of selective action of said compound on a polypeptide in the same or a parallel
 - 20 pathway,
 - (d) alternatively monitoring changes in morphologic and/or functional properties of components in said transformed, transfected or infected cells caused by the addition of the compound to be tested, and,
 - (e) identifying the compound.
- 25 43. A method of identifying compounds or polypeptides which bind to or modulate the properties of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi, which method comprises:
- (a) contacting a compound or polypeptides to be tested with at least one of the polypeptides as defined in claim 37,
 - 30 (b) detecting the complex formed between the compound or polypeptide to be tested and said polypeptide,
 - (c) alternatively, examining the diminution of complex formation between said polypeptide and a binding partner, caused by the addition of the compound or polypeptide being tested,

- (d) alternatively, examining the alteration in the functional activity of the polypeptide, caused by the addition of the compound or polypeptide being tested, and,
- (e) identifying the compound or protein.

5 44. A method for identifying compounds interacting with a polypeptide involved in a pathway eventually leading to programmed cell death of yeast and fungi comprising the steps of:

- (a) providing a two-hybrid screening system wherein a polypeptide of claim 37 and a protein interacting with said polypeptide or an interacting polypeptide obtainable by a method of claim 41, are expressed,
- 10 (b) interacting said compound with the complex formed by the expressed proteins as defined in a),
- (c) detecting a second complex, wherein the presence of said second complex identifies a compound which specifically binds to one of said polypeptide or to said second complex, and,
- (d) identifying the compound.

15 45. A method of identifying compounds which selectively modulate expression of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi which method comprises:

- (a) contacting host cells transformed, transfected or infected with an expression vector comprising a promoter sequence of a nucleic acid as defined in claim 36 joined in
20 frame with a reporter gene,
- (b) monitoring increased or decreased expression of said reporter gene caused by the addition of the compound being tested, and,
- (c) identifying the compound.

25 46. A method for identifying polypeptides involved in a pathway eventually leading to programmed cell death comprising the steps of:

- (a) providing a two-hybrid system wherein a polypeptide encoded by a nucleic acid according to claim 36 or a vector according to any of claims 3 to 7 as a bait and a yeast or fungal cDNA library as a prey are used,
- (b) detecting an interaction between said polypeptide and a yeast or fungal polypeptide
30 encoded by said cDNA library, and,
- (c) identifying said yeast or fungal polypeptide.

47. A method according to any of claims 41 to 46 wherein said yeast or fungus is chosen from *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Candida albicans*, or *Aspergillus fumigatus*.

48. A compound or polypeptide identifiable according to the method of any of claims 41 to 47.
49. A compound or polypeptide according to claim 48 for use as a medicament.
50. A method for preparing a pharmaceutical composition for treating diseases associated with yeast or fungi comprising admixing a compound or polypeptide according to claim 49 with a suitable pharmaceutically acceptable carrier.
51. A pharmaceutical composition comprising a compound or polypeptide according to claim 49 together with a suitable pharmaceutically acceptable carrier.
52. Use of a compound or polypeptide according to claim 48 or 49 or a pharmaceutical composition according to claim 51 or obtainable by the method of claim 50 for the preparation of a medicament for treating diseases associated with yeast and fungi.
53. A method for preventing infection with yeast or fungi comprising administering a composition according to claim 51 or obtainable by the method of claim 50 to a mammal in an effective amount to stimulate the production of protective antibody or protective T-cell response.
54. Use of an antibody capable of specifically binding to at least one of the polypeptides as defined in claim 37 or to a specific epitope of said polypeptide, for the preparation of a medicament for treating diseases associated with yeast and fungi.
55. Use according to any of claims 52 to 54 wherein said disease is associated with yeast or fungi, where the yeast or fungus is chosen from *Candida* spp., *Aspergillus* spp., *Microsporum* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis*, spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*, and *Sporothrix schenckii*.
56. Use of a compound or polypeptide according to claim 48 or 49 or a pharmaceutical composition according to claim 51 or a genetically modified organism as defined in claim 40 for the preparation of a medicament for modifying the endogenic flora of humans and other mammals.
57. A genetically modified mammalian cell or non-human organism in which modification results in the overexpression or underexpression of at least one of the nucleic acids as defined in claim 36 or a human homologue thereof or at least one of the polypeptides as defined in claim 37 or a human homologue thereof, which overexpression or underexpression of said nucleic acid or polypeptide prevents, delays or sensitizes for apoptosis of said genetically modified mammalian cell or in said genetically modified non-human organism.

58. A genetically modified mammalian cell or non-human organism according to claim 57 wherein said modification comprises the expression of an antisense molecule to at least one of the nucleic acids as defined in claim 36 or an antisense molecule to a mammalian homologue of said nucleic acid.
- 5 59. A method for identifying compounds for stimulating or inhibiting apoptosis comprising the use of at least one of the nucleic acids as defined in claim 36 or a human homologue thereof and/or at least one of the polypeptides as defined in claim 37 or a human homologue thereof and/or a genetically modified mammalian cell or non-human organism according to claim 57 or 58.
- 10 60. A compound identifiable according to the method of claim 59.
61. A compound according to claim 60 for use as a medicament.
62. A method for preparing a pharmaceutical composition for treating proliferative disorders or for preventing apoptosis in certain diseases comprising admixing a compound according to claim 60 or 61 with a suitable pharmaceutically acceptable carrier.
- 15 63. Use of a compound according to claim 60 or 61 for the preparation of a medicament for treating proliferative disorders or for preventing apoptosis in certain disorders.
64. Use of a nucleic acid selected from any of the nucleic acids as defined in claim 36 or a human homologue thereof for treating and/or preventing and/or alleviating proliferative disorders or for the prevention of apoptosis in certain diseases.
- 20 65. Use of a nucleic acid selected from any of the nucleic acids as defined in claim 36 or a human homologue thereof for the preparation of a medicament for treating and/or preventing and/or alleviating proliferative disorders or for the prevention of apoptosis in certain diseases.
- 25 66. Use of an antisense molecule to at least one of the nucleic acids as defined in claim 36 or an antisense molecule to a mammalian homologue of said nucleic acid for treating and/or preventing and/or alleviating proliferative disorders or for preventing apoptosis in certain disorders.
- 30 67. Use of an antisense molecule to at least one of the nucleic acids as defined in claim 36 or an antisense molecule to a mammalian homologue of said nucleic acid for the preparation of a medicament for treating and/or preventing and/or alleviating proliferative disorders or for preventing apoptosis in certain disorders.

68. Use of a polypeptide selected from any of the polypeptides as defined in claim 37 or a human homologue thereof for treating and/or preventing and/or alleviating proliferative disorders or for the prevention of apoptosis in certain diseases.
69. A pharmaceutical composition for use as a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases comprising a nucleic acid molecule as defined in claim 36 or a human homologue thereof or an antisense molecule to at least one of the nucleic acids as defined in claim 36 or an antisense molecule to a mammalian homologue of said nucleic acid or a polypeptide as defined in claim 37 or a human homologue thereof together with a pharmaceutically acceptable carrier diluent or excipient therefor.
70. A vaccine for immunizing mammals against proliferative disorders or for preventing apoptosis in certain diseases comprising least one nucleic acid as defined in claim 36 or a human homologue thereof or at least one polypeptide as defined in claim 37 or a human analogue thereof in a pharmaceutically acceptable carrier.
71. Use of an antibody capable of specifically binding to at least one of the polypeptides as defined in claim 37 or to a human homologue thereof or to a specific epitope of said polypeptide or said human homologue, for the preparation of a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases.
72. An expression vector comprising a human homologue of a nucleic acid as defined in claim 36.
73. An expression vector according to claim 72 which is an expression vector wherein said nucleic acid sequence is operably linked to one or more control sequences allowing the expression in prokaryotic and/or eukaryotic host cells.
74. An expression vector according to claim 72 or 73 which comprises an inducible promoter.
75. An expression vector according to any of claims 72 to 74 which comprises a sequence encoding a reporter molecule.
76. A host cell transformed, transfected or infected with the vector of any of claims 72 to 75.
77. An isolated nucleic acid comprising a human homologue of at least one of the nucleic acids as defined in claim 36.
78. An antisense molecule comprising a nucleic acid sequence capable of selectively hybridising to the nucleic acid molecule of claim 77.
79. A polypeptide encoded by a nucleic acid of claim 77.

Figure 1:

YBL002W, 896 bp, CDS: 501-896 (SEQ ID NO 21)

TGTTTGGATATTAAGTAGTCATGTTGTAATCTCTGGCCTAAGTATACGTAACGAAAATGGTA
GCACGTCGGGTTTATGGCCCCCAGGTTAATGTCTTCTCTGAAATTGCGATCACTTTGAGA
AATAATGGGAACACCTTAAGCGTGAGCTGTGCCCCACCGCTTCGCCTAATAAAGCGGTGTT
CTCAAAATTTCTCCCCGTTTTTCAGGATCAGGACCCGCCATCTAGTTCTGGTAAAATUGCGC
TTACAAGAACAAGAAAGAAACATCCCCGTAATGCCAAGTGAAGACACTTGGCGTCATAT
ATAAGGTTTTTGGATCAGTAACCGTTATTTGAGCATAACACAGGTTTTTAAATATATTATT
ATATATCATGGTATATGTGTAAAATTTTTTTGCTGACTGGTTTTGTATTATTATTACCT
TTTAAAAATTTTACTTTCTTCTGTAAATTTTTTCTGATTGCTCTATACTCAAACCAAC
AACAACCTTACTCTACAACATACTCTCTGCCCCGAAAGAAACCAGCTTCCAAAGCTC
CAGCTGAAAAGAAAGCCAGCTGCCAAGAAACATCAACCTCCGTGATGGTAAGAAGAGAT
CTAAGGTTTGAAGGAGACCTATCCCTCTTATATTATCAAAAGTTTGAAGCAAACTCAC
CAGACACTGCTATTTCOCAGAAAGTCTATGTCTATTTTGAAGTCTTTCGTCAACGATATCT
TTGAAAGAATTGCTACTGAAGCTTCTAAATTCGGCGCTTATAACAGAAATCCACTATTT
CTGCTAGAGAAATCCAAACAGCCCTTAGATTGATCTTACCTGGTGAATTGGCTAAACATC
CCGTCCTCGAAGGTACTAGGCTCTTACCAAATACTCCTCCTCTACTCAAGCCTAA

YBL002W, 131 aa (SEQ ID NO 22)

MSSAAEKKPKASKAPAEKKPKAARKTSTSVDGKKRSKVRKETYSSYIYKVLKQTHPDTGISQ
KSMSILNSFVNDIFERRIATEASKLAAYNKKSTISAREIQTAVRLILPGELAKHAVSEGTR
AVTKYSSSTQA

YBL064C, 1286 bp, CDS: 501-1286 (SEQ ID NO 25)

TTGCCAACCTCAAAGAAGAAGAATTATGGGCATATTGACCTTCTCCGGTTTCCCTCCCGC
GCTCTCGTATCCCTCTGCATTTCACCTCCGAGCAAGCGCTCCACTATCTCTATATCTTTAC
CAGTAAAACCTTTTAACGTTTTGTGATATTTTGAACCTCAACCCACATTCAGTATGCGGTG
TCTATATAAAGATATTTCTGATAGCACTATGTTTATCTTTATACAATATACAAAAGCTCA
CCCAGGACGAGCAGCGCGGCTATTTTTCTATCATTTCCGTGAATAGCGACCAACGGTCCGC
GCTATTTTATTTTGTGCAATTTTTTCGGGATGGGTTCCTCCGCCAAAAGCTAGCCCCGGA
GATTTTTTAATTACGTAAAGAAACAAGGGCCCGGATGTTCTGCTATTGGTATATAAAGAG
AGAAGGAGACATATAGAAAATTGTGCTTCTAGATTCTCGCAGTAGGATGAGATAAATTTTC
AAAGAAGCAGGAAGCAAGGATCTTTAGTGAATTTGTAGCGCTCAATTAAAGAGGACGCG
CATGGACCTTTCTTAAGCAGGCTCACTTGCATCACAGACGATTAAACATTTGCCACAG
CACCTATTTCTGTCCAAACATTTCAACCAAGTGATCAACCAAGACTAAGAATAAACTCTG
ATGCTCTTAACTTTTATGCTGACACAAAGGTTGGTAAAATCAATTTTACGACTACTTGG
GCGACTCTTGGGGGGTCTTGTTTTTCTACCCAGCAGATTTCACCCCTGTCTGCACCAACCG
AAGTCAGCGCATTCGCCAATTGAAACCCCAATTCGACACAGAGAAATGTTAAATGATCG
GGCTTTTCACTGCAAGATGTTGAGTCCACGAAAAATGGATTCAAGACATCAAGGAATAG
CAAAGGTTAAAATGTTGGTTTTCCCAATTAATTGCTGACACTTTTAGAAACGTGGCATTC
TATATGATATGCTAGATGCCGAGGATTCAAAAATATCAATGATGGGTCACTGAAGACCG
TGAGGTCTGTCTTCGTCAATCGATCCCAAGAAAGATTAGACTGATTTTTACCTACCCCT
CCACCGTCGGAAGAAACACTTCTGAAGTGTAAAGGGTAATCGACGCTTGCATTTGACTC
ACAAGCAAGGGGTAGTAACCTCAATTAATTGCGACCCAGCTGACGATGTCATTATTCCTC
CCTCTCTCTCAATGATGAGGCGAAGGCTAAATTTGGTCAATTTAATGAAATTAAACCTT
ATTTAAGATTCAACCAAGTCAAGAAATAA

YBL064C, 261 aa (SEQ ID NO 26)

MPSRICSAQLKREAWTLPEKAHLQSQTIKTFATAPILCKQFKQSDQFRLKENSDAFNFDA
DTTVGKINFYDYLGDSWGVLFSPFADETFVCTTEVSFAFKLKPEPDKRMVKLIGLSVEDV
ESHEKNIQDIKETAZYKKNVGFPITGDTFRNVAFLYDMVDABGFKNINDGSLKTVRSVFVI
DPKKKIRLIFTYPSTVGRNDSSEVLRLVIDALQLTDKEGVVTFINWQPADUVCIIPPSVSNDE
AKAKFGQFNEIKPYLRFLKSK

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YBR089C-A, 800 bp, CDS: 501-800 (SEQ ID NO 47)

TTTTCTAGCTGGCGCGGCAACTATAAAGTACAGCAAGTGAGGTTGAGGCAATACCTGGGAG
 TTTACACTATCGGGAGACAGCTCCTAACACCAAGCAGAAAAACGACTTTTTCGCAAGTAT
 GTAAGGCGCTGGGTGAGUCCAGCGGACGAGGATGSEUTTAATAAGAAGCTACAGTTTAGC
 ACAGCTAGAACAGCATAACCTAAGGGCAACTCTGCTTTTCCGAGAACTTAAAGAGGGG
 TAGACAATGATGGTAATCTTATAAACCAGGCTACAAAGAAGGTTGTAGCAGCAAGGAAGAT
 GATATTTTAAATACGCTTCAGGTGAAATGAATAGCTCGCCCATACCGGCATGCTCAACTTG
 TAACTCAGGACTCTAGCTTTCTACTGTACTATCCTCTAAAGGACTGCTGTTCTGTGCACC
 CCTTCTCTTTGTTTATCATAGCGCACGACAAGAGTACTAACTAATTAACCTTAGAACAATTA
 ACATATATAAACTAGCGCTATGGCCGCAACTAAAGAAGCAAAAGCAACCAAGGAACCAA
 AGAACAGGACCAACAGGAGAAAAGAGCATCCTAACGCCCTTAGGACCCGGTTGTCTAGCTT
 ATATGTTCTTTGCTAATGAAAACAGAGACATTGTCCGTTCGAGAACTCTTGACGTAACTT
 TTGGCCAAAGTAGGCAGAAATATTGGGTGAGAGGTGGAAAGGCCTTAAGTGTGAAGAAAAGC
 AACCTTATCAATCTAAGGCTCAACGACACAAGAGAGATACGAATCTGAAAAGGAATTGT
 ACAATGCTACACGTGCTTGA

YBR089C-A, 99 aa (SEQ ID NO 48)

MAATKEAKQPKPKKRTTRKKLPNAPKRLSAYMFFANENRDLVRSENPDVTFGQVCRZ
 LGERWKALTAEEKQPYESKAQADKKRYSEKELYNATPA

YBR149W, 1535 bp, CDS: 501-1535 (SEQ ID NO 57)

TTTCGCAAAACATCAACTTCTCCTTAATCGACCAACTGACAATGAAGTTTCAGGTTCTACGAG
 AGATCTCGCAATTTCCAGAAGGAAACAATAGGTGGGTAAAGAATGATCCTACCAAGATAAG
 GATAACTATATCAAAACACTGATGCAACATTTGAAGAAAAAGAGAGTACAAAGTTGATA
 AAAGACAGCAAGATGGCGCTCCACCTTAACATCTTAACAATTTGCTTTACTGAAAAATG
 CTACTAGTATATAATCATTAAGTAICTAACTATCACTCAATAAAAATATTATAGATCGCT
 TAAAAACTCCTTTATTCGGATTATAAATCCACCAAAAGCCGCTCTACCTTACCTCCGC
 CTGGAAAAATTATATATATAAAGTGAGCTCGTAATACAGGGCTAAAAAGGAAGAGGG
 GGATATCAAGCATCTGGACTTAATTCGCACTAGCTCCGCCCTTAATTGAATAAAGCCTCTT
 GATTTTAAATCAACTGCTATCATGTCTCTTCAGTAGCCTCAACCGAAAAACATAGTCGAAA
 ATATGTTGCATCCAAAGACTACAGAAATATACTTTTCACTCAACAATCGTCTTCCGTATCC
 CAGCACATGGGTTTGGGACAGCAAACTCTCAGGAAAAGTTAGCTGAAACAAAACAGCCCG
 TAAAAGCTGCAATCAAGCTGGATAAAGGCACAATGATAUTGCTTGGGCTACGAGACAG
 AGCCATTCGTAGGTGAAGCCATCAAGGAGTTAATTAGAAGATGGATUTATCAAAAGCCACC
 ATCTTTTTCATAACCACAAAAGTGTGCGCGGTTCTATGGGACGAAGTGGACAGATCATTGA
 ATGAATCTTTTGAAGCTTTTAGGCTTGGAAATACGTGACTTCTCTTGCACATTGGCCCGC
 TATGTTTTTGAAGAGATTAAGGACCCTAAGGGGATCAGCGGACTGGTGAAACACTCCCGCTTC
 ATGATCTCTGAAAAACAATCTATGCTGCGGACGCTGACTATTTAGAAACTTACAAGCAAT
 TGGAAAAAATTTACCTTGTATCTTAACGATCATCTGATGAGAGCAATTTGGTGTCTCAAAAT
 TTTCCATTGAGTATTTGGAACGCTCTCATTAAGGAATGCAGASTTAAGCCAAACGGTGAACC
 AAGTGGAAACTCACCTTCTTACCAAAAATCGAACTAAGAAAAGTTCTGCTTTTATGCACG
 ACATTCCTGTAAACAGCATACTCACCATTAGGTTCCCATGGCCCAACCAACTTGAAATCC
 CACTAGTGA AAAAGCTTGGCGAAAAGTACAATGTCAAGGAAAATGACTTTGCTAATTCTT
 ACCATATTAGACAAGGCACTATCGTAATTCCGAGATCCTTGAAATCCAGTTAAGGATTTCCCT
 CGAGTATTCGAATTCGCATCTTTGACAAAGGATGAATTACAAGAGTTGAACGACTTCGGTG
 AAAAATACCCAGTGAGATTCTCGATGAGCCATTTGCAGCCATCTTTCCAGAGTTTACTG
 GAAACGGACCAAACTTGGACAATTTAAAGTATTAA

YBR149W, 344 aa (SEQ ID NO 58)

MSSSVASTENIVENMLHPKTTETVYFSLNNGVRIPALGLGTANPHEKLAETKQAVKAAIKA
 GYRHIDTAWAYETEPFVGRAIKELLEDGSTKRECIETTKWVPLWDEVDRSLNESKAL
 CJFYVHLLQHWPLCFEKIRDPXGISGLVKTFVEDSGKTHYAADGDYLETYKQLEKLYLD
 PNDHRVRAIGVSNFSIEYLERLIKECKVKFIVNQVETHPHLPQMELEKFCFPHDILITAY
 SPLGSHGAPNLRIPLVKKLAEKYNVTGNLLISYHIROGTIVIPRSLNPVKYSSSEFAS
 LTKDELQELNDFCEKYPVRFTDRPFAAILPFTGNGPNLDNLKY

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YBR289W, 3218 bp, CDS: 501-3218 (SEQ ID NO 63)

GATACGATCTATAGTCTCTAAAAAGGTAAAACAATCAAGCGGGCTTTTGACTTCGAAGT
GGAGGCTAAGCACCAG/AAATTGAGCTTATTTATAACTGAGAAATACTTATAGACCTCTAA
ATCTCTTCCAAACCATTGAATGGTCTAAATAATCATCACTACTGCTATCTTCGAGCAATTG
AGGACATGTGTACGAACGGGATCCACAGCTCCCTGAAGGAGGGAGCTGTTCACCTAA
AAGATACTCGAAAATAAGTTTGTCTTTGTATCAGTGATATAGAAATGACAAATACATCTFA
TTTTGGTTGGGTGGTAAGGTTTACAGCCTCTGTTGTTGCCCAAGTCCCTGTTATCGCCAA
CTTTAAATAAATCTCTTCTTGTCTTTGACCAAAAATTTCAATTTTCGTCCGATTTAAAA
GAAACTGAAATTTCAACATAAACACCAAAACAAAGCATCATCAAGGGAACATATAGTAA
ACAACCTACAAAAAGCAACAATGAATAATCAGCCGAGGGTACCAACAGCGTTTCCAAATA
GTATTGGAAATATATTTAGCAACATTGGAACTCCATCTTTTAACATGGCGCAAAATTCGCG
AACAGCTGTATCAGAGCCTCACACCACAACAAATTGCAGATGATTGAGCAACGACACCAAC
ACTTACTCAGGAGTCTCTACACACACAAACAACAACAACAACAACAACAACTTCAACGCCAC
CGCAAAACCCATCAATCTCCACCCCTCTCTCGCAACAATCTCAACCCATTGCTAATCAAT
CAGCGACTTCTACCCCTCTCTCTCTCTCCAGCACCACTTACATCCCCAAATTTGGTC
AAGTGCCCTTAGCTCCAGCGCTTATTAATTTGCCTCCACAAATTCCTCAGTTACCTTTGG
CTACACAGCAACAAGTTTGAACAAGTTGAGGCAGCAGGCCATAGCAAAAAATAATCCAC
AGGTTGTCAATGCAATTACTGTTGCACAACAAGTGCAACGCCAAATTCAGCAGCAAA
ACGCACACCAAAACGGCACAACTCAGCTAGAACAGCAGAGGCAATTGCTGGTTCAACAGC
AACAGCAGCAGCAACTTAGAAACCAATACAGCTACAAACAGCAACAACAGTTTAGGCATC
ATGTGCAAAATACAACAGCAGCAACAAAAGCAACAACAACAGCAGCAGCAGCATCAGCAAC
ACAACAACAACAACAGCAACAGCAGCAACAGCAACAGCAACAGCAACAGCAACAGCAAC
AGCAACAACAACAACAACAGCAGCAGCAGCAGCAGCAGCAAGGACAAATACCGCAAT
CTCAGCAAGTTCTCAAGTTAGATCCATGAGTGGACAACTCCACCAATGTTTCAGCCCA
CTATTTGGCCAACTTCTTCAATTTCCAAAATTTAAACTTTACCCAAAGTACCAAACTATTCAAT
ACGATCCACCAGAAACCAAGCTACCATATCCAACTTATTEGTCAGACAAAAAGCAGATA
CGGATACTTTGTTGTACGAACAAATTTATCCAGCGTGATAAAATTAACAAATATTGCGCTAA
TAAGAGAAACCAATGGTTACGATCCGTTTAGCATTTATGGATTAGTAATAAAGAGTATA
TTAGTAGACTGTGGCATACTGAAGTATTATCAAGATTTGAAGAACACTAGAATGAAT
CTATCAACAAGCACTTCTCAGAAGATTCCTTCGGCAAGTATTTGGGGAAATGGTTACTCAG
GGTATGGTAATGGGATTACGAATACAACCTACCAGAGTTATTCACAAGTGAAGGTGGAA
ATAGGAAGCATTACCTAGAGGATAAATTTAAAACCTATATAACAGGCCATGAATGAGACAT
CGGAACAGTTAGTTCCCATAGATTGGAGTTGGATCAAGATCGTGACAGATTCTTCTCTA
GGGACACTTCTTATGCAACAAAAATGACAAGCTTATTTAAANTGACACTTTCTCCACG
ACATGTTGCGAGATTACCGATTTGAGGACGCTACGAGAGAGCAACACATTGATACTATTT
GTCAATCTATACAAGAGCAGATTCAAGGATTTCAAGGAAATCCATATATAGAGTTGAATC
AGCACCGTCTAGCCGCTGATCACTTCACAAATTAGTATCAAGCTGGATTTCTCTCTGGAC
AAAACCAATTAATCGATCAATTTGAGTGGGAGATCTCTAATAGTGATAACTGTCCAGAAG
AGTTTGCAGAGTCCATGTGTCAAGAATTAGAATACUAGGTAAGTTTGTGACTGUCATTG
CTCACTTCATAAGAGAGCAAGTTCAATGTATCTATAATCCTACCTGGCAGTGTAGGTTACA
ATTTTGAITGGATCAGCGATAGAAGATGATGACATFAGAAGCAGAATGCTCCCAACGATTA
CTCTTGATGATGTTTATAGGCCTGCAGCGGAAGCAAAATTTTACTCCAAACCTATTAC
AGATTTCACTGCAGACTTAGACAGATTGGATAAAGATAAGGACAGAGACACAAGAAGGA
AAGAAGACAAAGGTAGATCTAATAGACGTGGTATGCTGUCATTCTCCGGCACATCTGCAA
GTAATACATCTATGAACGGCGTTCAACAACAGTAGCAGCAGCAAAATGCTTCATCGTTGC
CAUCAGGAGAGATTTTACTGCCAGATATTGCAGATATTCCAAGAAGTTTCAGGACTCCAG
TACCTAGCACTTTAATGCCTGGTGGTGTGTTGACGTAGGCCCTTCTGTGGAATCGTACGAAT
TGAGAAACACAAACCACTTATAAAGCAGGCCAGATAGACCTAAGCCAGTTTCACTTCTTT
GTTATATTATTGACCATATTCCGGGTCAATTCCCTACTAATTCTATTTAAATGCTTGAAGA
AAGTTAATACAAAAGAGAGTTCCGAGCAGCGCCCAATGACACAAGTAGTGGCACCAATG
CAATGCTTCCCACTCCCAATCCCTCAAACTAAGCTGAATACTAACATTCCGCGCTCGTG
TGACGATACCTTCAATCCCAACCCGATTGCCAATCACACTGTTACTAATTACCCCAATC
CCACACTGCAGCCAGTAATCCAGGTGGGGCAGCTAGTAAATCGGTACCTACACCTAGTC
TTCCTATAGCACTCCAGTAGCACCATGATAGCCAAAGCAGACTTTGTTGACTAATAGCA
ATAATGGTAGCAGTAACAATAACACACAGAAATACATAG

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Y3R289W, 905 aa (SEQ ID NO 64)

MNNQPPQGTNSVPNSIGNIFSNIGTPSPNMAQIPQQLYQSLTFQQQLQMLQQQRHQQLLSRL
 QQQQQQQQQTSPPPQTHQSPPPPPQQSQPTANQSATSPPPPPPA7HKI,HPQTGGVPTA7A
 PINLPPOIAQLPLATQOQVLNKLRRQQAIAKNFQVWNAITVAQQQVQRQIEOQKGGQTAQ
 TQLEQQRRQLLVQQQQQQQLRNQIQRQQQQQFRHHVQIQQQQQKQQQQQQHQQQQQQQQ
 QQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQGQIPQSQQVPQVRSMSGQPPTNVQPTIGQLPQ
 LPKLNLPKYQTIQYDPPETKLPYPTYWSDKKADTDLTLLYEQIIRQDKINKYSLIRETNGY
 DFFSIYGFSSNKEYISRLWHTLKYYQDLKNTRMKSITSTSQKIPSASIWGNNGYSGYNGGIT
 NTTTRVIPPQVEVCNRKHYLEDKLVYKQAMNETSEQLVPIRLEFDQDRDRFFLRDTILLWN
 KNDKLIKIEDFVQDMLRDYRFEDATREQHIDTICQSIQEQIQETQGNPYIELNQDRLGGU
 DLRIRIKLDIVVQGNQLIDQFEWEISNSDNCPEEFAESMCQELELPGEFVTAIAHSIREQ
 VHMVYHKSALLCYNFDGSAIEDDDIRSRMLPTITLDDVYRPAAESXIPTENLLQISAAEL
 ERLOKDKDRDTRRKRRQGRSNRRGMLALSGTSASNTSMNGVHINTVAAGNASSLPPGEILL
 PDIAIDIPRTFRTFVPSTLMPGGVDVGPSVESYELRNTTYKSRPDRPKPVSPPCYITDHT
 PGHSLLLSISKLPQKVNTKEEFAAAPNDTSSGTKAMLPSPESLKTKLNSNIRAGVTIIPSP
 NPIANHTVTNSFNFTLQFVIPGGAASKSVPTPSLPIAPPVAPHDSEATLLTNSNNGSSNN
 NTQNT

YCR004C, 1244 bp, CDS: 501-1244 (SEQ ID NO 69)

TTAAGAAAATGAACGTTACTATTTCCCTTCCTCGTTTCTAGTTACATAAAAATTTACTAATCG
 TTGGAAAATTGCGGAAGCTATCACGCGATACTAGGTACACACGCATTATTTTATAATC
 CCATTATTAAATAAATCCCTTATGACCCCTTTTGTAAATAACTTATTAAAGAACCTCCGGTA
 AAATACTGTACTGCGGGGAAAGAAGGCGCTTCCCTTCTTGGAACTTAATATAAATAATA
 AATTTGCCTAAGGGCATTAGGUUTTACTGCTTGGCTAGCGTAATTATTTCTGATTTCATAC
 AATTTGCACTATTCCGGCAGCTAGTTGATACTATAACATCCTACATTTTACTTGTTTTA
 CGTTTCATTTTATTGAAAGTTTGTAACTTTATCAGAAAGAAAACAAGAAAGAGGAAAAG
 GAAAAGAGGGGTCAGCTTAGTATCAATAAAAAAAGAGAGTAAACAAAACAATACAGAC
 TCAATTGAAGCACTATAAGAAATGCTAAAGATTGCGATAAATTACTTACTCTTACCTACGGGC
 ACATAGACCTTTTAGCCCAAGCTGTTAAGAAAGCTCTCGAGCCAGCTTGGTCTTAAAGCTC
 ATATATACAGGGTCGAGGAACCTTACCTGATGAAGTCTTCACCAAGATGAACGCTCCTC
 AGAAACCTGAAGATATTCTGTTGCCACTGAGAAAAGCTTGGCTCGAATATGACGCTTTT
 TGTTCGGTGTTTCCAAGTAGGTTTGGTAATTGCGCGCTCAATGGTCCGCCCTTTTGGGATA
 AAACCGGTGGATTATGGGCCAAGGGCTCTTTGACGGCAAGCTGCGGGGATATTCTGTTA
 GTACTTCCAGTTACGGAGGCTGGTCAAGAAAGTACCGTTAAAGCCCTGTTTGTCTTATTTAG
 CTCATCAUGGAATTATCTTTTACCAGTGGGTTATAAGAATTCAATTTGCTGAGTTAGCCA
 GTATAGAAGAGGTACACGGTGGCTCTCCATGGGGTGCTGGTACCCTTGCAGGACCTGACG
 GCTCAAGAACTGCGTCTCCACTTGAAATTGAGAAATGCTGAAATCAAGGTAAAAACATTTCT
 ACGAAACCGCCAAAAAAGCTTTCCCTGCAAAAGAGCCAAGCCCTCCACTGAAAAGAAGA
 CCACTACCTCTGATCGGGCTAAGACACAACTAAACCTGCAGCACCTACAACTGCAGAAA
 AGAAGGAGGACAAAAGGATTATCTATCTGCTGTACTGTCATGTAA

YCR004C, 247 aa (SEQ ID NO 70)

MVKIAIITYSTYGHIDVLAQAVKKGVEAAGGKADIYRVEETLPDEVLTGMNAPQKPEDIP
 VATEKTLLEYDAFLFGVPTRFGNLPQWSAFWDKTGGLNWKGSLLNGKAAGIFVSTSSYGG
 GQESTVKACLSYLAHHGIIIFLPLGYKNSFAELASIEVHGGSPWGAGTLAGPDGSRTASP
 LELRTAETQKTFYETAKKLFPAKEAKPSTEKKTTTSDAAKRQTKPAAATTAEKKEDKGL
 LSCCTVM

YCR013C, 1148bp, CDS: 501-1148 (SEQ ID NO 77)

TGAAAAATGATCAAGGCACATTGTTAATTGAAGAAGAACAGAAAGAAAGAAACAAAATTAA
 AACCGATTGACCAATATATGTTCTCTGAATGCCAAGGATGGAAATTATTTGCAGAAGATTAG
 ACTTTTTTTTGTGCAAGTGGGATGAGCTTGGAGCAGGAAGAATACACTATACTGGATCTA
 AAGACTACAATAGATGCAATAGAAATATTGGCAGCGCAAAAAGGCTTCAAGCTTACACAAC
 ACGGTTTATTTGAAATAATATCCTTCTCGAAAGCTTTAACGAACCCAGAAATTTTCGAGT
 TATTAAACTTAAATACCGCTGAACCCGAACATAGAAATATCGAATGGGAAAAAAGAACTG
 CATAAAGGCATTAAAAGAGGAGCGGAATTTTTTTTAAATAAAATCTTAATATCATTAA

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AGATAAATAAATAGTCTATATATACGTATATAAATAAAAAATATTCAAAAAATAAAAATAAA
 CTATATATTTTAGCGTAAGGATGGGGAAGAGAAAAAATAATGATCTATCGATTTTC
 AATTCAATTCAATTTATTTCTTTTCCGATAGAAAGCAACACCTGGCAATTCCCTTACCTT
 CCAATTAATTCACAAGAGCCACCCACCCAGTAGAGACATGGGAGATCTTGTCTAGTGACAC
 CGTACTTCTTAGCGACAGTGGCAGTGTCCACCACCACCAATGATCACCCTGTTACCGACAG
 CAGAGCTCTTGACAACCTTCGTCTAACAAGCCCTTAGTACCAGCAGCGAACTTTTCGAAAT
 CGAAAACACCTGGTGGACCGTTCCAGACAATGGTCTTAGCCTTTGCCAACAGTACCAGCAA
 ACAACTTTCTAGATTCTGGACCATTGTCTCAACCCCTTSCCAGCCAGCTGGGAATACCTTCCT
 TGTCTAGTGACAGTCTTGGTGTCTGGCATCAGCAGAGAAAGCATCAGCAATGATGAAGTGA
 CTGGCAAGACGACTTCGACACCCCTTGGCCCTTGGCCCTTTCCATCAACTTTTGGAACTATTT
 CAGCACCAGCCCTTGTGGAAGATGGAGTCACCGATTTCACTGTTTTCCAAAACCTTCTTGA
 AGGCGAAAAGCCATACCACCCACCAATGATGATAGAGTCCACCTTGTCCAAACAGTTGTCAA
 TCAATTGA

YCR013C, 215 aa (SEQ ID NO 78)

MGKEKRKKLIYRFQNSIYFFSDKKATPGNSLPSNNSKEAPPPVETWEILSVTPYFLATV
 AVSPPPMMTVLPAAELIUTSSNKALVPAANFNSKTPGGPFQTMVLAFATVAANNFLDSG
 PLSNPCCPAGIPSLSVTVLVLSAERKASAMMKSTGKITSFPLALAFSINFGTISAPALSK
 MESPISVFSKTFKVKAIPPPMMIESTLSNKLIN

YDL059C, 1217 bp, CDS: 501-1217 (SEQ ID NO 83)

AAAGTATCAAGTTGCTAAATTTACTTCGAAGACAGAAGCCAGTAAATTTTGTCTTCTTC
 ATGGAAATAGTTTCCAAAAGTTCTTAGTAATTACCATATCTTCTTGTATCTGGCGCTGC
 GAAAGAAAGGTTAGCCGACCGGCATCACCCATAATTTGTATATATAGCAATGAAGCAACT
 TGTTCGAAGTTTCTTTAAAGTACTTATAGTATTGAATAATATCATGTTCACTTGATAAAAT
 TGGGTATTTTATTTGACUATTATATACCGCTTGGACACTAATGTCTTTCAAGTTGGTGTAC
 CTCACCTGCTTTTCAATGTACTGCGGCCAAATTGATTAGAGGAAGCCACAGTTTGGCAAGG
 GCAGATATAGGAAGCAGTAACCGCAAGGAAGGATAAGAACATCATTTGAGGGAGTCTG
 TGGCATTTAGCACATGCTTTGGACCATTAAGGCTTTACCTAGAGGAGAAGAGCATATTT
 CAGGATAAACAGACAAAATAATGACGATACAAGCGAAGCCCAAGTTCCGAGCATATCGTATG
 ATTCCGACTACATACGGGCACAGCACCCCGCTTCCATATATAACACTTCCAAAATCATCGAAG
 ATTGGAAATGGAAGACCTGCCAGCGCTTGGTCCGTGCAGAGGATTTGCCCTTCTACAGTCCA
 AGATGGAAAGGTAUAGGTACAATATTTACCACAATAATAAATATCGGAAGCACAACTTAT
 UTAAAGCTGATACUAGGUATGCTCTCTATTGAGTTGCTAATGAACATTCGGGTATGATG
 GTTGGCGAATGGATGTTATAGATGTTGAGGCCCGGGAGTGCCAGCCCTTCACCGCAGTAA
 ATAAATGGAGAAAACAUCAACACTAGTGAGGTCAAGTATACAGTTGTGGCAGAAGCCCAAG
 TAAAGGTTACCTTAAAGGATGGCACCAACACACAGTGTGGTGGGCTAGGTACAAATTACTT
 TCTCCTCCAGAGGTGAATGTTATAACAGGTTCGAAAAAGAGGCTGTAGGCGATGCGTTAA
 AGAAGGCGTTATTGAGCTTTGAAAAAATCATACTCGATTTATGAGACTAAGATTACAAATA
 ATTACTATGTGATGGCTTGTATGGCTCAAAAAAATTAATAATGAAGCTAACACCAATT
 ACAACTTATGTTCAGCCACTAATAGCAAGCCGACTTTTATCAAAATTGGAGGATGCTAAAG
 CCACGCATATCAAATAA

YDL059C, 238 aa (SEQ ID NO 84)

MPTQAKPSSSISYDSTTYGTAPGLDIKEFCIIIECWNGRPASAWSVQRIGLLQSKIERVY
 NIYHNNKYGKHNLKLIPLGHALIQFANETFGYDGRMDVIDVEAREQPFYAVNNNGENTN
 TSEVKYTVVAEAQVKVTLKDGNTNQCGGLGRITLSSRGECCYNRSKKEAVGDAIKKALLSF
 EKILLDYECKITNNYYVDGLYCKKIKNEANTNYNLLSATNSKPIPTKTRDAKGTHTK

YDL147W, 1838 bp, CDS: 501-1838 (SEQ ID NO 87)

ACTCTTCTCTGATTTTCAGCAATGGCCCTTTTTTTTTTCTTCCAGCATCATACTCCTTCGCTT
 GTCTTTTGGAAATTCCTTTTATTCTTACTTTTGACGTTTGTCTTGACCTGTGAGTCCACGGG
 CTTTCAAGGCGGCCCTTTAAATTCCTAAGTTGTGAACCGGCCCATGTATTTGATCTTCCCTT
 TTACTTTGCTTCTCAACTGTACTATTTACAGTAATAATTAGTCCAAACCTTCAGATTCCTTCT
 CGCTAAATGCTCATCTCTAATTATCATTTATTTCTTAATAAAATCTTAAATTTTTCAC
 TGGTTCNGTAUGGCTCATCGUCCAAATATTACCCGCTCTTGTATGTGATCTTTTGTACTTT

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TCGGTGCCAAATGCAAAAGGGAAATCCAAGGAAAAACCATTAACAGGACACTACATCAGAG
 ATANTCTTCANTTAACAGASTAGACGAATATACTGCTGGGCTCACTACCATTTTGTTC
 TAGAGTAAACGTAGAGAAAGATGTCAAGAGATGCACCAATTPAGGCTGACAAGGATTATA
 GCCAAATTTTGAAGGAAGAGTTTCTTAAGATUGATTGCTGCTCAAAATGATTGTAAC
 CTGCTTTAGACCAACTGTTAGTGTGGAGAGAAGAAACCAACACAGCTTCAGATCTGCCCT
 CCTCGAAAGAAGTTTGGCCAAAGATTGTAGATCTGCTAGCATCAAGGAATAAGTGGGACG
 ACCTAAATGAGCAATTGACTCTACTCTCAAAAAGCATGGTCAGTTGAAATGTCAATTC
 AGTATATGATACAAAAGGTTATCCAAATATTTCAAAAGCTCGAAATCTTTGGATTTAAACA
 CCAGAATTAGTGTCAATTGAAACTATCAGGGTGGTTACAGAGAACAAAATATTTGTAGAAG
 TGGAAAGAGCTAGGGTCACCAAGAGATTGGTGGAAATTAAGAAGCAAGAGGGTAAGATTG
 ATGAGCTGCAGACATCTTCTGTAGTTACAGCTTGACACCTATCCCTCCATCGAAATGT
 CTGAGAAAATTCAGTTTATATTAGAGCAATGGAATTGAGTATATTAAAAAGGTGATTATT
 CCCAAGCCACGGTGTCTTCAAGAAAAATCTGAAAAAACTTTTAAAAATCCAAAATACG
 AGTCNTGAAGCTAGAATAATTATAATCTTCTGCTAAAAATTAGTTTGCACAAGAGAGAAAT
 ACCTAGAAGTTGCGCAGTATCTGCAAGAAATTTATCAACACAGACGCCAATTAAATCAGATG
 AGGCTAAGTGGAAACCTGTCTTATGCGACATTGTATATTTCTTAGTCCCTTTCACCTTACG
 CCAATTTACAAAATCATTTAATTCACAAAATCCAGAATGATAACAACCTGAAAAAATTAG
 AAAGCCCAAGAATCTTTAGTAAAATTGTTTACTACGAATGAGTTGATGAGATGGCCAATTG
 TTCAAAAAAUCTATGAGCCCGTCTTAAATGAGGATGATTGGCATTGGGTGGAGAAGCTA
 ATAAGCATCACTGGGAAGATTTCAAAAAAGGGTCATCGAGCACAAATTTAACACTCAATT
 CCGAATACTATTCCAGAATTACTTTACTAAGATTGAATGAATTGCTGGACCTAACGGAGA
 GCCAGACGGAAACATACATCAGTGATTTGGTAAACCAGGGCATCATATACGCTAAAGTTA
 ATCGCCACGCCAAAATCGTGAATTTTGAAAAACCAAAAAACTCAAGCCAATTATTGAACG
 AATGGTCACATAATGTTGACGAATATTAGAACAATAGAAACAATAGGCCATTTAATTA
 CAAAAGAGGAAATCATGCACGGTTTGCAGCTAAATGA

YDL147W, 445 aa (SEQ ID NO 88)

MSRDAPTKADKDYSQLKEEFPKIDSLAQNDNSALDQLLVLEKKTRQASDLASSKEVLA
 KIVDLLASRNKWDLDLNEQLTLLSKKHGQLKLSIQYMQKVM EYVKSSKSLDLNTRL SVLE
 TIRVVTENKIFVEVERARVTKDLVEIKKEEGKIDEAADILCELVETVYGSMESEKIQFI
 LEQMELSILKGDYSQATVLSRKILKKTFFKPKYESLKLEYNLLVKISLHKREYLEVAQV
 LQEIYQTD AIKSDEAKWKPVLSHIVYFLVLSFYGNLQNDLIHKIQNDNNLKKLESQESLV
 KLFTTMELMRWPIVQKTYEPVINEDDLAFQGEANKHHWEDIQKRVJEHNLRVISEYYSRI
 TLLRLNELLDLTESQTEYISDLVNQGLIYAKVMRPAKIVNFEKPKNSSQLLNEWSHNVD
 ELLEHIECTIGHLITKEETMNGIQAK

YDR253C, 1076 bp, CDS: 501-1076 (SEQ ID NO 113)

TTTCCCCGCTAAATAAACCCAGATGCTTTCTATGCTTCTAATCTTTTACCAATTTACCTT
 TGTTTATTTCAATATAAACTTTAATTTACAGTCCCTATCTATTGCUUGACTGGACTAACA
 TGCACGTGACATTTTGTGATGTTTTTGGTCCCTTACTTAGTACGCTTAGTACGCCACAG
 TTTATATTTCTTTGACAATAATAAAGAACCTGATTGTGGGTTACAACCTGCTACACTTTT
 AGTTTAAAAATAAGCAGGAATTAATCTTCAGTTCTGTATCATTATTATAAATAAACTATA
 TTTGTTCTCTTTGTGCGCCCTCGGAACCTTTCCCTCATTACATTGACGAGGTATATATAGATA
 TAGTAGATATACATATCTATCCATGGTATATATGTATGCACCTCGATAATTGAATAGCGT
 TTCATGTATATGCCAAGAAATTTGTTAATAATATAGTGGAAAAAGTCAAGAGGTATTAT
 AAATTTCAAAAAAGTACCAATGGAGGATCAGGATGCTGCATTATCAAAACAGGCTACAG
 AAGCAATAGTGGATGTATCAATTAATATAGATAACATAGATCCTATATAAAAGAGTTAT
 TAGAAAGGGTAAAGGAATAGGCAAAACAGGTTACAAATTAATAAACACCACTCATACCGG
 CAGAAAATCGTGTTGATATAAATAGTCAAGGCGGTAAACATAAAGGTTAAAAAGGAAAAAG
 CATTACCAAAAACACCGAAGTCCAGCAAAAGCAAAACUCAAAGATCGTAGAAATAGTACTG
 CTGMAAAAGCATTTAAATGTGCGAAATGTTCTGTTGGAAATTTTCAAGATCATCAGATTTGA
 GAAGCCACGMAAAGACACACTTCGCCATATTGCCATAACATTTGTCCTCAATGTGGCAAAG
 GTTTTGC AAGGAAAGATGCATTGAAAAGACATTATGATACACTGACATGTAGGAGAAACA
 GGACTAAATTACTAACTGCGGGTGGTGAGGGTATCAATGAATTACTGAAAAAAGTCAAGC
 AATCCAACATCGTTTATCGTCAAGATAACAACCAATGGTAGCAGTAATGGCTGA

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YDR253c, 191 aa (SEQ ID NO 114)
MEDQDAAFIKQATEAIVDVSLNIQNTDPTIKELLERVRNRQNRLLQNKKPAIIPAENGVDI
NSQGGNIKVKKENALPKPPKSSKSKPQDRNSTGEKRFKCAKCSLEFSRSSDLERHIEKTH
FAILFNICPQCGKGFARKDALKRHYD1LTQRNRRTKLLTAGGEGINELLKKVKQSNIVHR
QDNNHNGSSNG

YDR276C, 668 bp, CDS: 501-568 (SEQ ID NO 117)
ACCTTTAGTTCCTTAGCATCACCAATCGCAGACATCCAACGTATCCGTGCGCGTAATCCTT
CTCTTNGTAGTTCGAGCACAGCATACAGAAAGAAGCCGCGCGAAGCGGTAAATGTCTTTCC
TCCGGCCTTCTAACCAACCAAAACCGATCTCGGAACATGGGGGGGGGAGGTCTCTGAAAT
CGAAAAACCCGAGACAGCGAGAGGGATTTCGAGAAATTACAAAGATCACTATTTACTG
CTCCCTTCACCTCCGAGTCCCTTAATAGCCGAAGATGCAATGGGTGTGGGCTCTGGGTG
CCCTTTAACCAAGCCCTCAAAGGGGGTCCCTGGTTATTTTGGCATGGGCGCCTCTATAAA
TACAAAAGAGCAACTGAGTCTTTTCTTTTTCGAAGAGCGAAAGCAAAAAAGAGCAAAAT
TTACTATACGGTTGTTCGTTTTCGCGAGTATAATACAATTGATTATACATTTTGAACATAA
CAGCACAGCACAAATACAACAATGGATTCTGCCAAGATCATTAAACATTATATTATCCCTTT
TCTTACCACCAGTCGCGCTTTTTCTAGCCCGTGGGTGGGTAAGTACTGACTGTATAGTGGATA
TCATTTTGACCATTTTGGCTTGGTTCCAGGTATGCTATATGCCCTTGATACATTGTCTAC
AAGACTAA

YDR276C, 55 aa (SEQ ID NO 118)
MDSAKIINIILSLFLPPVAVFLARGWGTDCIVDIILTLIAWTFQMLYALYIVLQD

YDR377W, 806 bp, CDS: 501-806 (SEQ ID NO 127)
AATACAAGACTTGGTGGTCAGCGGAGCGCTATCCTTAGAGATTCTATCGACCTCTCTAA
TATCAAGCACACCACATGGAAAGATTGGGAAAGAAATCAACAAGAAGGAATTGCTTCGGGG
CAAAAACGAAACACAAAACCTCCCTCAAAGTTTTTAAGTTTTGAAGAGTTGTGGAACGGTGT
AGAAAGCATATAAAATAGATCTCTTAATATATTTCTAACATCTTCTTGTAAATGTAAATAT
TTTAAAGCGCTTCATCTTATTTACCGAGAGAAACCAATCATATCGAAGGATTCTCAATAGT
AAGTATCCCGCGCGTGGTCCCTCGGGGAAATAGAAACGAGAAACTTCAAGTACTTGATAGCA
AGAAAGTGAGTGCTTGGCTTCCCCATTTTGATTATATAAGAAAGGCATTATTTTCTAGGGC
AAGAAAGACATTGTGAAATTGTTCCAGAACTTTCAATTTAAAGTCTTTTCGTGAACGA
GTGGACGTCAAAAAGAAATATGATTTTTTAAACGTGCAGTATCTACATTGATTCTCTCAA
AAGTCTGTCTTCCAAGAAATATAGGTTCGGCAACCAATGCCAAGCGCATTGCTAATGTTG
TTCACTTTTTATAAGTCTTGCCTCAAGGACCAAGCAACAGCCATCAAGGCTAACACTAGAT
TGGCCAGATACAAAGCCAAGTACTTTGATGGGGATAATGCTAGTGGTAAACCATTGTGGC
ATTTTGCTCTAGGTATAATTTGCCCTTTGGCTATTCCATGGAATATTACTTTCAATTTGACAC
ATCATAAAGCTGCCGGAAGAGCATTCG

YDR377W, 101 aa (SEQ ID NO 128)
MIFKRAVSTLIPPKVVSSKNICSAFNAKRIANVVFYKSLPQCPAPATKANTRIAFYKAK
YFDGDNASCKPLWHFALGIIAFGYSMEYYFHLRHHKGAEEH

YELC39C, 842 bp, CDS: 501-842 (SEQ ID NO 141)
AGTAATTTGCTCCCATTTTGGTATACGAGCTAGCAGGACCTTTTGGCCAACTGACCATTC
CATATTCATCCCACTCACCAACCGTCATCGTTGGTATTATTATTATCATTCGGCTTGAAGA
AAAGAGAAACGAAAAAGCAATGGATCAACAGCGGGTTATAGCGCCCTTATTGAATTAT
TTTCTCTCGTGCCTTCTCTGAGAAGGCTCTGCACTCCCCCGGAGGGTCTTTTCCAC
CTTTCTCAAGCTAATAACGATAACAGCGAGGGCATTATTCAGGTTCCAACCTACTATTAAG
TGGCCCCAAGGGGCAAGACAAAGGCACACACATATATATATATCGTGTGTGAAGCTC
GACAGATTTAGATCAGAAATAGTCTCTTTTGTGTGAGGTGAAACCAATCAAGACTTA
TACACGAGATCACATACAGCAATTTATTCACATTACTTTAAGTAAACTTCAGTAAACCA
CMTTACATCAAAAACAAACATGGCTTAAAGAAAGTACGGGATTCAAGCCAGGCTCTGTAA
AABAGGGTGTCTACATTCPTTAAACGAGGTGTGAGCAGTGTATACAAATACAAAGAGCTC
CTCCTAACAAAGTTGGACCTAATTTACATGGTATTTTTGGTAGACATTCAAGGTCAAGTAA
AGGGTTATTTCTAACACAGATGCAAACATCAACAGAAAGTCAATGGATGAGGATAGTA

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TGTCGGAGTACTTGACGAACCCAAAGAAATATATTCCTGGTACCAAGATGGCGTTTGCCG
GGTTGAAGAAGGAAAAGGACAGAAACGATTTAAATTACTTATATGACAAAGGCTGCCAAAT
AG

YEL039C, 113 aa (SEQ ID NO 142)

MAKESTGFKPGSAKKGATLFKTRCQQCHTIEGGPNKVGPNLHGIFCRHSCQVKGYSYTD
ANINKNVKWBDEDSMSEYLTNPKKYIPGTKMAFAGLKKRKRNDLITYMTKAAK

YER112W, 1064 bp, CDS: 501-1064 (SEQ ID NO 147)

TACTGAAGTCCCTCTAAACCTACTGCCCTTTATATTTTACGGCTTTAAATAAACCATGGACA
ACGTGAATTGGGTAGCAATCTTTTTPAATAGAAAGTTTATTTATGTATAAUAATAATTTA
AAGATATTCATAGTGATAAGTAATTTTAAATGAGTTTAAAGTACTACTTTTTCCTTTACCG
CCACTTTTCCTGTACTATCAAAAAGCCAAATTCGCCATTTGTAGCCGCCACACGCATTTTG
ATCATCAATTTACGAAATTTGCCGCACACGTGTACCGTGATAAGCACTCTTACTATCATGT
TTTACGGGAGTAGCAATGATGTTCAAATTTATTCGACGCTTTCTTTTCGTGAAATCGTAGTATCA
CAGACCTTCTCTAAATGATGGAAAGCCGTAAAGAAGGAAATCTGTAAAAGTAAATTAACGAAGT
AGTATTTAGTAAAAACAGAGTTTGAABAACTTGATAAAATCTTCAACTCGAACTGAAAAGAAACA
CAATAGAAATATTTTTCCTCAATGCTACCTTTATATCTTTTAAACAAATGCGAAGGGACAAAC
AAATGCAAAATAGAATTGAAAACCGGTGAAATATACAAAGGGATATTGACCAACGTAGATA
ACTGGATGAACCTTACTTTTATCTAATGTAAACCGAATATAGTGAAGAAAGCGCAATTAATT
CAGAAGACAAATGCTGAGAGCAGTAAAGCCGTAAAATTTGAACGAAATTTTATATTAGAGGGA
CTTTTATCAAGTTTATCAAAATGCAAGATAATATAATTGACAACCTCAAGCAGCAAAATTA
ACTCCAAACAATAACTCTATAGTAAACCGCCCTCCGCCATAAAACATACTACAACAATAGGG
ATTCAAACCAATAGAGGTAACTACAAACAGAAAGATAATAATAACCGGCAACAGCAACC
GCCGTCCATACCTCTCAAAAACCTCAATTAUAAACACAGCAACAGCAGTAAACATTAACAACA
GTATCAACAGTATCAATAGCAACCAACCAAAATATGAACAATGGTTTAGGTGGGTCCGTCC
AACATCATTTTAAACAGCTCTTCTCCACAAAAGGTCCGAATTTTAA

>YER112W, 187 aa (SEQ ID NO 148)

MLPLVLLTNAKGQGMQIELKNGELIQGILFNVDNWMNLTLNVTEYSEPSAUNSEDNAES
SKAVKLNELIYTRGTFKFKIKLDNIIDKVKQIINSNMNSNSNGPGHKRYYNMRDSNNNRG
NYNPRNDNNKGNRRRYPYQNRQYNNNSNSSLNMSINSINSNNQNTNGLGGSVQIHFNSS
SPQKVEF

>YPR010W, 2000 bp, CDS: 501-2000 (SEQ ID NO 153)

GAAATATTTCAACGGTGGTGCTTAATGGTTPCCCATGATATCTCTGTTATTGACTCTGT
TTCTAAGACAGTTTTCGCTTTTCAGACCAAGGTACTGTCAAGAGGTTCGAAGGTACAATTTA
CGACTATAGAGATTACATCTTGCAGTCTGCTGATGCTGCCAGGTGTGGTTAATAAGCATTG
ATTTATTTTAGGAAGCACCTCAGAATATATTTTCCATAGAAGCCTAAATTTAAGTATGCATT
ATAGCCCCATGATACTTTTTPPIGACTACTTGTATTTCGAATCTAATTGAACCTAAGTGG
GCATTCCTGGGTCTATTGGTATATGTATCACTTTTACGTAAAAAAGTAGTGGCTAATATAA
AACATAAAAATCTACAAGAAGGGTGAAGTGCTTTTCCGANTTTTGCCACTGCAAGTAATTGG
TGCAATTTGAAATACGAGATTTCGTTCTCTAAGACCATATAAAATAAGGAATTAGCCCT
ACCTATCCTTGTTGTTAAATATGAGCGGAGAAACGTTTGAGTTCAACATTAGACATTTCTG
GTAAAGTTTACCCAAATACACTTTTCCACTGATGCTACTTCAGCAGACTTGAAAAGCAAG
CAGAGCAATTCGACCAAGTCCCAAGTGCCCGCCAAAATACATGGTTAAAGCTGGCTTGT
CTGGCGAAGAGTCCATTAATAATATATCCCTTAATCAACCCAGCATCCACAGTAATGCTAT
TGGCGACTCCAGATGCTAACCTGATTTCTAACCAGCCAAAAGATAATTTCAATTGAAG
ACCTTGGCCCTTGAGCAACAAGTCAAAACATTTGCTCAATTGGCTGTTGGTTTCAAGAACTA
TGGGCAACACCTGTTATCTGAATGCTACCTACAGGCTTTATACAGAGTGACGATTTTAA
GGGATATGATTCTTAATTTATAACCTTCTCAACCTCTCTCTAACAGTGGTGCACAAGATG
AAGAGATTTCACAAACAAATCGTTATTGAAATGAAGCGTTTGTTTGAATAATTACACAACTA
AAAGTTTCAAGAGTGTMTTGCCAAATGTGTTATTAAACACCGCTAAGAAAGTGTATCCAC
AATTTGCTGAACCTGATTCACAAGGTTCCTTCTATTAACAACTAAGACGCTGAGAGTGTGT
TTACACAACTATTTCCATAGTATGAGTATTTGTTTGGGTGACAAATTTTCCGAAGATTTCA
GGATTCAATTTAAACATCCATCAAGACACAGCTAATGATACGATATTACTGTAAAG

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AAAATGAAAGCGATTCTAAATTACAATGTCTATATTTCTCGTACTACAAATTTTCATGAGAA
 ATGGGCTCCTGGGAAGGTTTGAATGAGAAANTTGAAAAAGATCAGACTTGACTGGCGCCA
 ATTCCATCTATAGCGTCGAAAAGAAAATATCAAGAATTACCAAGTTTTTTAACTGTTCACT
 ACGTTAGATTTTTTCTGGAAAAGGTCAACCAACAAAAATCTAAAATATTGCGTAAOCTCG
 TTTTCCCATTTTCAATTAGATGTTGCAGACATGCTTACCCUCAGAAATACGCAGCAGAGAAGG
 TAAAAGTTGCTGACGAAC TGAGAAAAGTTGAAAAGGAGAAAAATGAAAAGGAAAGACAGA
 TCAAAAGGCGTAAATTTGACCCATCATCCAGTGAAAATGTCATGACACCAAGAGAACAAAT
 ATGAGACACAAGTGGCTCTTAACGAAAGTGAAAAGATCAATCCCTCGAAGACTATAAGA
 AACATTTTCCCTCCAAACTTGGA AAAAGGTGAAAACCCATCTTGTTTATAACTTGATCG
 GTGTCATTACACATCAAGGTGCCAATCTGAGCTCTCGACACTATCAAGCTTTTCATAAGCG
 ACGAAGTGGACGAAAAATAATGGTACAAATTTAATGATGATAAAGTTAGCGTTGTTGAAA
 AGGAAAAAATTGAATCTTAGCCGGTGGGGGCGAAAGTGATAGTGCCTGATCTTAATGT
 ATAAAGGATTTGGTCTGTA

>YFR010W, 499 aa (SEQ ID NO 154)

MSGETFEFNIRHSGKVYPITLSTDATSADLKSKEELTQVPSARQKYMVKGGLSGEESIK
 IYPLIKPGSTVMLLGTPLANLISKPAKKNFIEDLAPEQQVQQAQLPVGFKNMGNTCYL
 NATFLQALYRVNDLRDMILNYPNSQGVSNSSGAQDEEIERQIVIEMKRCFENLQNKSTKSVL
 PIVLLNLTLRKCYPOFAERDSQCCFYKQQAEELEFTQLFHSMSIVFGDKFS2DFRQFKTT
 IKDTANDNDITVKENESDSKLQCHISGTFNFMNGLLEGLNEXIEKRSDLTGANSIYSVR
 KKISRLPKFLTVOYVRRFFWKRSTNKKSKILRKVVFPPQLDVAJMLTPEYAAAEYKVRDEL
 RKVEKEKNEKEREIKRRKFDPSSEENVMTFREQYETQVALNESEKQWLEEVYKHFPPNL
 EKGENFSCVYNLIGVITHQGANSESGHYQAFTRDFELDENKWKFNDDKVSVVEKEKIBSL
 AGGGESDSALILMYKGFGL

>YFR052W, 1325 bp, CDS: 501-1325 (SEQ ID NO 157)

CAGAGACATGTTTTTAATTCAGTGATGAGGCGGAAACGTGCAAGATCCTAAATGAAGGAT
 AAAAAGAGTTCTTAAAAAGGGAAGTAAGGAATAACAGAGTGA AAAAACCGAAAAGACAAC
 TTAACAAATCGGCAACACTTTTATGGGGCCCCGCTCGCCTGTGTGCAAGTAGTATTCGAC
 CTGGAACACGCATTTACCACGAGAAGACAGCAATAGTCCGTACAACATTAATTAAGTTTCG
 ACAATTCCTCGCCTTTATAAGCCATGCTAGTGCCCAATCAACACACTTTACTTGCCCTGAA
 GTTCCTTTTTTTCGCTAGCCTGTAACCTTAAATAAGCCATCTAACCTTTTTTTTTCTAAAAAT
 TTTCTTTATTACCTGTGCGCTTATTTCTIATTTCTACACATTATTTGCCACCCCATTTGAAA
 TTGTAGCTTGTATTAAATAGCGAAAGCCCCCAAGTATAACCGGTGGAAGTACTTATTTGAAG
 TGAGATAAGAAGCCATCGTARTGCCCTCGTTAGCCGAATTGACCAAGTCGTTAAGCATAG
 CCTTTGAAAACGGCGATTATGCCGCGTGTGAGAAGCTCTTGCCCCCTATCAAGATCGAAC
 TTATCAAGAATAACCTTTTAATACCTGACTTATCCATTCAAAATGACATCTTATTTGAATG
 ATTTGATGATTACTAAAAGGATCCTGGAAGTAGGTGCCCTTGCTAGCAACCAAACTTTTCA
 ATTTTGACAGCTTCGAGAATTACTTCAACCAATTGAAGCTTACTACTTTAGCAACCAATC
 ATPAATTATCTGAATCTGACRAGAATCGAAGCTGATAAGTCTCTGATTTGTTGAACTTAT
 TGTCTCAGAATAACACAACCAAGTTTCACTCGGAATTGCAGTATCTAGATAAACCATATCA
 AGAAGCTTGGGAAGACGATTCACTTTTGTCTTACCCNTCAAAC TAGACAGATGGCTCATGG
 AAGGTCGTACACAGAAAGCATGGGATCTTCTGCAATCTGGGTCCGACAAATATATCAGAAT
 TCGACTCTTTTACCGATAACCTAAAATCAGCTATAAGAGACGAAATTGCTAAAAATACCG
 AGCTATCCTACGACTTTCTCCCTCTCTCCAACATAAAGGCTTTGCTCTTTTCCAACAACG
 AAAAGAAACTGAAAAATTTGCACTAGAGAGAACTGGGCTATTGTCAACTCGAAACTTT
 ACTTCAATAACCAATCAAGGAGAAAGCTGATTACGAAGATGAATGATGCATGAAAGAAG
 ACCAAAGACAAACATTACCGAAAAGCAATGCGATTATGCCATAAGTATTGAAAAATATG
 TGTA

>YFR052W, 274 aa (SEQ ID NO 158)

MFSLAEELTKLSIAFENGDYAAACEKLLPPIKIELIKNNLLIPDSIQNDIYVNDLMTKR
 ILEVGA LASIQTFNFDSFENYFNQLKPYFYSNNHKLSESEKKSKEITSEYVJNTLSQNNTT
 KPHSELQYLDKHIKNLEDDSLSPYIKLDRWLMESYQKAWDIIQSGSQNISEFDSFTDI
 LKSAITRDEIAKNTELSDYDFLPLSNIKALLFPNNEKETKFALEARNWPVNSKVYFNNQSK
 EKADYSEDEMHHEEDQXTNIIKAMDYAIISIENIV

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>YGL072C, 860 bp, CDS: 501-860 (SEQ ID NO 159)

ACTCTTTTGTCTAGGGAGTTTCTGTGCTAAGAGGTTTGTCAATGACACCGAAAAGAGGAT
AATAGGTAATACTTTTTGTAAGTGTAAAGAATATTAAATCGTTTTACGGGAATTGGCCCTC
TTCCCTATATTCTATCCGAGGTTGTGTACTGTAGCGGTTTATACTTCAACCTGTGAAAGT
TATGTAATATGCGAATTCTGTTTCTGCTTGATAATCTCAAGAATATACTCTCGAGCACGC
GATGGAGCAGAAAGGGGAGCAATGAATACTGATGAGCTTAACGATGAGGAGGCCGTTTCC
GTTTCTCTTGATTACCCCTTTTCATCCAACACTCAATATAAGTACGCCAACTTGCCCTAAAA
CGGCCAATGTGACACCCAGTTCACCTCGGCAAGCCCTTCTCAGGCTCTCACTAGCTCGAATA
ACGAGAATCTTCACGACTCATCTACTTGGCATTTCCTGGGTGCAGTTCAACCTCACTCG
CGTCCGGCGGTGTGAGGTGCATGGGTGCCGGTATTTTTTTTAGTTCGCTCTCGGCCATTAC
GCGATCAGCTTCGAGAACATACTATATTAAATGATTATATACGCTATTTAATGACCTTGC
CCTGTGACTATTTCTTAGCTCGTTTGGGACGGCGGTGATCGTTGTACTTGTCTGGGTCC
TGTAATTCGACTATAGCCGGTTCGGGTATTTCTCCACAAATCTTTTCTTAGCGTTCTCG
GGCGCGGTGTCCGGCTGGGTGGAATAACTGTGCTCATTAAAGCTTGGCAGGTTATCACTC
ACTTTAGTGTCTTTCAGTGGCGCTGAACCTTATATCGGGGGAUACUUCTTGTACTTCCCTCA
CTAGTGTATTGTGCTTAG

>YGL072C, 119 aa (SEQ ID NO 160)

MGAGIFFSSLCALRDQLREHTILNDYIRYLMTLPCVLFLLSFGQAVIVVLCRVLYFDYSR
FRYFLHKSFLSVLCRRVGLGCITVVIKAWQVITHFSVFSOAELYIGCHPCTSIHVSIVV

>YGL080W, 803 bp, CDS: 501-803 (SEQ ID NO 161)

GAAGAAAAAGAGAAGGGGATGATCAGGAAGGAGAAATAGAACTTGAAATTATTAGAGTA
AAAPGAATAAAGGTCAGGACGAAGATAAAGAAGACGCTTACTTGCTTCTCGAAAAACAAG
AAPATTATTACCCCTCAGCACTCCAATAGTATGTGGTTACTACTAATAGTAATCTTGATT
TTTCACCGCCTACTATCGAATTAAATATAATTTTATAACCCAGTTCTATATTGCTGGGTG
GTATTATAGCTTCATGGCTACTCAAATAAGTGGAGTTTCTTGCTCTGGACGTGGCCTGTA
AAGTTCTCTTTTGGGACGGGCCCCCGCTTTTAAACCGAGGCGAAATGACAAGTGCTTTCTGG
CAAGAAGGAATATGCCACTACAACCTGCGGTCTCCACCTTTCTCCACCGATAATCTATT
AAACACTCACTTTGCCAATCAGCAAAACGTCAATACATCTACATATATACGTATAGATTTTA
TTGCACTGTGATCAAAAAGAATGTCTCAACCGGTTCAACGCGCTGCACACGCTCATTC
TTCAAAAATACATCAATAAAGAAACTTTGAAATATATTTTCACAACACACTTCTCGGGTC
CCGATTCAAATTTCCGATATCCAAATTTGCTGCTATATATGATCTGAAAAAAGACCTTACAC
TAATCTCTGGCCCAATGACTTTTGCCTTAGTTACCTATTTCAGGTGTTTTCTATGAAGTATG
CTCTTTTCAGTATCACCAAAACTACTTACTGTTGGATGCCACCTTATTAATGAAACTG
CGCAATTAGCTCAAGGCTATAGGTTTCTCAAAATACACGTATTTTACAACAGATGAGGAGA
AGAAAGCTCTAGATAAGGAATGGAAAGAGAAAGAAAAAACTGGTAAMCAGTAA

>YGL080W, 130 aa (SEQ ID NO 162)

MSQPVQRAARSFLQKYINKETLKYLFTTHFWGPVSNFGIPIAALYDLKKDPTLISGFMT
FALVTYSGVFMKYALSVSPKNYLLFGCHLINETAQLAQCYRFLKYTYFTTDEEKKALDKR
WKEKFKTGKQ

>YGR008C, 755 bp, CDS: 501-755 (SEQ ID NO 165)

CCCAATAGTTATGAACTTAACCGAGCTCAAATAATTTAAAGATAAAAGATAAAAGATAAA
AGATAAAGGACAAAAGAAAATTCTATGCCCATGTTGAAGTATCCAGCGGCAAAATGTTGC
TATCCAACAGAAAGTACCAAGCCAGTTTCAAAAAGGTACAGAAATTAAGTGATGCTATCCG
TCCCACAACATAATTTTCTCCAGCGGAGCAATATATACGCCAGCGGGGGGAGGAAAACCTCT
CAGTAAGCAATGAAGGGATAGATAATGGGGGCGCGGCTGCCTAGCTTAGGCTAAGAAAAT
CCTTCCGAAAACAGGCGGCTGCGAGCGCAGAAAGCGAACACTTGTCAATTTGTATAGAACGAC
TATTTATAAGTTTGTCTTTTGTCACTCTCTTGGCCCTAAATTACCAATACCTATTGTATCAA
TTGTTCTGTAAACTCAATTATACAAATAAAGCAACCAATCAACAGTAACAAACCGCTCAAG
TGTACATCCAATCAGAAAAAATGACGAGAAACAAAACAAGTGGACCGAACCTGAAGGAAAGG
CTGATCCAAAGTACTTTTCGCACACTGGTAACCTACGGTGAATCTCCAAATCACTCAACA
AGCAAGCTTCCGGCAAGGGTAATTTGGGGTAAGCCAGGCGATGAGATTGATGACTTAATTTG
ATAAATGGTGAATTAACCCUAGTGTTCAAGAAAGATAGAAAGAGGCTCAAAATTTGCAATCGC

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ATGAACAAAAGTTTGAAAACGTCCAAAAGGAATGA

>YGR008C, 84 aa (SEQ ID NO 166)

MPTRTNKWTEREGKADPKYFSHTGNYGESPNHIKKQSSGKGNWGXPGDEIDDLIDNGEIPP
VFKKDRRG5NLQSHQKFENVQKE

>YGR023W, 2156 bp, CDS: 501-2156 (SEQ ID NO 167)

TTAGATCATGGCTAGGGGATCTGGGAAGTACAATGATGTGCTCTCCCCCTCTCAAACACA
ACACCAGCATCAACTAAGCCCTCATCTCGAAAGTCGAAGGTGCTCTCATTCAGGTTAATTAG
TGGTGGCTGTTGTGTCTTCCATGAACAAGGAGCACTTAATTAATTTGTTGCAATGAGAT
ATCATTFTTTTFTTCCCTCTTCTTGGGCTCTTGACAGTCATCAAATCGAAGTTTGTAG
TTTTTCTTCTTCCGCAACATCAATTTTACCTAGAAAAGTGTACATGAAAACCAAGGATA
CTGCTATTTTACGTAGTAAGTACTCTTCGGTCCATATTGGAAGACCAAGGCATAATAAGGATA
TATTCCGAGGAGATAAATTGGGATATAATCTTCCATTGCTTCCGAAATTTGTTTAAACACT
TCTAGTTTCATTTCCGGGTGGTTGATCTTCCGTTTCCACTTTTAACTTACTCCCAAGTTAGT
ATAATATAAGTAGTTAAGGTATGGCAAGCTGCAATCCGACCAGGAAGAAGAGCTCTGCTT
CAAGCCTATCTATGTGGAGAACGATTTCTCATGGCGTTAACAACACTACCGCTAAGTGTTC
TTTCCGACGAGTTGGTTCCAGCTAATAGCACAAACATCGAGCACAGCTCTTCCATCACTT
CGCTTTTCCGAGTTGAGTCATTTACGTCCAGTACCGATGCAACGAGCAGCGCAAGTTTAA
CAACGCGGAGTATAGCTTCAGTATCCTTTACTTCCCTTCCGACAAAGTTCTTCACTGCTTA
CTCTTTTGTCAACATTATCCTCAGAACTTTTCTCTTCTGTCATGCAAGTTTCCGCTGCTT
CAACATCGTCTGCTCTTCTTCCGAGGTTACGTCATCATCGTCATCATCAATATCTCCTT
CCTCTTTCATCATCAACAATAATATCATCGTCAATCATCACTGCCGACATTCAGTGTGGCAT
CAACATCTTTCGACAGTTGCTTCTTCTCACTTTTCTCACTAGCTCATCGTTGGTTATCTCTA
CGTCTTCCGTCACGTTTACGTTTAGTTCCGAAAGTTCAAGCTCTTTGATTTCCCTCTTCAA
TTTCAACATCCGTTTTCGACTTCTTCAGTGTACGTTCCCTCTCTTCAACTTCATCTCCAC
CTTGGTCCCTCATCCGAATTGACATCACTCTGTACTCAATCACTCTCATCTCATCCACCC
TCTTTTCTACTCTCTCTCATTTTTCATCATCTCTCATCTCTCATCTCTCATCTCTCTCT
CATCTCTCATCATCATCATCATCATCATCATCATCATATTTTACCCCTCTCCACATCTTCTCTT
CATCCATATACTCGTCTTCTGTCATATCCTTCACTTTTCACTCTCTCTCTCAAACCTTA
CCTCAATCAATCACTTCTACATCGGCTCATCTTCTATTACTCCCGCTTCCGAATATTTCCA
ATTTGGCAAAAACCATTAAGTAGTATAAGAGGCCAGACCATCTCTCTAACTACTATA
CCACATAAAGTATTACCGACAGCATCCGCATCTTCAGGAAAAAATTCACATCACTCAG
GCTTATCAAAAAAGAATCGTAATATTAATCATCGGTTTGTTGTTGTTGGCATAGGTGCCCCCC
TCATCCTAATTTCTACTAATATTGATTTACATGTTTTGTGTTGAGCTAAAAAACGGATT
TCATTCACTCTGACCGTAAATTTCTCAGAGCTTATCGTAGTAACATTTTCAACCAAAATAT
GGTATTTCTTGGCTGGGTAAAAAATTTGGTGATATCGATCCAGAGATATACTTAAACATG
ACAACCCCTACACCCCTAAACACACTAATCTTCAAGCCTACCAAGCAAGCAAGCAAGCAAG
ACGCTAATGATGAAAACCTATCATCCAACTTCCATAACAGAGGCATAGATGATCAATGCT
CACCTACTAAATCTGATCATATTTCAATGTCCGATAGTAATAGTCAAGATTAACAAGCAAG
CAGATGAAGTAATGCACGATGAAAACATTCATCGTGTTTATGATGACAGCGAAGCTAGCA
TCGACGAGAACTATTACACGAAACCAACACAGGCTTAAATATCACGAACATTTAA

>YGR023W, 551 aa (SEQ ID NO 168)

MASCNPTRKKSSASSLSMWRPILMALTTLPISVLSQELVPANSTSSSTAPSITSLSAVES
PTSSSTDATSSASLSTPSTASVSFTSPFPSSSLLTSLSSLSSELSSSSMQVSSSSSTSSSSS
EVTSSSSSSSSLSFSSSSSTLSSSSSLPTFTVASTSSSTVASSTLSISSSLVISTSSSTFT
FSSESSSSSLISSSISTSVSTSSVYVPSSSTSSPPSSSELSSSYSSSSSSSTLPSYSSS
FSSSSSSSSSSSSSSSSSSSSSSSYFTLSTSSSSSTVSSSSYPSPSSSSGNNPTSSITST
SASSSITPASEYSNLAKTILSILEGQTLLSNYYTFTITYSFTASASSGKNSHHSGLSKKNR
NIIIGCVVGIGAPLILILLILTYMFCVQPKKTDFTDSGKTVTAYRSNIFTKIWYFLLGK
KIGETERFSSDSPICSNNIQNFGUIDPNDLNNNNKYTFKHTNVEGYDDDDDDDDANDENL
SSNFHNRGIDDQYSFTKSASYSMKNSMSQDYNDADEVMMHEDENIHRVYDDSEASIDENYYT
KPNNGNLNITNY

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>YCR034W, 1244 bp, exon1: 501-525, intron1: 526-879, exon2:
880 1244 (SEQ ID NO 169)

TATAAAAAAATTTCTTGTAGACAATAAAATAAGAAATGCCCATTTTGTAACTTAGCGAAAGATGCCAGTACACCCCTTTTACACCCGTGCATTAAAGGTGTTTGGGTTAATAGGAGCTTTATCATATCTCTTTGATTTTTTTTCTGCTGTCTCTGGGCTTGAGGGACTCACAGAGATCTGGAAATTTTCAGATTGTCACTGCTTAGGATGGGTGTCACTAGACGGTGGCCGCCGTGGATGGGAAATCTCATACGTTTACACACATAGTGTTTGGAAATTAATAGTAGCAATAGCTATCTGGCTACTGTTTTTAAAGTATTACCCCGTTTCTCACTGCTTCTTTTAAAGCAATAACAACGGCAAGACCAAAGATATATCAATATAGGCTAAGCAATCTCTAGGTATGTTTGGAGGATACGAATACAGATAGAAAACATGAGTGAATTTCCGTCACCGAAAAATGCTTAACATAAAATGCAACAGACAATTAATCAATATGTTAAATATTGTAAAACAATGTCTATCATCAGCAGCAATGTACCTTAAGCCAAAAAAAATAAAAAAAAATAAAAAAAAAGAAACAGCTTTTGCATTATCAATCCAGGCATAGGGCGACTATTTAGCACTCAACGATTTTTTAAGCTTCTGTATTGCTGACATAAAATTCGGGCTTTAGAAATCCAATATTGAAAAACGTGAGTACCGCAGAGCACATAGAAAGAAAGTAGGAAGTTTACCGTTTATATTTGATTGTGAAATGCATACTCCGTTGGATGTGGGCAACATAGATTTAAGTGTGGATGAAAATTAATGTGCTCATTTGTGAAAAAAAAGTTTTGCTTTTACTAACAAATTTTTTATTATTTGTTTTCAATAGACGTTTCTCTCACACAAGAAAGGCCAGAAAGGCTTATTTCACTGCTCCATCTCTGAACGTCGTGTTTTGTTATCTGCTCATTATCCAAGGAATTGAGAGCTCAATATGGTATCAAGGCTTTGGCAATCAGAAAGAGACGATCAAGTCTCGTTGTTCGTGTTTCCAAGAAGGCTCAAGAAGGTAACATTTTATCTGTTTACAGATTCAGGTTTGTCTGTTCAAGTTGACAAGGTCACCAAGGAAAAGGTCACCGGTGCTTCGTTCCAAATTAATCTGCACCCCTCCAGGCTGTTATCTACTAAGTTACACTTGGACAAGGACAGAAAGGCTTTGATCCAAAGAAAGGCTGTTAAATTCGAATAA

>YGR034W, 129 aa (SEQ ID NO 170)

MLNYCKTMYVSSDRRKARKAYFTAPSSERRVLLSAPLSKELRAQYGKALCPIRMEDVLLV
VKGSKGQEGKISSVYRLKPAVQVDKVTKEKVNCASVPINLHPSKLVITKLHLDKDRKAL
IQEKGCKLE

>YGR069W, 836 bp, CDS: 501-836 (SEQ ID NO 171)

TTGCAATTATTTTGTGTAAGAACAGGGCTCGAAAGTGATCTCTTGCTTAGAAATATTGCGT
TGCCGCTGGTGTCCATATCTTGCTTGCTTGACTGCGACCGCTACTACTGTTATGTTGAT
TTTCCGCAATTTCCCCACCGACTAAAAACATCCCTTTTGAAGAAACCAATAAGTTTGTCC
AATAGCATTCGAAATCTTAAGCTTTTCCCTTAACCTAGACTTGCCAAACTACTGCTATTCT
TCTTATATCGGCCAACTTGCAAAACCTCCAAATTTGAATCTTCCCTACCAATCTCAGCGAA
TTTTCTTTCACACGATCTCCATTTTTCACGTGAATCTACTAAGTTTCCCTGATAAAGGTATAG
ACGACAGTTCCAACGGTGACCTTTCGATCAGAAATTAATGTCCTTGACGGGGAGTTTATTC
TAATATCAAAATAACTTTATCTCTCTTTTCTTCTGCTCCGAATGCCACCGCTGCTAG
ATAGCGAATAAGTGAAACATGGTCTTGCTTCACCTTACTTCTCGCCGAGAGCTGTACAA
GATAITTTTTTACTTTTGCCATCTTATACTCATCTAATCACTGTTTCATTTTCCCTCTA
TTTCITTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCAGTTTTCGAAGAAACTCCCTTTTTTA
CAATTCGTAAGACGAGTGAAGTATTCAGCACTATATTACATACATACAAAGCAAG
CAAAAGAAACATTTTATAGCTTAACATTTACTTCAATTTGTTTTGTATTCTTATAATA
AGAAAGACCTGCTGTTTAAATGTGGAGTAATCCGTCCTTACTCGATCTTCAATAA

>YGR069W. 111 aa {SEO ID NO 172}

MVLDDHPLASSCTRYFLLLPSTHNPHLHFHFSISFFFFFFFFFSSRRNCLFRIVKDEV
 KYSGVVYYIHTKODKETFLDTFYFNCFCLPYNKKDLLFNVGWIRPLDLO

>YGR070W, 3968 bp, CDS: 501-3968 (SEQ ID NO 173)

AAGAAACATTTTTAGATCTAACATTTTACTTCAATTGTTTTTGTATTCCCAATAAAGA
AAGACCTGCTGTTTAAATGTGGGAGTAATCCGTCCCTACTCGATCTTCAATAAATTGTCA
TCTTGTATCTAAAGGAGCGCTCCAGTACTCCAATTAAGCACCACCAAGTGGTCTAGTGT
CGATTTTTTTTTCACGCATACGTTTGTATGTTTCTTAAATTTTCCCATGATTTTTTTGTGTGC
CAATGTCATATCTACAAACTCTATACGGAAGTAACCGCACTTCACTTTTTTGCCTTAA
ACGGCAATATTTTAAAGACATATCATAGAGGGGCCAAGGGAGAAATUGTTAAATTTTAAACTTTT

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CTTTGGCTCTTGAATGAAAAAGTAAATAAATAAAACTAAATCAAAAAGAAAGCCACGT
 TTGAATTTTAAAGCAAAAATTTTGTGGATTAGTAATGATATAAAATAAACCAAGTCGTT
 GGTAAAGAAATTTGGTTAGGTTATGAATAGTAATGAACTGGATCTAAGAAATAAATATTTTT
 ATGAGATATTTCCGTAAGAAAAGAAAATCAGATACTTCAACCCCTACTCAGTTGTTCTCCG
 CCTCCAAAGTTCAGACAAACATCAATGAAATTTCTATCACTAACGATCAGGATGAAGATA
 GTACTGAAGATGAAAAATAGGCTTCATTGAAGGATTATACACTAGGGCAGGACACCCGGT
 CACGGTATAGGATAGCACCCGACTGTTCTTCCCAACAATTAAGGCATCTCCTGTCTTAC
 ATATTTCAACCAACCTTAATTCAAGTCCACAATCCTTCACAGGGGATCAGATTTCACCTA
 CTAATAAAAAAATTTCAATAAAATGATCGACCAGACAAGATAAAGGTAAACAGTTGCACTA
 CCACTTTCATCACCCTTCCTCAAAAAGATCGAATGTFTTGGCTTCCTCAGCTAAGAAAACATT
 CATCTCCTTCACATATTATCATTTTCCAAAAACAGTGGCAGTCATATGGGGATCCAAACC
 AGCTATCTACGCCCTCCACCTCCCAAAAGTGCAGGTCACACGATGGAGTTACACAGTTTCAT
 TCAATGSAAAACATAGTTCTTCTAGCACCTCTTCTTTATTTGCATTAGAGTCACTGAAAA
 CCCAAATAGACGCTCATCAAACTCTTCCAAATCATCTAGTCAATATCGACGCCACTACTA
 ATCAACACCAACCTCATCTATCTCAAGGTCCAAATCAAGTCCCTCTCTCTGAAUGAAATAT
 CCTGATCAAAAGGCACGCCCTTTGGTTTATCTCTGCACTTTTATCACTAATAGCAATTAAT
 TCAABACAGACCATCAAAATTGAGCACGCATAAAAAAGATGGGCTTACTTTACAGAGATTCTT
 TTACAGSAAACCAAGCAATTGATACTTTATGCTTGATCATAGGAAGCTTAGATCGTAATTT
 TGGGCACTGTTGATCGGAAAACTGGCTGCAAGCTCAAAAATTGTTCCATGACGTACTTTATG
 ACCATGGCTTAAGACATTTCTGTACTGGACATTTACAGCTTATCTTCAGAAATCAAATTTTA
 TGGCAGCATCAGTCGCAGAGTTCTACTTCAATTGCCAACACATTTTCTTCATCATCTTCTT
 CAGTTAATTCGCTCCGTACTCAAACTGAAATATATGGTGTFTTTTGTCCCATTTGACACAT
 GTTATTTCTCTACATGCTCTCTCGAAAACTTTGCTACTCTATTTCTTGGCCCCAATCGTT
 TGCAACACAGGCTAATTTACATTTTAAATTAGGTGGTGGTCTTAAGAGAAATATTTTCGT
 TAGCACTCGATTAAGGAGGATGATGAACGAATTTCTTGGACAAATTTCTGTACCAAGAGCG
 TATGGGAATCATTTATCCAAACACAAATCAAAAGGCAGGAGGCAATATATGAGTTGTTTA
 CTACAGAAAAGAAGTTTGTAAATCTTTTGGAAATCATCCGAGATACTTTTCATGAAGAAAT
 TATTTAGAAACGAATATTATTCATCTGATGTAGGATAAAATTTGTAAAGCACGTTTTCG
 CACATATCAATGAAATATATTTCTGTCAATAGAGAAATTTTCAAGGCTTTAGCCACAAAGGC
 AATCATTAAGCCCCAATTTGTCTTGGAAATTGCAGATATATTTTTCAGATATCTTCTTCT
 TTGATCTCTTTCTGTCTATACATAGCATCAAGACCATACGCCAAAGTATCTAATTTGAAACCC
 AAAGATCAGTTAATCCCAATTTTGGCTCGTTTGTGACGATGAAGTGTCTAATTTCTTCCCTCA
 GGCATTTGGATCGAATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT
 TGGTAAAGAGAAATAATACACTTTCTGGGACCCAGTAAACAGACAAAGATGATTTACAAATGC
 TAAAGAAAGTCCAAGATCTTTTAAAGGATCTAATGAAAAGGATTGATAGAGCAAGCGGTG
 CAGCACAAGATCGTTATGAAGTTAAAGTGTAAAGCAGAAAAATTTCTATTCAAAATGAAT
 ACGTTAATCTGGGTTTGAATAACGAAAAAAGGAAAAATCAAGCATGAAGGTTTACTCTCMA
 GGAAGGACGTGAACAAAACAGATGGGTCTTTTTCAGGAGACATTCAAATTTTACCTACTCG
 ACAATATGCTTAATTTCTTGAATTCAAAAGCTGTAACAAAGTGGCAACCAACACACTGTAT
 TTACAGAGACCAATTTCCACTCCCTTTTACTGTTTATTTGTCTGGGCTGAGGATATGCCACCCA
 TAAAAAGATNTGTACACAAAAACCAAAATTCCTCAGCCGGTCTGCTCTTAACCCCAATATC
 AAACGAGCAATCCCAAGAATGCTATTCTATTCGCCTATTACGGTACGAAACCAACATATC
 AAGTTACTTTGTACGCCGCCGCGAGCCGGATTACAGACATTAATAGAAAAGGTGAAAC
 AAGAGCAAAAAGGCTCTCTTTGATGAAACTAAACATATTACTTTTAAAGCAAAATCGTAGGT
 AATTTCTTTCACTCATACATAAATACTAATCGCGTCAACGATGTCTTAATCTGTCTATGCTG
 GTAAATTTTATTTGGTTGCAACAAATATGGGACTCTTTGTCTTAAATTAATGCTACATCGA
 TCAATCAAAAACAGTGCACCTTCTGCACAAAATATCAATTTACACAGATCTCTGTATTGG
 AAGATNTAAAGTTATGATCTTCTAATTTGACAAAAACCTGACGGCTGTCTTTTAGAGG
 TAATCGACGATGCAGAAAAATCCAGATTTTCTTTTCGAAAAAAATCTTAAAGTGTATTTA
 AATATGTTGCAATGTTCAAAGACGGTTTCTGTAATGGTAAAGAAATCATTATGATTGCAAC
 ATCATTTTGTGACGCCGCACAAATATTGATTTGTAAATCCTTTGATATTTGATTTTAAAT
 GCGGTAAATTTAAAAAAAACCTAAAGGCAGGCTTGGTAGATTTTAGCGTTGATTCTGAAC
 CTCTGTCTTTTCTTTTGGAGAAATAGATCTGCATTTGGTTGTAAAAAAATATCAAAA
 TATTAAACGTACCGGAAGTGTGTGATAAAAATGGATTTAAATGAGGGAGCTTTTAAATC
 TACATGATAACAAAGTTTATAGCGAACATGTATAAAGAGACGTTCAAAGTAGTTTCCATGT
 TCCCGATAAAAAATTCAACTTTTGCATGTTTTCAGAACTCTGCTTTTTTCTCAATTAAGC

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AAGGGAAGAGGGAGGAGACAAACGGATOTTTTCATTGCGAGGGGCAACCAGAACAGTTTCG
CGTGTTCCTACCCCTTATATTGTGGCAATTAATAGTAACCTTATTGAAATTAGACATATAG
AAAATGGAGAACCTGTCCCGCTGTGTACTTTGGAAACAAGATAAGTATGTTAAATCATATG
CCAAGAAGATCTTATATTGTTATGAGGATCCTCAAGGATTTGAAATTATCGAACTGTTAA
ATTTTPTGA

>YGR070W, 1155 aa (SEQ ID NO 174)

MNSNELDLRNKYFYEIFGKKRKSSTSTPTQLFSGSEVQTNINELISITNDEDEDSTEDENK
ASLKDYTLGHDTGARYRIAPDCSSSHQLKASPVLHISTNLNSSPQSPTGDIPTNKKISL
MDSTRQDEKGNSTTTSSPSQKRSNVLLPHVRKHSSPSLLSPSKNSGSHMGDPNQISTPPT
FKSAGHTMBELHSSFNKGKSSSSSTSSLPALSLKTQNRSSNSSMHSSQYRHTNQHQHH
SRKSSSPVSLTEISMIKGTPLVYPALLSLIAIKFKQTIKLSTHKKMGLLYRDSFTGKQAT
DTLCLIGSLDRNLCLMIGKSLEAQKLPFDVLYDHCVRDSVLEIYELSSSIPMAHQSSQS
STSIANTFSSSSSVNSLRTKTEIYGVTVPLTHCYSSSTCSLEKLCYISICPNRLQQQANL
HLKLGGLKRNISLALDKEEDERISWTSNVPKSVWESLSKQQIKRQEAIVEIPTTEKKFV
KSLEIIRDFTFKKLLLETNIIIPSDVRINFVKHVFABINEIYSVNREPTKALAQHQSLSPIC
PGIADIFLQYLPFFDFELSYIASRPYAKYLIETQRSVNPNFARFDDEVSNSSLRHGIDSF
LSQGVSRPGRYSLLVREIHFSDPVTOKDOLQMLMKVQDLLKDLMKRIDRASGAAQDRYD
VKVLKQKILPKNEYVNLGLNNEKRKIKHECLLSKQVNTDASPSGDIQFYLLDNMLLF
KSKAVNKWHQHTVFQRFIFLPLLFICPAEDMPPIKRYVTENPNCSAGVLLPQYQTSNPKN
AIVFAYYGTQOQYQVTLYAPQAPAGLQTLIEKVQEQKRLIDETKHITFKQMVGGQFHSYL
NPNRVNDVLIHAGKILLVATNMGLFVLNYATSINQKPVHLLHKISISQISVLEEYKVMY
LLIDKILYGCPLDVLDCAFNADFIKRNKSKVIKQYVAMFKDGFONCKRIIMIAHPLHAA
QLLIVNPLIFDFNSGNFKKMLKAGLVDFSVDSFPLSFLENKICIGCKKNIKILNVPEV
CDKNGFKMRELLNLHDNKVLNMYKEIFKQVSMFPIKNSTFACFPELCFFLNKQGGKREET
KGCPHWEGEPEGFACSYPIVAINSNFIEIRHIENCLVRCVLGNKIRMLKSYAKKILYC
YEDPQGFETTELNF

>YGR132C, 1364 bp, CDS: 501-1364 (SEQ ID NO 177)

CATACATGTATCAGACGTATAGCTCCACGATTCTCAAGAATCCAGAAGCTTGGCATATT
ATGCTATAAACCCGATGATTATGTATATTTTATGTTGTCTCCAGTAAGTGGCAGCATAAACC
CGCCCACTCTGCCCTGCATGCTGTGAAGCAATATGCGATATATACCACATATATTCC
GCTCCCGTTCCAGGATTTCCGAAAGAGAAACTTCAGTGAATGACTATGACTACATAGTTGG
AGTCTTAGACCATTCGCAANTGACTTATTCAAGTATCAGAGATCAACACTGATGAGAATAA
ACTCGTCTTCATGATGATACGGGTAACCGCAATGTATGCCATCAATAAATTTCCAGGGAAA
GGGAGTTTGACGATCTCATGGATGCAACGGTTGAGGATATATAATATTAGCAGAAAGAAC
AGGAAAAAATAAANTCCGTAACCAACCATCAACCCATACCAAACTTACATTCCAAATCA
ATAATTTACTTTTAGAAAAAGATGTCTAATTCTGCCAAACTTATCGATGTATCATCAACCAAGG
TGGCGTTGCCCAATKGTATAATTGCTASCGGGATTGAGTACTCCATGTATGATGTGAAGG
GTGGTTCCTGCTGGTGTTATTTTCGACAGAAATCAATGGTGTAAACCAACAGGTTGTGGGTG
AAGCCACTTCATTTCTTGGTGCTTGGCTACAGAAGGGGATCATATACCATGTGAGGACGA
AACCAAGAGCATTTGCTACCAATACTGGTACGAAGGATTTGCCAATGGTGTCAATTGACCT
TGAGAGTCTTACATAGACCAAGGTCCTTACAGCTACCCGCAATATACCAAAATTTGGGTCT
TCCATTACGACCAAAAGAGTGTACCAATCTATCGGCAATGAGGTTTAAAGTCTATAGTAG
CTCAATTTGATGCTGCTGAGTTAATTACTCAGAGAGAAATTAATTTCTCAAAAAATCAGAA
AAGAGCTTTCTACGAGGGCCAAACGAATTCGGTATTAAGTTGGAAGATGTCTCTATCACTC
ATATGACGTTTGGTCCCGAATTCACGAAAGCAGTTGAGCAGMCCAGATTGCCACACCNAC
ATGCCCAAGAGCCAAATTCCTTTGTCGAAAAGGCAGAGCAAGAGAGACAAGCTTCTGTTA
TCAGAGCTGAAGGTGAAGCAGAAAGTGTGAATTCATTTCAAAAGCCTTAGCTAAAGTTG
CTCATGCTCTCTTATTGATTAGAAGATTAGAAGCTTCTAAGGACATCGCTCAAACATTAG
CAAACTCATCTAACCTCTCTATTTACCAAGTCAACATTTCTGGTGGTGGTAACAGCGAGT
CTTCGGGATGACCAAAATTCCTTGTCTTTGAACATTTGGCGTTAA

>YGR132C, 287 aa (SEQ ID NO 178)

MSKSAKLIDVITKVALFGLIASGIQYSMDVKGGSRGVI7DRINGVKQVVGEGTHFLV
PWLQKAIIDVRTKPKSATWNTKDLQMSLTLRVTHRPEVLQLPAIYQNLGLDYDERV

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LPSIGNEVLKSIVAQFDRAELITORELISQKLRKELSTRANEFGIKLEDVSLTHMTFGPE
 FTKAVEQKQIAQQDAERAKFLVEKAEQERQASVTRAEGEAFSAEPISKALAKVGDGLLLI
 RRLEASKDIAQTLANSNNVYLPQHSGGGNSSESSGS?NSLLLNIGR

>YGR135W, 1277 bp, CDS: 501-1277 (SEQ ID NO 179)

TTCTGAAC TGAATCTGAAATGTGTTAAACCTGTTTCCCTCAAAGCCTGCAAACAAAGACGA
 TAGTTCCCTTATTACACCTTGCTTAGTTTTATCGCTGATTACTCCTTCGACACCCAGCT
 GAACCCCTCCAGGAAGAAGGGTGGTGTCTACCGATGGTAAGATTTTCCCATTGCCCAAAGC
 CGATAAGCCTATCCCACCTTCATGAATATATAACACTCCGACAGCTCGATGTTGGAGACAG
 TGAGTGAGCAGTGAATTCCTCATGTTTCTCTGCTCCTCATTTAATGACAAATTAGCCAT
 GTAATAACATCTTGAGGCAGTTAAATATTGCTTACCCCTGCAGGTGCCAAAAAATTTATAG
 AATAAAAGCATAAAAAAGATGGATATCTATGTAAATAAGGAAACATTGGCAGAGCGAAGAGA
 ACAGACTGCTTTCTATATAAAAGTTTTTCGATCAGTCTCTATTTTAAATAATTGATTATTGGA
 TATAGTTAGTAGTGTATAACATGGGTTCCAGAAGATACGATTCCAGGACAACAATTTTCT
 CUUCTGAGGGACCTTATATACAGGTTGAATACGCTTGAATTCUATTTCAUATGCAGGTA
 CCGCAATGGGATTATGGCATCTGATGGGATTGTTCTTCGACGACAGAACGCAAGTCACAA
 GACTTTACTAGAACAAGACACCTCTACCGAAAACTTTATAAGTTAAAACGATAAATTTG
 CGCTTGCCGTTGCTGGACTGACTGCAGATGCAGAAATTTCTAATAAATAAGGCTAGAATTC
 ACGCTCAAATTTACCTTAAACCTTATAATGAAGATATACCACTAGAAATTTTGGTGAGAA
 GCTTAACCTATATAAAACAAGCTTACACCAACATGCTGCTTAAAGACCATTTGGTGTCT
 CCTTTATCTACGCCGCTATAGACGATAGATACGGTTACCAATTGTATACATCTAATCCAC
 CGGGAAACTATACAGGCTGGAAGGCTATTAGTGTGCGCTAACACATCAGCAGCACAAA
 CCGTACTTCAAATGGACTACAGGATGATATGAAAGTCGATGATGCCATTGAAGCTGGCTT
 TAAAAAGCTTATCCAAACTTACCGACAGTAGCGCGCTGACTTATGACAGGTTGGAAATTC
 CTACTATCAGAAAGGGTGCTAATGACGGAGAGTGTATCAGAAAGATTTTCAAGCCTCAAG
 AGATAAAGGATATATTGGTAAAGACTGGTATTACCAAGAGGATGAAGACGAAGAAGCTG
 ATCAAGATATGAATAA

>YGR135W, 258 aa (SEQ ID NO 180)

MGRRYDSRITIFSPEGRLYQVEYALESIHAGTAIGIMASDGIVLAAERKVTSTLLSDQ
 TSTEKLYKLNDKIAVAVAGLTADAELINTARIHAQNYLKYNNEDIPVEILVRRLSDIKQ
 GYTHQGLRPFQVSVFIYAGYEDRYGYQLYTSNPSGNYTGWKAISVGANTSAAQTLQMDY
 KUDMKYDDAIELALKKIKSKPTDSSALTYDRLFAPIRKGANDEYVQKTFKPQEIKDILV
 KTGITKKDEDEADEDMK

>YGR155W, 2024 bp, CDS: 501-2024 (SEQ ID NO 181)

GTGTTCTCATCCGACCCCTCTGATTCAATTGCTGGCCATTACATTTTCCCTCAATGACACA
 TCCCTTATTTCATAACTGATTAAAAATGGTAATGGCAGGTGATAGTAGTGGCTCACAAA
 CAAAATTTCTTTCTCAGCGCTGACAAAGCTTCATTTTCATTTCTAACTTATTCACAAACA
 CTTCAACTTCACCCAAGTAAGGATAATCAGCTCTGTCGCTGACTGATAAATGCTATATCCG
 GCATATGCAAGTCCACACGGCATTACCGTTTTCACTAATTTATTGCCATTTCTCTCCACAGT
 TTTGCAACCGAAAGGCAAAAAAGAAACCAACACCGAAAAATTTTTTCTCCTAAAGGTAAA
 GTAAAAGGCAACACTTGAAGATTTCTGTTGTAGGCCACTTGCTCAAAGGACATCTAGATA
 AATACGACGTAAGAATAAAATGACTAAATCTGAGCAGCAAGCCGATTCAAGACATAAAG
 TTATCGACTTAGTTGGTAACACCCCATTTGATCGCACTGAAAAAATTCCTTAAGGCTTTGG
 GTATCAAAACACAAATTTATGCTAAGCTGGAACTATACAATCCAGGTGGTTCCATCAAG
 ACAGAATTGCCAAGTCTATGGTGGAGAAAGCTGAAGCTTCCCGTAGAATTCATCTCTCCA
 GACTACTCTGATCGAACCTACTTCTGGTAACACCGGTATCGGTCTAGCTTTAATTCGGCG
 CCATCAAAGGTTACAGAACTATCAACACCTTCCCGGAAAAAATGTCTAACGAGAAAGTTT
 CTCTCTTAAAGGCTCTGGGTGCTGAAATCATCAGAACTCCAACCTGCTGCTGCCTGGGATT
 CTCCAGAATCACATAATGGTGTGCTAAGAAGTTGGAAAAAGAGATTCTTGGTGTCTGTTA
 TACTTGACCAATATAACAAATATGATGAACCCAGAAGCTCATTAATTTGGTACTGGTGGC
 AAATCCAAAGACAGCTAGAAGACTTGAATTTATTTGATAATCTACGCGCTGTTGTTGCTC
 GTCTTGGTACTGGTGGGACTATTAGCGGTATTTCCAAGTACTTGAAGAACAGAAATGATA
 AGATCCAAATCGTTGGTGGCTGACCCATTCGGTTCAATTTTAGCCCAACCTGAAAACTTGA

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ATAAGACATGATATCACTGACTACAAAGTTGAGGGTATTGGTTATGATTTTGTTCCTCAGG
 TTTTCGACAGAAATTAATTGATCTTTTCGTATAAGACAGACGACAAGCCTTCTTTCAAAT
 ACGCCAGACAATTGATTTCTAACGAAGGTGTCTTGGTGGGTGGTTCCTCCGGTCTCGCCT
 TCACTTCGGGTCGTGAAAATCTGTGAAGACCAACCTGAAGTGAAGATGATGTTCATTG
 TTGCCATATTTCCAGATTCCATCAGGTCCGTACCTAACCAATTCGTGGATGACGATGCT
 TCAAAAAGAACAAATTTGTGGGATGATCAGGTGTTGGCCCGTTTTCGACTCTTCAAAGCTGG
 AGGCTTCGACGACAAATACGCTGATGTGTTTGGTAACGCTACTGTCAAAGGATCTTCACT
 TGAACCCGGTTCCTTCCGTTAAGGAAACCGCTAAGGTCACTGATGTATCAACATATTAA
 AAGACAATGGCTTTGACCAATTGCTGTGTGACTGAAGACGGCAAGTTGTCTEGTTTAG
 TTACTCTCTCTGAGCTTCTAAGAAACTATCAATCAATAATTCAAACAACGACAACACTA
 TAAAGGGTAAATACTTGGACTTCAAGAAATTAAACAATTTCAATGATGTTTCTCTTTACA
 ACGAAAATAAATCCGGTAAGAAGAAGTTTATTAAATTCGATGAAAACCTCAAAGCTATCTG
 ACCTGAAATCGTTTCTTTGAAAAAACTCATCTCCGTTATCACTGATGGCTTGAABCCAA
 TCCATATCGTTACTAAAGATGGATTACTGAGCTACTTAGCATAA

>YGR155W, 507 aa (SEQ ID NO 182)

MTKSEQQADSRINVIDLVGNTPLIALKGLPKALGIKQTIYAKLELYNPGSSIKDRIAKSM
 VEEAEASGRHHFSRSTLIEPTSGNTGIGLALIGAIGYRTIITLPEKMSNEKVSVLKALG
 AEIRPTAAAWDSPESHIGVAKKLEKMI PGAVILDQYNNMMNPEAHYFGTGREIQROLE
 ELNLFONLRAVVAGAGTGGTISGISKYLKEQNDRIQIVGADPFGSILAOPENLNKTDITD
 YKVEGTGYDFVTQVLDFKLIDVWYKTDKPSFKYARQLISNEGVLVGGSSGSAPTAVVKY
 CEDHPELTEDDVIVAIFPDSIRSYLTKFVDDDEWLKKNLWDDQVLA RFDS SKLEASTTKY
 ADVFGNATVYKDLHLKPVVSVKETAKVTDVILKLNKGFDQLPVLTEDGKLSGLVTLSELL
 RKLSTNNNNNDNTTKGYLDPKKIMNFNDVSSYNENKSGKKKPTKFDENSKISDINRFFF
 KNSSAVITDGLKPIHIVTKMDLLSYLA

>YHR095W, 935 bp, CDS: 501-935 (SEQ ID NO 207)

GACACCTTTTCCGGTGTTCGAGGGGCAACGGCGGCTTGCACCTTGACTTTCACTTAAAGTT
 GTCGTGAAAACCTTTCATTTTACCTTCTGGAGTATTCATGGCTTTGAACGACCAGATTC
 CAATTCATATGAGTTGGATGAATTGGATTTCGAGGAGATATTAGATCGGGAGTTGAATT
 CATCATTTTACGTATATCAACTAGTTGACGATTATGATATCTTTATAGATTTTAAGGTGG
 GGAAAGCAACATGAGACCCAGATGGAATTGATTATGGGGACATTGTTGCCCTTATATATA
 ATTTCAATATACTAATTCAAATGATTAAAAACGTGAGGGGACACGCAACTTCGGGTGTT
 AAGAAATATTTTGCTACATTAGATAATGGTGGAGTTTCCTGGCTTGTCGGATAAAAGCCA
 TCAAATGTGCGAGCAGCTCATCTTTACGTTTCTGTCTTCTCCCCACCTCATATGAGTGG
 TATCTTTCTATCAGCACTTGATGAATATTCTTPTTCTCATATATCTGAAAGACAAAAGAT
 CGGCACGGCAATGCCCTGCAGCAITTTCTTCTAGTTTTTCCGAATTTCCATTACGTATTG
 GATCTTGTCGGCATATTTGTCACTCCTTCACGGAAAAAAGAGCACTCCGTCACCTT
 CGGAAAAACCTTTTGACTCAATGCAACAGTGTCAATACTCTTTGCGCTGTCTCTTCAAGA
 AAAATCAGGAGTGCAAGATATCGATTAAATCTTGGAGTTATGATGGTTAGTCTTAGTT
 TAACTCTCTTGAAGAAGGGTTTTTTTCAAGTTGGTCAACACTCTTTAGAGGTAAAAA
 AAAAAAAGAGAATTCTTCATGTAATTTACCATGATTCTACCTTTTGCAG
 CAAAAATGAAGATAATCCGAGCGCATGCCAAGTAG

>YHR095W, 144 aa (SEQ ID NO 208)

MMILFLIYLKDKRSARQCPAFLPSFSEFLRIGSCAHICQSFTKXKEHWVTSEKLLTQ
 CMSEVILCAVSLKKNQECKISINSLEVMMVSLSLTLKKGFFSWSFLFRGKKKKKKKKR
 ILHVIYHDSFTLQAKMKIIRAHAK

>YHR138C, 845 bp, CDS: 501-845 (SEQ ID NO 209)

CTACGAAATTAAGCAAAATTAATAAATAAACAAACAAACAAACAAACAAAC
 AAAAAAACAANCAAAACACATATTTCTTATGATGACTCCACCAAGAGATCGTGGTGA
 CTTCCTAATTTGTTTGTCTTCAGTACAGTTACTATCAGTGTCTCTTTCTTTTATATG
 ACTATGTGATGTTACTGATACATCACGGCGCTTCCTTTATGTTTCTTTTATGTTCCG
 TACAGGATTTATAGTTTTTACACTATATGACTTCAATAATTTCTAATATTCAGTTCCCA
 TTAAATTTGATTATTCGATTAGATCGGTCCGCGCTACCAAAAGAGGCGAAGAAAAGAG

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GAAAAACGCAAGTGGATAAAAGGGGTGGGGGGCAAAAGTATTTAAGAAAAAGCGATGCGATG
 GAGAGAACAANTGGATAAGTTGCGTTTCCTCGTTATATTACAACATTTAAATCTATTGTG
 TAACAGACTATAGCATATATATGAAGGCCAGTTACTTAGTTTTGATTTTCAATTAGCATAT
 TCTCCATGGACAGGCATCTTCCTTATCATCATACATCGTAACTTTCCCCAAGACGGATA
 ATATTGGCTACCGAACCAGAATAGCATTATGAAGATGTCAAAAAATATGTGGTGGACATAG
 GGGTTAAAATAACACACGAATATAGCTTGATAAAGGGCTTTACAGTGGACTTAUCTGATA
 CCGACCAATTTTGGACGGTCTGAAAGAACCTTTGAGCTATATTGAAAGCGAGTACGGTG
 CTAATTGCAATTTGGAAAAGGATTGAGAAGTTTCATGCTCTAAACCGTGACCATTAGTTG
 CTTAG

>YHR138C, 114 aa (SEQ ID NO 210)

MKASYLVLIPLSIFEMAQASSLSSYIVTFPKIDNMATDQNSILEDVKKYVVDIGGKITHE
 YSTIKCFTVQLPDSQILECLKERLSYTESSEYGAKCNLEKDSFVHA1NRDHLVA

>YHR179W, 1703 bp, CDS: 501-1703 (SEQ ID NO 215)

ATATCTTACGTAATCAACTTCCGTAATCAACTTCCGTAATCAAGATCTCTTAGCATCTC
 TTGTTCAATCTTCAGACTCTACTAAGTGTCTTACCAACCATTGGATGCTCATTACAAAT
 GAATGAATATATTGCACGGAAACGGAAGCGCATGCTTTTCCGTCCTCGTGCTTAGTAA
 AGCAAAACGGAGTAGAATCGGTAAGAACTTCCTTTTGGGGTGGAAAATCATTGCCATTG
 TTTTGGACACCTTTCTTTTTCCTGTTATGTTTCGAGCACCGCGTTCTTTTGGGTACTTGAT
 GAGGTAGCAGATTCTTGGAACTGCTTTCTCTCGAGGTAACCTGCCCTGTTCTCTCTGGT
 GACTTTCTTAAAAATATAAAAGGAAAAGCATATCTCTAGTTTCGAGTTTTTTCTTCATACTT
 TATTTCTCTTATCTTAAACCGCTCCAGATATAGAATAAAATCATCATATTAAGCTAAATATAG
 ACGATAATATAGTATCGATAATGCCATTGTGTTAAGGACTTTAAGCCACAAGCTTTGGGTG
 ACACCAACTTATTCAACCAATCAAAATGGTAACAATGAACCTTCTACACCGTGCTGTCA
 TTCTCTCATTTGACTAGAAATGAGAGCCCAACATCCAGGTAATATTCCAAACAGAGACTGGG
 CCGTTGAATACTACGCTCAACGTGCTCAAAGACCAGGAACCTTGATTATCACTGAAGGTA
 CCTTTCCCTCTCCACAATCTGGGGGTTACGACAATGCTCCAGGTATCTGGTCCGAAGAAC
 AAAATTAAAGAAATGGGACCAAGATTTTCAAGGCTATTTCAATGAGAATAAAATCGTTTCGCTAGG
 TCCAATTAATGGGTCTAGGTTGGGCTGCTTTCCAGACACCCCTTGCTAGGGATGGTTTGC
 GTTACGACTCCCGCTTCTGACAACTCTATATCAATCCAGAAACAACAACAAAAGCCTAACA
 AGCCTAACCAACCCACAACACAGTATTAACAAAGGATGAATTAAGCAATACCTCAAGAAT
 ACGTCCAAGCTGCCAAAACTCCATTGCTGCTGGTGGCGATGGTGTGAAATCCACAGCG
 CTAAACGGTTACTTCTTCAACCACTTCTTGGACCCACACTCCAATAACAGAACCGATCACT
 ATGGTSGATCCATCGAAAACAGAGCCCGTTTCACCTTGGAAAGTGGTTGATGCAGTTGTGG
 ATGCTACTTGGCCCTGAAAAAGTCCGTTTGAGATTGTCTCCATATGGTGTCTTCAACAGTA
 TGTCTCTCTGCTGCTGAACCCGCTATTTGTTGCTCAATATGCTTATGCTTTAGGTGAACCTAC
 AAAGAAGAGCTAAAGCTGGCAAGCGTTTGGCTTTTCGTCCATCTAGTTGAACCTCGTGCTCA
 CCAACCCAAATTTTAACTGAAGGTGAAGGTGAATACAAATGGAGGTAGCAACAAATTTGCTT
 ATTCTAATCTGGAAGGGUCCAATTATTAGAGCTGGTAACCTTGGCTCTGCACCCAGAAGTGTG
 TCACAGAAGAGCTCAAGCATCTCTAGAACATCGATCGCTTACCGTAGATTTTTTATCTCTA
 ATCCAGATTTGGTTGATCGTTTGGAAAAAGGTTACCATTAAACAAATATGACAGAGACA
 CTTTCTACAAAAATGTCAGCTGACGGATACATGACTACCTTACGTAACGAAGAAGCTCTAA
 AACTCGGTTCCGACAAAAATTA

>YHR179W, 400 aa (SEQ ID NO 216)

MPFVKDPKPKQALGDTNLFKPIKIGNNELLHRAVIPPLTRMRAQHFGNIPNRDWAWEYYAQ
 RAQRPTLLIITEGTFPSPQEGGYDNAPGIWSEEQIKEWTKIFKATHENKSPAUVQIMVIG
 WAAFPDITLARDGLRYDSASDNVYMNACQEEKAKKANNPOHSLTKDELKQYVKEYVQAAKN
 SIAGAGDVEIHSANGYLLKQFLDPHSNNRTDEYGGSIENRARFTLEVVDAAVDAIGPEK
 VGIRLSPYGVFNMSGGGAETGIVAQYAYVLGRIFRRAKAGKRLAFVHILVEPRVTNPFLTE
 GEGEYNGGSKFAYSIWKGPILRAGNFALHFEVVRREEVKDFRTLIGYGRFFISNPDLVDR
 LKXGLPLNKYDRDTFYKMSAEGYIEYFTYEALKLGNLKN

>YIL074C, 1910 bp, CDS: 501-1910 (SEQ ID NO 219)

CGGGAGTCTTTAGCAAGTTCCGGCAATATCGATATCAATAGTATTGCTAAATAAACCTTT

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TTTATTCOCATTEACTGTCCCTTTTATACCTGGCTGACCCCTTAATTCCCTAGCAATCTTTGCCT
 GCACCCCGTACCAGGAAGCGTGATAGAATCGGTAGCTACAAAATTTTATGATAGTTAATA
 AGTGCCTATTCGTTTTCATAATGTCCAGTGCACCTATCAATAATATTACACTCTTGTTCTTG
 CCAAACTATACACAAAATGCCACATTTTTTTTCTTTACACCGAAGAATTTGGCCGTCAGCCG
 GACAGCGCTCAGATTAAATGTGCGCTAGATTCCTTTACCGCTGGAAACGAGTCACCGTTATG
 AAAACTAATGGAATCTCCAGGTTTAAATACAATAGAAGGTTACGAGCTACTACATTAAAA
 AATACTTTTGTCTGTTTATGCTGTAGATTATTCTAACATTAAAACTAACAAACACTGATT
 TCGGGTATTTCCCTCCCTAACATGTCTTATTTCAGCTGCGCGATAATTTACAAGATTGATTCC
 AACGTGCCATGAACTTTCTGCGCTCTCCTGCTGCGAGTCTCAACCTCAOCAAACCTCAGTCAT
 TTTCAACACACTACCTCCTCGTGTAAAGCATTACAAAAGCAACCAAGGCTTTAAACCTTT
 TTTCTACTTGGTGACATGAATATTCTACTGTTCGAAAATGTCAATGCAACTGCAATCAAAA
 TCTTCAAGGATCAGGGTTACCAAGTAGAGTTCACAAAGTCTTCTCTACCTGAGGATGAAT
 TGATTCAAAATAACAAAGACGTACACGCTATCGGTATAAGATCCAAAACCTAGATTGACTG
 AAAAAATACTACAGCATGCCAGGAATCTAGTTTGTATTGGTTGTTTTTGCATAGGTACCA
 ATCAAGTAGACCTAAAATATGCCGCTAGTAAAGGTATTGCTGTTTTCAATTCCGCATTCT
 CCAATTCAGATCCCTTACCAGAAATCGGTAAATGCTGAGATTCATTAGTTTAGCAACACAAT
 TAGGTGAATAGATCCATTGAACCTGCATACAGGTACATGGAATAAAGTCGCTGCTAGGTGTT
 GCGAAGTAAGAGGAAAAACTCTCCGTATTATTGGGTATGCTCACATTGGTTCCGAATTAT
 CAGTTCTTGCAGAAGCTATGGGCCGTCATGTGCTATACTATGATATCGTGACAATTATGC
 CCTTAGGTACTGCCAGACAAGTTTCTACATTAGATGAATTGTTGAATAAATCTGATTTTG
 TAACACTACATGTACCAGCTACTCCAGAACTGAAAAAATGTTATCTGCTCCACAAATTCG
 CTGCTATGAAGGACGGGGTTATGTTTATTAATGCTTCAAGAGGTAAGTGTGCTGACATTC
 CATCTCTGATCCAAGCGTCAAGGCCAACAATAATGACAGTCTGCTTTAGATGTTTATC
 CACATGAACCAAGCTAAGAACCGTGAAGGTTCAATTAACGATGAACCTTAACAGCTGGACTT
 CTGAGTTGTTTTCATTAACCAAAATAATCTGACACCCACATATTGGTGGCTCTACAGAAG
 AAGCTCAAAGTTCAATCGGTATTGAGGTGGCTACTGCATTGTCCAAATACATCAATGAAG
 GTAACCTCTGTCGGTTCTGTGAACCTTCCCAGAGTCAGTTTGAAGTCTTTGGACTACGATC
 AAGAGAACACAGTACGTGTCTTGTATATTTCATCGTAAGCTTCTGCTGTTTGAAGACCG
 TTAATGATATCTTATCCGATCATAATATCGAGAAACAGTCTCTCTGATTCTTCACGGCAGAG
 TCGCTTATCTAATGGCAGACATCTCTCTGTTAATCAAAGTGAATCAAAGGATATATATG
 AAAAGTTGAACCAAACTTCTGCCAAAGTTTCCATCAGCTTATTTATACTAA

>YIL074C, 469 aa (SEQ ID NO 220)

MSYSAADNLQDSFQRAMNFSQSPGAVETSPTQSEFMNTLPRRVSTIKQPKALXPFSTGDMN
 YLLLENVNATAIKIFKQGGYQVEFFKESLPEDELIEKIKDVHAIGIRSKTRLTEKILQHA
 RNLVCIGCFICIGTNQVDLKYAASKGI AVFNSPFSNSRSVAELVIGSII SLARQLGDRSIE
 LHTCTWNKVAARCWEVRCKFLGIIIGYCHICSQSLSVLAEMGLHVLVYDIDVTIMALCTARQ
 VSTLDFVJNKSDFTLHVPATPETEKMLGAPQFAAMKCGAYVTNVRGTVVDIPSLIQAV
 KANKLAGAALDVYPHEPAKNGEGSFNDELNSWTSELVSLPNILTPHIGGSTEEAQSSIG
 IEVATALSKYINEGNSVGSVNFPEVSLKSLDYDQENTVRVLYIHRNVPGVLKTVNDELSD
 HNIEKQFSDSHGEIAYLMADISSVNQSEIKDIYEKLNQTSARVSTRLLY

>YJR037W, 992 bp, CDS: 501-992 (SEQ ID NO 221)

GATTTCATGCTTTTTCGCGGAATTTCCCTCCACCAACGCTTCCATTCGAGACCTGTCCCGTGA
 TGTCGAGGACACGATAGACAAATTTCTCTGCACCGTATCTCTTTGCAAAAGACTGCAGAC
 CAGCTTCCGTCTTTGCTACGCCGTAGACGATGCATTTCATCGTCTCTCTTCGATAACAGATT
 TCACCAATTCGAGGCCAATCCCACGGGAGGCACCTGTAATCAAATAACCTTGCCCATAT
 CCGTTCTTTGACAGATTATAAGTTGTTTTCTCTCTGTTGCTGTTCCGACAGCCCTTATTTCT
 CTGTATTCCCTCTCTCTTTTCTGCAATATCGTTTCTAGCCACTTACGAAAAAGGTCAAA
 AAGTGAAAAAAAGAGGGAAAAAACCATGAGGAACAGTATGCTCCCTTAATATCGGAAAAG
 CAATAGTAATAAAAAACAGCATCAGAGCTTTCCACGTCTCTCTCTTCCAGCTCTCATCTC
 GTAAAGTATTCAAGTTTATCATGTGCAATTTCTATAAGCTAGCACCTGTTGACAAGAAAG
 GCCAACCATTCCTCTTCCACCAATTAAGGGGAAAAGTGGTGCCTTATCGTTAATGTTGCCCT
 CCAATCTGTCACCTCACTCTCAATACAAAGAACTAGAGGCCCTTGTCAAAACCTTATAAGC
 ACGAAGCATTTACCATCATCGGGTTCCCATGCAACCAGTTTGGCCACCAAGAACCTGCGCT
 CTGATGAAGAAATGCCCAGTTCTGCCAACTGAACATATGGCGTGACTTTCCCATTTATGA

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AAAAAAATTGACCTTAATCGGTGGCAATCAGGACCCTGTTTACAAGTTTTTTGAAGAGCCAAA
AATCCGGTATGTTGGGCTTGAGAGGTATCAATGGAATTTTGAAAAATCTTAGTCGATA
AAAAGGGTAAAGTGTACGAAAGATACTCTTCACTAACCAACCTTCTTCGTTGTCCGAAA
CCATCGAAGAACCTTTTGAAAGAGGTGGAATAG

>YIR037W, 163 aa (SEQ ID NO 222)

MSEFYKLAPVDKKGQPPFFDQLKQKVVLLVNVASKCGFTPQYKELEALYKRYKDEGPTII
GFPCNQFGHDEPGSDEBIAQFCQLNYGVTFPIKKKIDVNGKNEDPVYKFLKSQKSGMLGL
RGIKWNFEKFLVDKKGKVYERYSSLTKPSSLSSETLEELLKEVE

>YJL161W, 1043 bp, CDS: 501-1043 (SEQ ID NO 229)

TCATAAAGTCTGGCGGGTATTCCCTTGACACAATTTTCATATCTTCCCATATGAATACCTG
TTAGTCCGTATCACCAAGTGTAACTGTTCTTTACCAATGAGAACATCTAGAGTCTTTCTG
ATATCGGTAACITCTGCCTCATTAAATTTAAAAATTTCTTCATAGTAAATAGCTTATTGCT
TTGGAGCAGATGATCGACATGTATTTTAGGAACATAAACTGCCATAAAATATAATAGATCA
GCTTAAAAAATAACAATGCCAATCAACAAAGTTGTATTTCCCTATCTTCCGATATTCCGAGT
CCACCATTCAGACCTCTGGTGAGATAGTTTGCCCTGCTTTTGCTCCCTTCCAAAGTGCTGA
TAAAAACCTCCGTGATTTTTTGAATACTCCCTGAATGTCTATTTTAAGTATATTTATAAA
ATTAGTTTAAAGTTGGTGCGGATAACGAAAACCTTGATGCAAGGTAAATAAATCAAGTATAT
CATAGAGTTCTTTTCAATTCATATGCTATACACAAGGTTTGTTACGTCACAACCTCACAAATCA
CCAAGTTTTTCAGGCACATCGCCCAATCTTGGCTCAAAACCTTTATTTTGAAGGGTAATT
TGTACACTAGTCTTTTATGACAACTGTATGGGACAGGTCCTGCCATGCCCTATATCTTAG
AATCAAAATAGCTTGAATAAGTCCAAAGAGCAAGAAGATCCCCATGCCATCGCAGAAGACG
ACATTGTAAATATAGTCCATGACGCTCCCAATAGAATATTCAGCCAGCAGCTTGATACCT
ATCAAGAGAAAGAGCTTGACTTACAAAAGAGTGACCTCCATAAAGTACTTCATTCTTTGA
CGTACAGTGATCTCTCTCAATTTTCCATTGTTTGGGGGTTTCTCATTCAACTTTTCGAGCC
TAATAGGCAATTCACCTTAGGCAAAAAATCCATTCTTTATAAGGGAAGTGTCGTTAGTG
TTTTAGGGTTCCACCGTTGATTTATATGGCACTTAAACTTAGGATGAACAGCTCGAAA
AAGCTGGAGTGCGCTTTGAGTAA

>YJL161W, 180 aa (SEQ ID NO 230)

MLYIRLLNHSQPTKFSGTSFNLGSKPLFSKCNLYTELLVTTLYGTGLACLYLESNSLNK
SKEQEDPHATAEDDIVNIVHDAPNRIFKPALDITYQEKELDLQKSDLHKVLHSLTYSVDSQ
FSIVWCFLIQLSSLICNSTLSEKKSILYKGSVSVVLGFPLIYMALKLRMKQLEKAGVRF

>YJR096W, 1349 bp, CDS: 501-1349 (SEQ ID NO 233)

CTATATTCAACAAGCAATGACACACCCAAAACCCAAAGCCATTAAAGTAGATGATGAACCAATG
GGACTACAAAATGAAATATAGAAAAAATAGAAATAGGCTAGAAGATCAATTTATTATTCGC
CCTATTCTTCTTTATTACCTACACAAAAATAAAGCAGCAACAAGAAACAAAAACAAAAAT
GAAAAACAACCAATAAATCTATGTAAAGCACTACTCAATTTCAATTGATATTCAATTACTTG
ACTTTTTTGTCTTATTGTAGGCTCCATAAGCGCGCCATTTTCCCTACTCCCTTTTTTC
GTAAATAGTAATAATGTGCTGAAAAGAACAATGAAGTAGTTATCATACATATTCCGTCGT
GTCCATATGAGGGGAGGTGTCCTCTCTCTCTCATCCCTTGTCGCAACCTCCAATATATAAG
AGCAATAGCAACCTGATCTTACTTTTGTAAATTAACCTTAOCATACCTAGCCCAAGGAAGAA
AAZAAATTCACCTCAACAACATGGTTCCCTAAGTTTACAAAACCTTTCAAACGGCTTCAAA
TCCCCAAGCATTGCTTTTGGGAACCTACGATATTTCCAAGATCGCAAAACAGCCGAATTTGTCT
ATGAAGGTGTCAAGTGCGGCTACCGTCATTTCCGATACTGCTGTTCTTTATGGTAATGAGA
AGGAAGTTGCGGATGGTATCATTTAAATGGTTGAACGAAGATCCAGGGAACCATAAACGTG
AGGAAATTTTTCACACTACATAAAATATGGAATTCGCAAAACGGATATAAAAGAGCTAAAG
CTGCCATTCGGCAATGTTGAATGAAGTCTCGGGCTTGCAATACATCGATCTTCTTTTGA
TTCAATTCGCCACTCGAAGGTTCTAAATTAAGGTTGGAACTTTGGCGCGCCATGCAAGAAG
CGGTTGATGAAGGATTGCTTAAGTCTATAGGGGTTTCCAACTATGGGAAAAAGCACATTG
ATGAACTTTTGAACCTGCCAGAACTGAAGCACAAAGCCAGTGGTCAACCAAAATCGAGATAT
CACCCTGGATTATGAGACACGAATTAGCCAGATTACTGTAAATCTAAAGGCTCCCGTCGTG
AAGCCCTTTGCCCAATTTGTGTCACGGCTACAAAATGACTAATCCAGATTTAACTAAAAGTTT
GCAAAAGAGGTGGACCGTAATCCAGGTCAAATTTTGATTGCTTGGTCTTTACAACACGGTT

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ATTTTACCACTACCGAAGACTAAAACITGTGAAGAGGTTAGAAGGTAACCTTGCAGCCTACA
ACTTTGAACTGTCAGACGAACAGATGAAATTTCTTGATCATCCTGATGCTTATCAGCCTA
CCGATTGGGAATGCACAGACGGCCATAA

>YJR096W, 282 aa (SEQ ID NO 234)

MVPKFYKLSNGFKIPSIALGTYDIPRSQTAEIVYEGVKCGYRHFDTAVLYGNEKEVGDGI
IKWLINEDPGNHKREEIFYTTKLWNSQNGYKRAKAAIRQCINEVSGEQYIDLLLIHSPLEG
SKLRLETWRAMQEAVDEGLVKSIGVSNYCKKHIDELLNWPCLKHKFVWNQIETSPWIMRQ
ELADYCKSKGLVVEAFAPLCHGYKMTNPDLLKVCKEVDNRNFGQVLIRWSLQBGYLPLPKT
KTVKRLEGNLAAYNFELSDEQMKFLDHPDAYEPTDWECTDA?

>YKL065C, 1121 bp, CDS: 501-1121 (SEQ ID NO 241)

CTGGGCTTAGGTTTCACATATCAAAAAGAASTTATGGCTTATGTGCTCTTTCTAAGTTTGA
CTTTTATGCCAATAATTTCTCCCTAGATCGCCGCCCGTTGAAGCAGCAGAATATTTTAAGT
GCCGCCATAAAAACCCTAGATAGAAAAGAAAGGAGAGAACATAAACGCAGAACACCACTACT
TTTAAAGGCGTACGCAAACTGTTGGGCTTATCTATATTGTACTATCTACCTACTTGCACCG
TCCTTTTACCTCCTCGATACCTACTCCTTATGCCCTGAACAATTTACATGTAACCCGCAAC
TGCATGCTATATACAGGATACGTTAACATAAAGGGGGCGCTACTAAACCCCTCTGGCGCA
GTGCAAAAATAGAAATATATGCCAAGTGGGACCTTGTATAGTTTCTGGTTTAAAGCTACT
CCTTCATGCCAACGCTCCTTTCTGCTATCCTTTTCGCAAGTGGCAAGTACTGAAAACCGA
GAAGAATAAATAATATATGCGATGAGTTTATACTTTACGACATTATTTTATTGCTCACTG
TTGAGGTGGTAATGCTCTTCATCTTCGTTTTCGCTTTGCCATTCCCGATCCGTAGGGGTA
TTTTTAGCACCTATAACCAATTGACAGCGAAGCAGCAATATAAATCTATAATCTTTATAA
CGGGTTGTCTGTGTTGGGCTGTCTGTTTATTGATTCATGCAAAAGCTCTCAAATTCGTGTTT
CATTATACCACAACGACAACAGTGGCTCAATCGGGTCATCTGCTGTAACCTCCAAATACAGG
CACFAGCAATCAAGAGCGTACAATCAAAGAAATATGTATATTTCCGGGTTCATATTGTACT
TTTCTATCTCTATCCCACTCTCATCTCTTCTTCTCAAGACACTGCTCAAAATACCAAGGCT
TAATCAACGAACACAAAACCAAAAATGAACAAACCTTCTCTCAACACCAAGAAAGCACT
CAAAATGAAGCTGATTCACCAACCTCAAGAGGAACCTAAGGAAAAAGCAAAATTTCTCTGG
AGGGCCTACAAAAGCAAGTCAAAAACCTGGAGAAATATTTTGATGAGAAGAAATCAACCTG
GAAATGTAGCAGCTGCTGAAGCTTCCAAGAAAGGAAACTAA

>YKL065C, 206 aa (SEQ ID NO 242)

MSLYFTTLFLLLTVEVVMLPFPVLPLPFRIRRGIPSTYNQLTAKQIQIKTIISTGTCLVGL
LFTDSWKRQIRVSTVHNDNSGSSICSSAVTPIQALASRAVNRNMYISGFTLYFSJCTPT
VMSIVKRLVQKYQGLINEQEKQKLKFESENCKDNEADSTKLQZELRKKQISLEGLQKQV
KNLEKYFDEKNQPGNVAAAASKKGN

>YKL196C, 1103 bp, CDS: 501-1103 (SEQ ID NO 253)

AAAGAGGCTTCCTATTAGGAGCAATAAAATATAAASCACCAGCCATAGAAAGAATCCCCA
TTATAAAGCCUGCTGTTTTTTCTTGATTTGGAGTTCTTACCGAACTGAGGGGAGGACGCCA
TGAGACGCTCTTGTTTGGTGTGCGGCATAACCCCTTCCCACTTGAATTGACGGCCTGTTTC
TGCACGCATTCCCTGACGACTAAGTTGCCAAGCATTTTACTGATAATATACACTCTTTTGA
TCGAGCCTACTTCCAGTTGGTAATTGGTGTTCACAAATTTACGCAATTATATGTTTTTAA
CCAAATTCGGCTCCTTTTCCCTTTTTTCTTATTGGCTGGCGTGCCGTACAGAAACGATT
GGCTTGGTGTGAAATCAAGAGCAAGCACANTAGATATCAACATGAACAATATACAAAAGT
CTCTGGCACAGTTTGACTGGCTTAGACACAGGCTAGGGCAATTTCTGAAGCTTTACGATCA
CTAGAGAAGTTATTTTGGCAATGAGATCTACTACATCGGTGATTTTCTGCTCTGGAGGAG
AAAAGGCTCTAGAGTTGAGTGAAGTTAAAGACTTCTACAAATTTGGTTTCTTTGAAGGT
CTAGTGTGTGGCCAGTTTATGACTTTTTTTGCTGAAACGGTCCGCTCTAGAACCTGGTCCAG
GACAAAGACAAACCTATAGAAAGAGGCAACTATATTGCCCACTTTATGCTCAGGAGTGAGG
GCATATGTGGTGTTTTGAATCACCGACAAACAATATCTGTGAGACCAAGCATACACACTAT
TAAACAAAATCTTGAATCAATATTTAGTCCGACATCTTAAGGAAGAGTGGGCGAGATGTGA
CTGAGACCAATGATGCATTGAAAATGAAGCAACTGGACACTTACATTAGCAAAATATCAAG
ATCCTTTCACAGGCTGACCTATCATCAAACTTCAACAAGAACTGGATGAGACGAAAATCTG
TTTTTGCACAAAACGATTGAGAAATGTTTTACAAAGAGGTGAAAAGTTGGATTAATTTGGTGG

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ACAAATCGGAGTCATTAACGGCAAGTTCCAAAATGTTTTATAAGCAAGCTAAAAAATCCA
ATTCCTGTTGCATCATCATGTAG

>YKL196C, 200 aa (SEQ ID NO 254)

MRIVYIGVFRSGGEKALELSFVKDLSPQGFPERSSVCGQFMFFFAETVASRTGACQQRQSIE
FGNYIGHVVARSEGICGVLTIDKEYPVRPAYTLNKLDEYLVVHPXEEWADVBTNDAL
KNKQLDITYISKYQDFSQADAIMKVQQLDETAKIVLHKTLENVLQRGEKLDNLVDKSESILT
ASSKMFYKQAKKNSCCIIIM

>YKR076W, 1613 bp, CDS: 501-1613 (SEQ ID NO 259)

TAAATAGTTGAGGCTTTTCCTGCAATCTGTCAAGAAGGGTATGTGTATGAACATGCAAAAT
CACACTGTAAATGATTTCATTACCCGTGATTATGGAGTGATTTTCTTTCTCTTTTCTTTT
ACATTTTAGTTTCATTATTATGCAAAATFAGAGGGTATACAGTTGAGATTTTAACACTTTTGA
ATTAAAAAGTGTGTACAGAGGAAACCGACGCAAAAAGGCTTGGTGACGCAAACTTTTCCATC
TTTATTTTCACCTCTTCAGACGGTCTTAAGACCTTTTGAACGTATCAATATAGTTTTCATCA
TCTGTTCTCTGTTGTTCTCCGTTACTAAGATATTAGTCAGCTCTTGAAATTTTACACCCCC
TATTTTATTTGTCTTAGCGTCCAACCCCTCTCAACCCCTTTTCCATTTCTTGTATAAAGCTA
GTTAATTAGGTAACGCTGCTCTTACCATCACTACAGTGCTTACGAGAATTTACCCAAACC
CTGCGCAACGATAAAATAAGAAATGTCGAAACAGTGCGCGAGTGGTACAAACGGAGCTTTCA
AAAGACAGGTTTCTGCTCTTCAGAGAAACAATCTCTAAGCAACACCCCAATTTATAAGCCAG
CAZACCGCAAGATATTGGTTGTATGTTCACCTTGCATGCCCATGGGCCCATAGAACACTAA
TTACGAGCGGCTTTGAAAGGATTAACCTCTGTTATAGGATGTAGCGTAGTCCATTGGCACC
TTGACGAGAAAGGATGGAGATTTTTTCGACATGGAAAAGCAATTGGAGGACAGTGAGAGATT
TTTTGCAACATTGCCACGATGTTGCACTGTGTTATTAGAACTGCTAAAGAGGATTCCAGCA
AGAGCTTCGCCGAGATCAAGAATGACAGTCAAAGATTTCATGGTTGATGCTACCAATGAGC
CTCACTATGGATACAAGAGAATCAGTGACTTATATTACAAGAGCGATCTTCAATTACTCGG
CAAGGTTCACTGTCCTGTCGACTTAGAAACCCAAACAATTTGTTAAACAACGAAA
GTAGCGAAATTAAGGATTTTGAATCTTACTGCGTTGCGATCAATTTGTCCACGACGATC
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GGGTTTACGACAGCATCAACAATGGTGTATACAAACACUGGATTCCGAGAGAAAGCAGAAG
TTTACGAAAGTGAAGTCAACAACGTATTTGAACATTTGGACAAAGTGAGAGAAATCTTGA
GTGACAAATATTCCAAATTCAGGCCAATTAACGTTGAAGAAGATAGACAAAAATCTTGG
GTGAGTTCTTCACTGTGGGTGATCAATTAACAGAAAGCTGACATTAGATTGTATACAAACCG
TCATAAGATTGATCTGTGTACGTCCAACATTTCAAATGCAATTTTACCTCTATTAGAG
CCGGATATCCATTTATTCATTTGTGGGTAAAGAAATTTATACTGGAATTATGATGCCCTTCA
GGTACACAACAGATTTTGACCATATCAAGTTTACACTACACGCGTTTCCACACAAGGATCA
AACCCTTGGAATTAACGCCCTTGGGACCCAAAGCCAGATATTGCTCCTTTATAA

>YKR076W, 370 aa (SEQ ID NO 260)

MSKQWASGTNGAFKRQVSSFRETISKQHPYKPAKGRYWLIVSLACPWAHRTLITRALKG
LTSVIGCSVVI:WHLDEKQWRFLDMKQLEDSEDFLEHWEIVAGGIRTAKEDSSKSFAEIK
NDSQRFMVDATNEPHYGYKRISCLYKSDPQYSARFTVPVLWDLETQTIVNNESSEIIRI
LNSSAFDEPVDHDKTDLVFAQLKQTQIDDFNSWVYDSINNGVYKTGFAEKAEVYESEVN
NVFEHLDEXEKLSDKYSKLKAKYGEEDRQKILGEEFTVGDQLTEADIRLYTTVIRFDPV
YVQHFKCNFTSIRAGYDFIHLWVRNLYWNYDAPRYTTDFDHIKLYTRSHTRINPLGITP
LCPKPDIRPL

>YKR092C, 1721 bp, CDS: 501-1721 (SEQ ID NO 261)

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ACATAAATTTGTTTTTTCACCTCCAAATAGCCAGTTAAGTCAATTTGTTTTATTACAGAA
GGTGTACCTTCTGTTGAGTTATTTTACTCTTGTTTTGTAGTTTGTACATCTCTTTATGT
CTTGAATCAAAACGATAATTCGAAGCTTATTGCAATTTAGTTCTCTTACCCATTTCTTTAC
AACGGGCCCGAGAAAAAGTGGAGTTGGTCCGAGGAAGCTTTCAACGGCAAGAGGAAAAAAC
CTTCCCATCCCTCCAGCATACAATTTTTTTTTTTTCAATGCAGGCTGAAAAAAAATTT
CACTTGATGATGTAAGTCACTCATCCACITTTATACAAAGCAAGAAAGAAACCCAGTCCGAG

[illegible]

MASKKIKVDEVPKLSVKRKKETFEKSSSSSSSSSSSSSSSSSSSSSGESSSSSSSSSS
SSSSSDSSDSS7SES6SSSSSSSSSSSSSSSSSSSDSLSSSESDSSSSGSSSSSSSSSDESSSES
ESEDETKKRARESDNEDAKETKKAKEPPESSSSSESSSSGSSSSSESGSESDSDSSSS
SSSSSDSES09ESDSQSSSSSSSSSDSSSDSDSS8SD8SSSDSD8888SSSSSDSDSDSDS
SSDSDESQGSSSSSSSDSSSDSDSDSDSDSDSDSDSSSSSELETFKEATADFSKARETPA
SNES7PSASSSSANKLNIPAGTDEIKEGGQKHFSRVDRSKINFEAWEFLTONTYKYGAAG
TWGEKANEKLGVRVGKDK3KKNEMRGSYRGGSITLES6SYKFOD

AGACAAGTCTTTCAACGACAACTCTAAGATCAGAATGATTGAAATCATGTTGCCAGTCTTT
CGATGCTCCACAAAACCTGGCTTGAACAGCTAAGTTGACTGCTGCTACCAACGCTAAGCA
ATAAGCGATTTAATCTCTAAATTATTACTTAAACTTTTATAAGCATTTTTATGTAACGAAA
AATAAATTTGGTTCATATTATTACTGCACCTGTCACCTTACCATGGAAAGACCAGACAGAAG
TTGCCGACAGTCTGTTGAATTGGCCTGGTTAGGCTTAAGTCTGGGTCCGCTTCTTTACAA
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AAAAAAAAAACCGATGAATTAGTGGAACTAAGGAAAAAAAAAAGAGGTATCTTGATTAAGG
AACACTGTTTAAACAGTGTGGTTTCCAAAACCTGAAAAGTGCATTAGTGTAATAGAAGAC
TACACACCTCGATACAAATAATGGTTACTCAATTCAAACCTGCCAGCGAATTCGACTCTG
CAATPCTCAAGACAAGCTAGTTTGTCTGATGATTTCTACGCCACTTGGTGGCGTCCATGTA
AAATGATTTGCTCCAATGATTGAAPATTCTCTGAACAATACCCACAAGCTGATTTCTATA
AATTGGAATGTCGATGAATTGGGTGATTTTCAACAAAAGAATGAAGTTTCCGCTATGCCAA
CTTTGATTTCTATTCAAGAACGGTAAGGAAGTGCAAAAGGTTCTTGGTGCCAACCCACCGG
CTATTAAAGCAAGCCATTGCCGCTACGCTTAA

MVTQFKTASEFDSAIAODKLVVVDYATWCGPCKMTAPMIIEKFSEQYPQADPYKLDVDEL
GDVAOKNEVSAMPTLLSEKNGKEVAKVVGANPAAIKCAIAANA

AACTACTGGGGATATATTTTGAGATTTACCACTAGTAGATACGGTGGTGTAGATACGTATGAT
TCCATCTTGAGGGACCAATCCACGATCATGGAACCTTTTAGATAAACGGTGTGCCATTTCA
CTTCCAGTACTGTTTCGATATATGACCGCTAAAGAACGTGATCATCATCCCGATTCTTATCAA
GATACAAATCACGAACCACTGGAGTCAATTAATATTAAAAAATTTGTTGATTGTTAATA

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AGGGGTGGGATCGCGGAAATTCATGCUCTACAGTAGAAGCGGTTGTTGCACAAATGAATT
 AAATCTTTATCTCCAACTCAAACTATCCCGATAGATGCATAAATATCTCCAGCTTCTA
 AACAGCACGGAGTGATGATRAATAAGGCATATATGTATATATATATCTATGTGCATATGCA
 CGTCCTTTTAAACTCAAATACAAATTCCTAGTAAATCCTTTTGTTCACACACGTCGG
 AACAACTCAGGACGGACTTAATGGATATGCTTCATAATAAATGTAGTGAATGCATCAAAA
 GCACCTCCAAATAGCAATTGAGTAATGAGGTAGACAAACAAAATTCGAATACCATGACC
 TCGGGAACACCGGATTTCTGAACTATTTGAGATGGAATCTCAAGATAATAATGATAGCA
 TAGAGGATTTCTTGTCTTTAATATAAATTTAACCCAGGAGGTTCAGTTTCGAGAACCAAA
 GACAATAAGACACACGAAAAACACAAAGACATAACCCATTCTATGTACCGTCAGAGG
 TAGTCCGAGAGATGGTCAAGAAACACGCATTGAATGGCAGAATATAG

>YLR053C, 1GB aa (SEQ ID NO 272)

MDMLHNKCSDAIKSTSNLSNEVDKQKLQYDDLGNITGFSELFEMESQDWNDSIEEFLFF
 NINLTQEVFENQRQYEHKKTKKHNFYVPSFVVRVMYKKHALNGRT

>YLR390W, 939 bp, CDS: 501-839 (SEQ ID NO 291)

CTGAATTCAGACTCATAGCTCAGACGTCACCAATTGAGTGAGGAGTGGTTTAGTTACA
 AATGACAGAAGAAGAAGCTAAAAGAGATACGCCCATACAGAGCAATATCAAAATGAGCAAG
 AATGAGGTCTTCGAATGGTTGGTTCTGACTTACTATTTGATTTCACTTCTCTGATTCAT
 CTCACCAACAAAGCCCGAAGTCTCTCAAAATGAAAATTTCAACATCATTAACAGACCGGC
 GCGCGCCTTTACAATTTAGTATGTACCCACCAATAAAGCTGCTTAAACATTAAGCTAG
 AAAGCCCAAGGGTGTTAAATAGTACAGCGAACCTTCAGCAACGGTACATCAACACACCC
 CTTGAAAAGAAATAGAGACAATACAGCTACAGTCAATCCCTTCCTTTGTAATTTTGGCCAC
 AATTGATTTGATTACATCATATTTGCTGTGCGCTTCTCTCATTTTTTCCGCATAAACT
 AGGGGAAACGGGATGAAGAAATGCAATTGGCTGAAAAATACAACAATTTGTAGTGTATTCA
 GTCATTTCAACTGACAAAAGTAACAAACACAAGAAACGTCAAGTCCAGTGCAATATGCGAA
 AGAACACTTTAGATATGCTCACTATACCTATCCCATGCTTGTGGGACTCTACACGGGCA
 CGAGATTTTTTCGAGCCCATTTGTTATCGATAGATTCGCTAAGGATCCAACTTCAGAACCC
 ACATTCCTCATCCCAAGATACGACGAGGACCGAAATCTGTTAAAGGTACCGCCCTTTTAT
 CATCCACACCAGCTGCACCACTTACACCACTTACACCTCTACTCCACCACACACAGTAA

>YLR390W, 112 aa (SEQ ID NO 292)

MZWLDKNITIVVLFSSHSPDKSNKHKRQVQXNMRKNITLDMVTIGIACLVGVYTGTRFFEP
 VIDRLRKDGNDKTDIFIPFYDEDDGMLDKVTPSLSSSTPAAPPTPPTPTPTPPQQ

>YMR251W, 1601 bp, CDS: 501-1601 (SEQ ID NO 315)

ACTCCAGAGCGCAAGAGTTCGTTTCATCTACGAAATGTTGCTGCGCATTCGCACAA
 CATGACATCCCAACCCCGGATGAAATCGAAAAGAAAAATAAGCTAAAGGAAACAAACACG
 AGAAACTATAGAGGAACATGTTGAGTTGAAAAGGTCAATCAATATACCGCCCCCTATATG
 TATGTACCTTTACCTTTTATTTAAGTACTAGTGTCTGTTTASTTAGGTTATGTGAAGGCAC
 GGGTTTTGTCTTTTTTTTTTTTTTTTACTATTACTTTCTTTTTCAAGCTTTTAAGCG
 CCGAAATGATATTTAAGCSAACATGACTAAAGGACAGCGACGAGGATTCAGCCTGGACA
 GTGATAGAAAAGTTATGCGGGAATACGTATATATAGTTGTATAAATGTGTGTTATAGAAC
 ATCGCAGCGCCTTTAAATATATTGTCCTTTTATTTCAATCTTATTCCATCTCTCTCTTGCA
 ACCACGGCAAGGCTGGAGCTATGTCTGAAAAATCAGCTAGCAATAACAAAGCTGAATTCAT
 AAAGGCAGTCATCGCCATTCAGAGAAATCATCTCTGCGGATCAACCAATTTATATACCTG
 CTAAGGGAAGCTACTGCTGTATGTTGGCGTACCATGCCCATGGGACAAAGAACCTTGA
 TCACCAGGGCCCTGAAAGGGCTAGCCCTATAATCGGGTGCAGTGTAGCGCATTTGGCACC
 TGGATGACAAAGGCTGGCGATTCCCTGAAGAAGGAGATGGGAAAACCAATGAAGGCACT
 GGTTTGACATTTGACGGCGGAATTAGCTCAGTAAATTTAAATACCACTACCTCTGTGCTTA
 ACATACCAATAACGCGCATCGGTTCTTGGTCCAGCGAACAGATGAACCGCATTTACGGGT
 ACAAGAGACTAAGCGACTTCTATTTTCAAAACAAAGCCAGACTATAAGGGAAGATTACCG
 TACCTGTCTTTTGGGACTTGGAAACATGCACTATAGTAAACAAATGAAGGCAGTGATATCA
 TCGGAATATGAATTCGGCTGCGTTTGTATGAGTTTGTGCGGGAAGAAATACCGTCAAGTCC
 GTCTGGTACCTCGGTCTCTAGAGGCAAGATTAACAGATTCAACTCTTGGGTGTACGATA
 AAATCAAAACGGTGTATACAAGGUCGGTTTTCAGAGATTTGACAGAGGTATACGAGAGGG

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ACGTAACAAGCCTTTTTCATATCTTGACAAATTGGAAATCTTCTGGACAAGAGGTACA
 CAGATTTGGAGGCGGAGTATGGTAAGAACACACAGGACAAGATACTAGATCCCTACTTTG
 CCATCGGAGACACTCTGACCGAGGCGGACGTGAGACTCTACCCACGATAGTAAGGTTCCG
 ACGTGGTATACCATCAACACTTCAAATGCAATCTGGCCACCATCAGAGATGATATATPCCC
 GTATACACACGTGGCTCARGAATATATACATGGCGCCACCAAGCCTTCCAGCGCACACCGG
 ACTTTACCCACATAAACTCGGATATACTCGCTCGCAGCCACGGGTCAACCCGATTGGGA
 TCACCCCACTGGGGCCCAAGCCTGATATCCGACCTCCATGA

>YMR251W, 365 aa (SEQ ID NO 316)

MSEKSASNNKAIEFKRQSSPFREIISADHPIYKPAKGRYWLIVLPCPWAQRTLITRALKG
 LAPLIIGCSVAHWHLDDKGWRFLEEGDGKTNERHWFDIAGGTSVNLNTSTPVANIPNNAH
 RLLVDGTDEPHYGYKRLSDFYFKTKPDYKGRITVFPVLWDLETCTIVNNESSDIIGIMNSA
 AFDEFVGEYRQVRLVPRSLERQITEFNSWVYDKINNGVYKAGFAECAEVYEREVTSLFPQ
 YLDKLENLLDKKYTDLEAEYGGKWKDKILDYFAIGDTLLEADVRLYPTIVRFDVVYHQH
 PKCNLATIRDDYSRIHTWLXNIYWRHEAFQRTTDFTHIKLAGYTRSQPRVNPIGITPLGPK
 PDIRPF

>YMR273C, 3248 bp, CDS: 501-3248 (SEQ ID NO 321)

AAATTGGTCTCAATCTGSAATAGTGCTACTTCGCACTGCTGGTCCTTGGATTAATATCC
 CTGAAGGATACCCITACAACTCTGGTAGGAACCTCCGGTTATAGAAATACCCTTTAGCCT
 TTTTTCAGTACTTGTATACCGTTTAAATTTCCCTATGTACTATAACCTTTTTTCACTACT
 ATTATCGAATTCTATCGAGCGACCGGGCTTTTGTACGGAAGAGTGAAGAAATCGAGTTT
 TCGTCTTTTGGTGAAGCAATTTGGAGGACTATAAAGTACCTATACTTTGTATTACGGACT
 CAATAACAAGTCGTTTCGTGTCAGTGGTATTGAAGTTCGTACATCTAAGAGTAGAGAGAAG
 GTGGCATCTAATAGGTTTCGACGTTTTTCTTTTTTCAAGGTTTTTATTTGGTCTCCTAGA
 ATTTAAGGTTCTAGTTAGTTTGGTTTGTGTTTGTGGGTTACATAATTTCAATTCAAAGGA
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 CAAGCGATAAGGGGATCGCTAGTCAAGGGGATAAAGCGAAGTCTGAAGTTTTGATTCTCTG
 CACAGTCCCTTCGACAATGAATCUGGACGCTAAAAAACCTAAAAAGATTGTCGATTGGGT
 CAATGCCATTACTTTATGTATCCAGAATTAGATATAAAATTCGGTGGGGAATCTAGTGGGA
 GACGATCATGGTCTGGCACGACATCCAGTTCTCGGTCAATGCCAAGTGACACAACCACCG
 TTAATAACACACGATATACCGATCCAACTCCGCTAGAGAACTTGCAATGGGAGGGGTAAGT
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 CCGCCAATCAACACCCCTAACCTTAAGCCTGATAATTTCCCTAGAGCTTGTAAGATACTT
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 ACACTATCAACTTCGAACAGGGGGCTTCTAAGGCATGGAAACGGCTCACTAATACGAAGCC
 CTTCAACATTTGCGGAGGTCATATACAGAGTTTGATGATAACGAAGATGACGATAAATAAGG
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 GACCACTGTCTGTTAAGAGATATAACTGAAGAACTGACAAAGATCTCAATAGTGCCAGGAC
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 CGTCACAAGAGCCAAGAAAAAGAGTAGAAACAAAGTGTGGATGAAATGAAAAACGACGACG
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 CTTTTAGACAGCAAGATGAGGACTCTGAGAATATGAGTTCCCTCGGTCAATTCGGTGATT
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 TAGAGAAAGAAAGCCGAGAGGTACCCGTCAAGGTTGAAATGACACAGTAGAAACAAGACT
 TACACTTAAGAGAGGGGAACAACAGACATGCTAAAGCCAAAGCGCAACGGATGACAAACAAG
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 AACACGATAACGAAGAAACCAAGGGGACGATGAAAAATGAAGAAAAAGTGGATTACAAA
 GAATCGAGCTCGACAAATTCAAAAACATTTATTTCTCTATTTAATGGCGGTGAGAAGA
 CGGAGGTGTCAAATAAAGAAAGAAATGAACAAATTCAGTACTTCCACCGCCACATTCACAGA
 CAAGACAGAAATTCAGAGAAACTTTTTCCGAACCTATTCAGAAGAAAGCCACACCAAGC

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ATGATGCATCATCATCACCCCTCGTCGTCACCATCATCGTCACCATCAATACCAAATAACG
 ATGCCUATGCACGTCGCGCTGAGGAAAAGCAAAAAGCTTGGTAACAAAAGTGGAAAGGGAGC
 CGGTTCACACCCATTGTGTTCGCAATCGCCCTCGTCTCTACCGGTACCATCACAGCCGTC
 ATGGTTCCCAAAAAATAAGCGTAAAAACCCCTTAAAGATTCTCAGCCGCAGCAGCAGATAC
 CATTACAACCACAATTGGAAGGGCGCAATAGAGATAGAAAAGAAAGAGGAAAGCGATTCCG
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 CCAACCAACAACACTCCAAACACGTCCAAAAAGGAGAATAACCGATGAGCAAAAAGCTCAAC
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 TCCAAAAATCAGCCCCAGTCCAAACTTCAGCCCCAGTTGAAGCTTCAGCTCAAACTCAGG
 CTCCAGCGGCACCAACCATTTGAACATACCTCCATATTGCCCCCAAGAAAGCTTACATTTG
 CAGACGTCAAAAAACCTGACAAACCAAACTCCCCGTTCAATTCACACACACTGCCCTTTG
 GGTCCCACTGCCCTTTGCTGACAGTGTCTACGTTTATCATGTTTCGACCACCGTCTACCAA
 TTAACGTCGAAAGGGCCATATACCGGCTGAGTCACTTGAAATTGAGCAATTCGAAGAGCG
 GACTGCGGAGCAGGTATTACTAAGTAACCTTCATGTATGCTTATCTGAACTTGGCTAATC
 ACACTCTGTACATGGAGCAGGTAGCCACCACAAGAACAAACAACAACAACAACAAC
 AACCCTGA

>YMR273C, 915 aa (SEQ ID NO 322)

MSNRDNESMLRRTSSDKALASQDRKRSEVLIAAQSLDNEIRSVKLNKRLSIGSMDLLID
 PELDIKFCGESSGRRSWSCITSSASMPSDTTTVNNTRYSDPTPLENLHGRGNSGIESSN
 KTKQCNLYGIKKGVHSPSRKLNANVLKKNLLWVPANQHPNVKPDNFLELVQDTLQNIQLS
 DNGEDNDGNSNENNDIEDNGEDKESQSYENKENNTINLNRGLSRHGNASLIRRPSTLRS
 YTEFDDNEDDDNKCDASSETVNVKVEERISKIKERPVSLLDITEELTKISNSAGLTDNDAI
 TLARTLSMAGSYSDKKDQPPRGHYDEGDTGFSTSQANTLDDGEFASNMPTNNPTWPPER
 SSLRRSRFNTYRIRSQEQEKEVEQSVCEMKNDDEERLKLTKNTIKVEIDFIKSPFRQQDE
 DSENMSSPGSIGDFQDIYNHYRQSSGEWEQEMGIEKEABEVPVKVRNDIPEQDLELRGT
 TDMVKPSATDDNKETKRHRRRNGWFWLNNKMSREDDNEENQGDSENEENVDSQRMELDNS
 KRHYISLFNCGEKEVEVSNEEMNNSSTSTATSQTRQKLEKTFANLFRKPKPHKHDASSSP
 SSSPSSSPSPINNDVAVHVVRKSKKLGNKSGREPVEPIVLFNRERPHRHHHSRHSQKIS
 VKTLKDSQPQQIPLQPLQLEGATIEEKKESDSESLPQLQPAVSVSSTKSNRDRREEEEA
 KKKNKRRSNTTETISNQQHSKHVQKFNTEQKAQIQAPAQEQVQTSVPVQASAPVQNSAPV
 QTSAPVEASAQTQAPAAPFLKHTSIIPERKLTADVKKPKDKPNSPVQFTDSAPGFPLPL
 TVSTVIMFDHRLPIINVERAIFYRLSHLKLSSNKRGLREQVLLSNFMAYLNLVNHNTLYMEQ
 VAHDKEQQQQQQQQP

>YNL112W, 3143 bp, exon1: 501-1773, intron1: 1774-2775, exon2: 2776-3143 (SEQ ID NO 327)

CTTGATGGATTCTATCTGACGTTGTAGAATCTAAGTTTACTGAAAAAATCAAGAGCATGTA
 GATGTTACGGATCGACTCAAAGACCCCTGTCTACTCTGAAATCTCTAATAATTATGCACA
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 AATTCCGAATTCCTTTTTTAAGGCGTATCCGTATTGAATCATTGAAAAATTTATTTCTT
 TTTTATTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTACGCCGATGCTCATCAGAAAAT
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 ACTACAAGTCTAGAGGTGGCGAATTCGGCGGTGGAAGAACTCTGATAGAACTCTTACA
 ATGACAGACCACAAGGCGGTAACCTACCGTGGTGGTTTCGGTGGTCTTCCAATTACAACC
 AACCCAGGAATTGATCAAAACCAAACTGGGATGAAGAAATTACCCAAATTGCCAACTTTCC
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 AGTTACAGAAAGGAAAATGAATGACTATTTCCGGACACCAATATTCAAAAGCCAAATACCA
 CTTTTCGATGAAGCTGGTTTCCCAAGACTACGTTTCTGAATGAAGTGAAGGCTGAAGGATTG
 ACAAAACCAACTGGCAATTCATGTTCAGGGTTCGGCCAAATGGCTTTATCTGGTAGGACATGG
 TTGGTATTGCTGCCACTGGTTCGGGTAAAGACTTTGTCTTATTGTTTACCAGGTATTGTTC
 ATATCAACGCTCAACCATTAATGGCTCCAGGCGATGACCAATTGTTTTGGTTTTGGCTC

[illegible]

MFYGGRRDQQYKNTNYKSRGGDFRGGKNSDRMSYNDPRPQGGNYRGGFGGRSNYNQFQELIK
PNWDEELPKLPTFEKNFYVEHESVRCRSDSEIAQFRKENEMTISGHDIKPKPITCFDEAGF
POYVLNEVKABGDFDKPTQICQCGWPMALSGRDMVGIAATGSGKTLSCPLPGIVHINAQPL
LAPGDGFIVLVLAPTRRELAVQIQTECSKFHSSRIINTCVYGGVPKQSQIRDLRSGSEIV
IATPGRLIDMLEIGKTNLKRVTYLVLEADRMMDMGFEFQIRKIVDQIRPDRQTLMWSAF
WFKEVKQLAADYLNDPHQVQVGSLELSASHNITQIVEVVSUFEKDRNLNKYLETASQDNE
YKTLIFASIKRMCDDITKYLREDGWFFALALHGGDKDQHRDWWLQGEFRNGRSPKVAITHVA
ARGIDVKGINIVINYNDMPGNTIEDYVHRIGRTGRAGATGTALSFFTEQNKGGLAKLISIMR
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RCRSNY

CAAAAAGAGCTAATCAACTCCTTGAAGCTTAGATAAAATACGCCATAAATGATACAGTGAAG
GAATGCCCTGTAATCTCAAAAATCTTTAGAAAATACCTGCCAAGGCCAAAGGCGTCTCTCAGT
TTTAAAAACCTGGTAAAAAGAGAACGACTGAAAAGCCTGAAGATACTATAGACAAAGAGATG
AAAGCTATGAAAAAACCCAGAAAGTCTAAAAAGCTTGCAAATTAAGCGTTCTACTCTTTG
TCAAAACCCCTTTTAAAGCTTTTACTTAATTTGTACAAATAATATAGAAATAGAAACA
AGTTGATGTTTGAACCTTTACATATCTCTTCAATCGTGTGAGCGATATAAGTATTACG
ATTATGTCGCGCGAAACCTGAAACCCGTTTAGACAAATTTCAATCAACATACTCCACTCCGT

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AGTGAGTAACCTTTTGGAGTAATACGAAGTAACCAAAGAGGTCAAAACGGAACTATATACC
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ACAACGACGTTGTGATGATGAAGATGACCTCTGAATAGTGAATTTGAAGATCAATTTGATG
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GACAAACAATCTCTAATTTTTTTTGGTTTACTAGCTCTTTTGTGAGAAATGCTTTTCACAA
AATCCCGAAACCTTGCTTGGACTTTGACCCACCCTGCTTTGTTACTCGGTGTGCCACTAT
CCTTATCTATACTTGCCGAAACAACAGCTAATCAGAAATGAGAAAAGACAATTTGATTTACAAA
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>YNL131W, 152 aa (SEQ ID NO 330)

MVELTEIKDDVVQLDEPQFSRNQAIVEEKA SATNNDVVDDEDDSDSDFEDEFDENETLLD
RIVALKDIVPPGKRQTI SNFFGFTESFVRNATKSGNLAWTLTTTALILGVPI SLSTLAR
QQLIEMEXTFDLQSDANNILAQGEKDAAATAN

>YNL143C, 893 bp, CDS: 501-893 (SEQ ID NO 333)

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AGCCACACCGATCCATCCCATGTTGGCCAAAGTCAAAATGTGTATTCAAATCTGTGTCTCAA
CGAGTTACCAACCCGCTTCCTTCGCCTGTAGGCGTACCTGTAAAATTGTAAGACATTGTTGA
TATTGTATTGTAATATATTAAGTATGATATATTACAAAACATAAATCTCTTTCAAAGCTCT
GTCCACACTTATTATTCAAGAAGGATATCTTAATTTGAAAGGACGTGAAAGCACGAATGAT
TACTACCCACTGATGTTCTGGTTAGCACATGTGTAACCTACTGCTTATATATGCTGCAGAAA
AGTGGCTTGGGAATGAACAUCTCTTTGTAUTGAATACCTTCATTTGATTAAGGCACAGGGCTTC
ACGCCGCTTACTATTCTCTCGATCCGTCACCAATTGAAGCTTTTTACGAGGGGAATAGTCG
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AAAAAAGAAAAAAGATGTCTTATCTTATCTTTCTTATCTTAAAGACCTACCATTTGTCTC
CTTTTCTATTTTGGCAGCCCGGGTATTCGCAAGGGGAAAAAAGCCCAAGACAGCATTCCT
TGTTTATTATGACTATTACAAAGCCAGGAATGATTTGATGGCCGACATGAATTACGTCG
TTTCAAGAACAGAAGCTTAAACCGTCCCTGCTGACCGGGGGCGGTAATCCGTCGA

>YNL143C, 130 aa (SEQ ID NO 334)

MREQLKLFTR EIVDFPFLILSGFDYYQTLLISSNSKKRFKDSLLSEKKKKKKKKKKDV
LSYLSYLKDLFFVFLFWQPGYSQRERKNPRQHSIFIMPTTKPGMISHADMNYYVSKNRSL
NRPAERGCNR

>YNL179C, 938 bp, CDS: 501-938 (SEQ ID NO 335)

ACAGCGGTAAATTTCAAATACCTAATCGGAGGTCTTATCTTATTTTTCAAGGGCPAGGC
TCTCCACATCGGTAAGTGTGACCCAGATAATGGAAAGTAGCAGAATTTTATTTATGTGCC
ATACAAGCCCCGGAGAAACGAGTAGCTAAAAAATTAAGGCTGTGCAAAAGTGGTTTGTCTC
CCGAGCCCCGGGCCCTTTCTCTCCCTGAATCTTTTCGTTCCGGCCCCCTCTCTCAATA
CCAGATCTGATCTATACTAAAGCTGCAGTGAGAGTAAACCGGAAAAATTAATCCCTGGGTGT
TTGCTTCCGTCTTAGCTTTTACTTTGGGTATCCGAGAACCTCTAAGAGCTTAGACCGGTCT
TCTTCCCTAAAAAGGAAATTTATAAAAGGTTATTATCTGCACTAAAGCAAAAAAACA
CGTTTCCGGCTCCGCTCAAAATTTTCATTACGCTTCTTGGTCAAATCAGTTACGTAACGG
GTTATGACGAATACGATGAGATGAGTAATTGCAGAACCTCTCTATGCACACACCTAAGCA
GTGCTTAATTTGAATTAATTTCCCTTTTAAATTTCTTTGATATATCTGTCCTTTTCTCTCTCTATC
TTAGTTCTTGGGAGTACTGGCAATCACTGTTCTCTCTTTTTTTTTTCTTTTTTTTTTATTTT
TTTTTTTTTTTTTACTTTTCAGTTTCTCCTACCTTTTCTTATTTTCTTATTTTAAAGTAA
GTTTAAATAGTACCTTCACTAAACACGTACGCGGATCCACCAACGAACAAAAGCACGAT
CCTTGACCCATCATTTGATTTCCAAAGGTTGCAACATTCATTTTTTTTTCCTGCTCTAT
TGCACAAGACAATATCCAGATATTTCAGTTGATAGGAATACAAGACAGGTGGCACCCA
CAAAGCACACGCGGAATATTTATTAAATACAAATATAG

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>YNL179C, 145 aa (SEQ ID NO 336)

MSNCRLLCRQLSSAYLNYLPFYFLIYRPFSLYLSSCEYWQSCPSFFFLPFLFFFFFTF
 QPLVAFPIILLFKVSLNSTLTKHVRPIHORKARSLTHHCIPKRWNIHFFFSGLLHKTISR
 IPSWIGNTRQVAPT KHTPKYLLNTI

>YOL150C, 812 bp, CDS: 501-812 (SEQ ID NO 349)

TTCCCATTTCCACTGCTATTCTCTGTTGCTATTGTCAGAACCATTTGTTTACTTGAATGTAA
 TTACTTACCATTTTTGTGAATCAAAAATATCTACTTCTTGTGGGGAGACGGGTAGAAGATTT
 GTATTTTACGAGACGTCCTCTCAATATATATGGCCAAAACACCTTGATATTCTAGTTTATTTC
 CATTCGTCTCTCTTTGAAGTCCCATTATATACAGTGACGCATGTGGTGTGTGAAAAAGTAGT
 TGCTTTATTTTGGATCGTATCTCCCAATAACGTTGAAATTCAAGCTTTTCTATAGAAT
 TCTAACTGTGTGGCAGAGTTTCTGTCTGCAGTTGCTGCTCCGGTCATTGTGCACAGCTTT
 TCTTGTGTATGCTTGTCAAAGATAAATGCTTATCTGAACGTTCTCTCTATTGTTTTTTCGTG
 AATTTTCTTTCTTTCTTCTGCTTCCGCTTTTCCACATATTAAGCTGTATATAGAAGAGAAA
 AATGGCGCAGAGATGTACTAGATGATAAAAAATAATTTGTAATAACGTTAATATATATAAAT
 ATTATCTATTTTCATTATAAGTTTATATTCTGCCCCCAAATTTTAAATTTGGGAGGCAG
 TGTCGTCAATGGTCTCTTTCAAGTTCTGAACTTGAAACCTAACAAFTCTTACTCTTTT
 TTTTATCAAGAGTAGCACCAAGGGTATATGGGTAGCACCAAGACCTGGTTTCCCACTG
 GAATATTGCTTTTAGAACAGGGAATCTTCTGTTAAGGATATCGAGAACAATCTGTCAATAG
 TAAATCTGGCTCCGATACCATTACTCTTTGA

>YOL150C, 103 aa (SEQ ID NO 350)

MIKNNCNVNVIYKYLFSEKVVILPSNFKIWEAVSSMVSFKFLNLKPNFLLFLSRVAP
 RVLWVAPEPGFPTGILFFRTGKSSLRISRTSTVNLASTMTST

>YOL151W, 1529 bp, CDS: 501-1529 (SEQ ID NO 351)

GCGTGAACATGTGCATATTTGCGATTTTACCTACAAATAATATCATCATTTATATTAT
 GTTTGCGATAGGTTCTACAAATACATGTGTGTAACCTATAGTTCTCTTTCAAAACTAGA
 AAGAAFTTCGTAAACAAAATAATCTCTCAATATTTTATAGCACCTTATTAATATCAATGCTGC
 AATACCTTCTCATTTCAACCAATTGGCCCCCACCTCTTTGTACAAAAAACGTCGCCATTG
 ATAAAAATAAGTAAGAACCATATAAATTGCAATGTCCATTACGTAAAAAGAAAAAATCATG
 TGTACATATTACGTAATAGAAATACGGAAATTTTCTCGCGGAAGTAGATCTTCCCTGCAAAA
 AAAGGAAAAAGTCCGATCAATTAATGAAAAAGGGATCCTTAGTTTCCCAACTATATAAGGA
 GGAAAAGTCTATCTCTGTAGCGTTGATATAACCTGTACGATTTTCAAAACAAACAGATAGC
 AGTATCACACGCCCCGTAAATATGTCACTTTTCTGTTTCACTGCTAACCGGTTTCATTCCCC
 AACACATCTGTGATCTCTCTGTGAAAGGAAGACTATAAGGTCATCGGTTCCTGCCAGAAGTC
 AAGAAAAGGCCGAGAAATTTAACGGAGGCCCTTTGGTAACAACCCAAAATTTCTCCATGGAAG
 TTGTCGCCAGACATATCTAAGCTGGACGCAATTTGACCATGTTTTTCCAAAAGCACCGCAAGG
 ATATCAAGATAGTTCTACATACGGCTCTCCATTCTGCTTTGATATCACTGACAGTGAAC
 GCGATTTATTAATTCCTGCTGTGAACGGTGTAAAGGGAATTTCTCCACTCAATTAAAAAAT
 ACGCCCCCTCATTTCTCTAGAACCTGTAGTTTCTACCTCTTCTTATGCAGCTGTGTTCGATA
 TGGCAAAAAGAAAACGATAAGTCTTTAACATTTAACGAAGAATCCTGGAACCCAGCTACCT
 GGGAGAGTTGCCAAAAGTGACCCAGTTAACGCCCTACTGTGTTCTAAGAAGTTTCTGTGAAA
 AAGCAGCTTCCGAAATTTCTAGAGGAGAAATAGAGACTCTGTGTAATAATCGAATTAATTCCTG
 TTAACCCAGTTTACGTTTTTGGTCCGCAAAATGTTTGACAAAGATGTGAAAAAACACTTGA
 ACACATCTTGGCAACTCGTCAACAGCTTGATGCAATTTATCACCAAGAGGACAAGATAACCG
 AACTATTTGGTGGATACATTTGATGTTTGGTGATGTTTGCAAAAGGCTCATTTAGTTTGGCTTCC
 AAAAGAGGGAAACAATTTGCTCAAGACTAATCGTATCGGAGGCCAGATTTACTATGCAGG
 ATGTTCTCGATATCTTTAACGAAGACTTCCCTGTTCTAAAAGGCAATATTCAGTGCGGGA
 AACCAGGTTCTGGTGCTACCCATAACACCCCTTGTGCTACTCTTGATAATAAAAAGAGTA
 AGAAATTTGTTAGGTTTCAAGTTTCAGGAACCTTGAAAGAGACCATTGACGACACTGCCCTCC
 AAATTTTAAATTTGAGGGCAGAAATATA

>YOL151W, 342 aa (SEQ ID NO 352)

MSVFSVGANGFIAQHIVGLLIKEDYKVIIGSARSQKAEINTFAFGNNPKFSMEIC/PDISK
 IDAFDHFVQKHGKDIKIVLHTASFFCFDITDSEKULLIPAVNGVKILHSIKKYAADSVS

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RVVLTS SYAAVFDMAKENLKS LTFNEESWNPATWESCQSDPVNAYCGSKKFAEKAWEFL
 EENRDSVKFBLTAVNPFVYVFGPQMFDDKDVKKHLNNTSCELVNLSLMHLSTEDKITELFGGYI
 DVADVAKAHLVAFQKREFIGQRLIVSEARFTMQDVLDDILNEDFPVLKGNIPVGKPGSGAT
 HNTLGATLDNKKSKLLGFKFRNLKETIDDTASQILKFEGRI

>YOR131C, 1157 bp, CDS: 501-1157 (SEQ ID NO 359)

TCCTGAACGGAGCTGCAGTTTGCCTCACTACCTACACGCTCCTCTGACATACAAGATGAT
 CCATCTGTGTTTGTTCGAGCAGGTTTCAGAACTCTTCCTCCTGGGGCTCAGCAAATGGATTG
 TTATCCAGATCATCATATGGATCATTAAGGTACAGCCGAAAGTCATTGTTTCAGAGGATAGAT
 GGATTGACTAAGGGTACAGTACGGCAAAAAAAATTAGATCAGCTTTTCAAAAACAACTA
 TTTTGGCGTTTACCAAAACCAAACAGTATATTCAACTAGTTCAATCACTCTTGAAAACG
 TCCCCCTTCTACAAAATTAGGCTTTGAACGGGTGCTATGCAAAAAAGTGTAAAGAAAACG
 AAAAAACCAGAAAACTCATATATATCTTATAACGAAATATCAGGGTGTTCGACTCAATCG
 CCAGGTGCCGCTAACACAATCATPAGGATAGTCCGGCAATATATACGGTTCAATAGTCAC
 TGAAAGTGTATACAGAAATAATGACAAAGCTACAAGGACTACAGGGATTAAAACACATCA
 AAGCGGTGTATTTGATATGGATGGCACATTATGCTTACCCAGCCCTGGATGTTTCCAG
 CAATGAGAAAACGCCATAGCGATTGGAGGACAAATCGATTGATATCCCTCATTTTCATTGATA
 CATTTGCCCAACAGAAAAAGAAAAAAGAAGCGCATGATAGAAATAGAATTAGTTGAGGCAA
 AAGCCATGAAGSAGATGCAACCCGAGCCTGCTCTGTTGACATAATGAGGTATTTGACGA
 AAAATGTTATTAAGCAAGAACATACTGACAGAAATGTCGGAGCCCCGGTAGAGACTTTTG
 TTAAAAGATTTATCCATCCGAGCTTTTCGAGCTTTGACTATATTGTGACAAGGGAGTTTA
 GGCCTACAAAACCGCAACAGACCCATTATACACATCGCCTCGAAGCTAAATATAAGGC
 CTTTGGAAATGATCATCTGATAGGAGATTCATTTGACGACATGAAATCCGGTAGATCTGCTG
 GATGTTTACCGGTATTACTCAAGAATCATGTGAATGGACATTTACTGCTCGAACATAAAG
 AACTAGTAGACGTTTCAGTAGAGGATCTTTCCGAAATAATTGAATTGATTCAAAATATGA
 ATAAAGAAAGTTTCTAA

>YOR131C, 218 aa (SEQ ID NO 360)

NFKIQGLQGGLKHIKAVVFDMMIXTLCLPQPMPPAMRNAIGLEDKSIDILHPIDTLPTKHK
 KKEAHDRIELVEAKANKEMQFGPLVDIMRYLTKNGTSKNICTRNVGAPVETFPVKRFIPS
 ELSRFDYIVTREFRPTKQFDPDLLHLASKLNIRPLEMIMVGDSPDDMKSGRSAGCFTVLL
 KNHVNGHLLLEHKELVDVSVEDLSZIEELIQNMNKESF

>YOR286W, 950 bp, CDS: 501-950 (SEQ ID NO 367)

CATCTGAGTACTCGATTGTTTCATATTCCTGCTTCCATCAATGTGCCATATAGATCGCAACC
 CTGACGCATTTGCCTTAGATCCCTTAGAATTTGAGAAACAGATTGGCATCCCCAAACCTG
 ACAGTGCCAAAGGAGCTAATATTTTATTGTGCTTCTGGCAAAACGGGGGGAGAGCTCAAA
 AAGTCGCCCTCCTTCACATGGATATTCAAACACCTCACATATATCTTGGCTCTATGAATGATT
 GGGTTTCTCATGGGGCTGATAAACCTGACTTATAGCCTTGTATACCTCAGGTATGTACCC
 TGCTGATTTTTCGTAAGCTAGTAACCTATTATGCCATTTATGTCACACCGTTTCATAATATT
 TGCCATTATGCATTTGGCTCTCATAGCCGCGCCGCAAAATAATTAGGAAGTATAAAAAAAA
 AATACAAAACCTTAATCTGAATGGAAATAAGATAGCGATAACTCTCAACAAATGGAAGCGAG
 ACAGAAGAAAAAGACCAACGATGTTCAAGCATAGTACAGGTATTCTCTCGAGGACAGPTT
 CTGCAAGATCGCCTACATTTGGTCCTGAGAACATTTACAACGAAGGCTCCAAAGATCTATA
 CTTTTGACCAGGTGAGGAACCTAGTCCGAACACCCCAATGATAAAAAACTATTGGTAGATG
 TAAGGGAACCCAAAGGAAGTAAAGGATTACAAGATGCCAACTACAATAAATATTCCGGTGA
 ATAGTGCCCCCTGGCCTCTTTGGATTGCCCGAAAAGGAGTTTCACAAASTTTTCCATTG
 CTAAACCACCTCACCATAAACAAATTGATTTTTTTCTTTGTGCCAAAGCAGTAAGAGCCAAA
 CTGCCGAAGAGTTGGCTCGATCTTATGGGTACGAAAACACTGGTATCTATCTGCTGTTCTA
 TTACTGAGTGGTTAGCTAAAGGTGGTGTGACGTTAAGCCCAAAAATAA

>YOR286W, 140 aa (SEQ ID NO 368)

MFKHSTGILSRVTSARSPTLVLRFTTKAPKIYTFDQVRNLVEHPNDKKLLVDVREPKEV
 KDYKMPCTTINIPVNSAFGALGLFEKBFHXVFQFAKPPHDXELIFLCAKGVRAKTAEELAR
 SYGYENCQIYPGSITEWLAAGGADVKKPKK

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>YOR382W, 962 bp, CDS: 501-962 (SEQ ID NO 375)

AGTAAAGCTCCCTACAGTGAATATCTGGGTCCTACTGACGCCAAGCCCTACAGCGATCGGA
 ATGCGGGAACCGGAAGTTAACGGGGCTTCCAGAACGGCGGAAGCGAATTGAACGAGGACGG
 CAAACAAAACACCCCAAAATTTCACTTACTTAGAATGACUCCAGAGCAGGGGTGCAATTT
 ATCAAGCGATCATTGAACTAACTAAGTTTCATATCCTGTATAGGATTTAAACAAATGCACC
 CTAAGTTCAATGCACCCCCCTCGCCCCGACGGGACCCCTGAACAGAGAAGCTGTTTCG
 AGGTTACCCCAATTTGGATCACTTGTATAATTTGTAAATCGAGTTTCGGATAAGATGTATACG
 AATCTAACTGGGTGCAGTATAATTAGCATTTTATATTTACCTAGCAATATATGTATAAAAC
 AGGAATGCTGTGGCTGCTTCAGGCAGAAATTTTACCGTCCCTGTAAAAAAGTCTATCATAAA
 GCCATCACAAACCAATTAATATGAAATTCACACATTTTCGGAGCTACTACAGTTATGA
 CTGCCGTCTCGGCAGCAGCTGTGTGAGTGTAAATGACCACTAAGACTATTACTGTCTACTA
 ACCCTAATAACCTTTTACACTAAGCTCGTTACCGACACCCCTGACCCCTATCATTAGTTACA
 GTACCACTAGAAGCTGTGTTGTGAGTAATAGTGAATGCTACTTACACAAAGGTTGTACCCG
 AAGGACCAAGATACCACTCTCTGAAAAGAGTACAAACAAAGACACTTACTTTGACAAACCGTT
 CAGGTTTCATCAACCAACCTTTTACCAAGACCGTCACTCAAGCCGTGGAATCATCTACAT
 CCTCCTCATCTCTCTCATCT
 CTGCAATCCAAGGAGCAAGTGTGCGGTGCATTGGCCCTTGGTTTGATTTCTTACCTATTAA
 AA

>YOR382W, 153 aa (SEQ ID NO 376)

MKFSTLFGATTVMITAVSAAVSSVMITKTITATNGNNVYTKVVTDTADPIISYSTTRTVV
 VSKSDATYTKVVTGPDFTTSEKSTTKTLTLTNGSCSSFNLYTATVTQAVESSTSSSSSSSS
 SSSSSASSSGAAPAAFQASVGAALGLISYLL

>YPL078C, 1235 bp, CDS: 501-1235 (SEQ ID NO 379)

TAAACTGTGTTGTGACGCCAACTGCAACTCCCAGATGAAATACGGTCCGGTAAAGATAGGA
 ATATTCCTACTCTTACAAGCATGAATATTTTAAACCGCGCGCAGTACTATACAGCATAACA
 GGTCTTCCACGCATGAGAACTGTCCATGGCTAAATTAGTTCTCTACACAGAATTAGAAA
 TGTGCTGTGACAAATGGCACATACGTAGATATAAGATAAAATATAATTCAGAAATGGCTGTGG
 CGACAACCTATTATCATAGAGGTGTCCCATCGAGCGAGCCTCATTGCCCCGGGTAATCGACA
 TCAATAATTGAACCAATCACGACGCTTTTCTCTTTTACCCGCTCATTTCCGACCTTCAACCACA
 GGTTTGGGTAATTAAATAGCAAGGGATTATAATTGCAGTTAGCAGTTTATGTTGACAAG
 TTTTACTGTCTTAGGAAGGGTTATATTTTATTTAAAGACTGACGAGAATTCACTACCTC
 CTAAGTTCGCAAGAGATAAAATGAGCATGAGTATGGGTGTCCGTGGCCTACCGTTAAGGT
 CCGTTTCTTAAACATTTATTTAGCCAAGGTGTTTCGTGTCTCTGATGGTGAATGGAGCCC
 GTTATATGTCTTCCACTCCAGAAAACAGACAGATCCAAAAGCAAAGGCTAACTCTATCA
 TCAATGCCATTCACAGGTAATATATTTTGACAAAGACGGGGGTPTTGGGGACTTCTGCTG
 CCGCTGTCTATTCATGCCACTTCCAATGAATTGTACGTTATCAACGATGAAGTATTTTAT
 TGCTCACTTTCTTGCTTCTCACTGGTTTAGTGGCAAGTATTTGGCCCCAGCATATAAAG
 ATTTTGGCGATGCAAGAAACGAAGAAAGTCTCCGACGTTTTTAAATGCTCGAGAAACAAAGC
 ATGTCGAAGCTGTTAAAGATAGAATCGACTCTGTCTCTCAACTACAAAATGTTGCTGAAA
 CTACAAAGGCTTTGTTTGTATGTTTCCAAGGAAACGTTGAACTTGAAGCGAAGCCTTTG
 AATTGAAACAAAAGGTAGAATTAGCTCACGAAGCAAAGGCAGTCTTAGATTCCGTGGGTTA
 GATATGAAGCTTCTTGGCTCAATTGGAACAAAGGCAACTAGCAAAATCTGTCACTCTCCA
 GAGTTCAGTUAGAATTGGGTAATCCAAAATTCGAAGAGAAAGTTTIGCAACAGTCTATAT
 CTGAATTTGAACAATTGCTTTCTAAATTTGAAGTAA

>YPL078C, 244 aa (SEQ ID NO 380)

MSMSMGVRLALRSVSKTLFSQGVRCPSMVIGARYMSSTPEKQTDPKAKANSIINATPGN
 NTLTKTGVLGTSAAAVIYAIISNELYVINDESILLTFLGFTGLVAKYLAPAYKDFADARM
 K<VSDVLNASRNKHVEAVKLRIDSVSQLQNVAEFTTKVLPDVSKETVELESEAFELKQKVE
 LAHEAKAVLDSWVRYEASLRQLEQRQLAKSVISRVQSELGNPKFQEKVLQQSISETEQILL
 SKLK

>YPL085W, 7088 bp, CDS: 501-7088 (SEQ ID NO 383)

TTTTTCATGAGGAAGAGCCAGTACACTAAATAATAAAAGGTGAATGATTAAACAATGA

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AAGCGGCAGAAAAATAAAATCAACACAGTGGCAGTATTGACTTTTGAAAATCAGAAGTTCA
TCCTAAGTTAAGACTTTCTCTTTTAAAGTGCTTTCTCTCTCTCTCACTCTCTTTATCGCTG
TATATCTCATTGTTGAATTAATATAACACAACGTTATPAAGTGATCATCACTTTCTGATCCA
TAATTTCAAACCTCAAGCCACCGTACATGTGUCATTTTUCACTATAAACCTTACGAGCAAG
AGAAAGATATACGGAAAAGCTTAATTOCCAGGTTACACAAAGATTTTGGTCATTGAATBT
TGCAGCCCTCCTGCTTGAGAACTGGACAACAACCTGTTATCAATATTCCCTTTTCAAAAT
AGTGGTATTTAACTGGCCATAACCAACGAAACCGTTGTACCTATTATTTTGTATAGTCTT
CATTTAATAACGTGTTAAGPATGACACCTGAAGCCAAGAAAAGGAAAAACCAAAAGAAGA
AGTTGAAGCAAAAGCAAAAAAAGCTGCTGAGAAAGCTGCTAGCCACAGTGAAGAACCAC
TTGAATTACCAGAAAATACGATTAAACAGCAGCTTCAACGACGACTCGGTGAACCGTACAG
AATCTGACATAGCTTCAAATCTGATGTTCTCTCCGCTCTCATCATCTACCAATATCTCTC
CGGCTAATGAAACACAATAGAAATACCTGATACTCAAGAATTGCATCATAAACTGCTCA
ACGACTCTGATCAACATGATATTACCGCGGACTCAAATGATTTGCCAGACAACCTCAATCG
TTGAACATGACTCTGTTATTACCCAAACAAAACCCAGCCATGTCTCAAGAATACGAACAGA
CTGCCGCTCACTTATCTTUGAGAAATCCATCGCTCGATGTAGTCGCGGAGAACTTCACA
ATAATAATGAACATAACCCAGAAAATTGCCGTATCCGCTGTGGAAGAGGATTCTTTCAATG
AAGAAGAGGGTGAAAATCACGACAGCATAATAATTTTCATCATTAAACCATCTTACCCCTT
CTCAATATAATCATTTTCTCCCATCCGATGGCAATCTTCTTTCTCCAGAATTATCTTCTG
GTGATACGCCAACTCACAACTGCTCTAGGCACAAAAGACAATGAAATAAATGACGATG
AGTATTGTAATGATTAAGGAAAATAGTTTGAACCCAAATATGTCTTCTCTCATGAACCTT
CAAAGGAAGAAGATGAAAGATTAAPACTAGAAACGCATGTATCAACCGAAGAAAAGAAAC
AGGATATCGCTGATCAGGAACTGCAGAAAACCTTATTTACGTCTAGTACAGAACCATCTG
AGAATAAAATAAGAAAATTCTGGTGATGATACCTCCATGTTGTTTCAAGATGACGAAAGTG
ATCAGAAGGTTCCATGGGAGCAAGATGCGAAGAAAGATTTTCATAATGAGAAACAAATA
ATACTCAAGAATCGGCACCGAACACAGATGATCGTGATAAGGGTTATGAAGGAAACGAAG
CTTTGAAAAAGTCCGAAAGTTGTACAGCCGCGGACGAGAGGTCGTACTCTGAAGAAACTT
CAGAAGATATCTTTACGGACACGACAAACAGGTAGTTCAACGCCAAATGATTTCACTC
GGAAAAATATTGAGAATGAAGCCAGAAATTAATCGGGCAAGCGAATCATAACTATCCGT
TGCTTCGCGAAGCTGACATTATAGAACCCTGGTAAGCATATTCAAGATCAAGCCGAGGATT
TGTTTACGCAGAGCAGCGGAGACTTGGGAGAAAGTTTTGCCATGGGAATCTACTGATAAAA
ACCGCTGATCTAACCAACCAATCCCAAGAGAAACATGAAGATTTATTTGCTGCTTCTGGAA
ACCATCACAACTTCTTTGGGAGTTTCTGACGGTGAAGTATCATCGGGAAAGACGGAAA
ACAGCATGCAGACTATCTAGTGAAGAAATAGCTGAGUAAAAGTTTTCGTTTTGGAAAACG
ACGACGACCTTTTGGACGACGACGACAGCTTTTGGCTTCTTCTGAGGAAGAAGACACAG
TACCTAATACCGATAATACAACGAATTTAACCTCAAAACCGATTGAAGAAAAAAGGCTT
CAAGATATAAACCTATTATCGAGGAGGAAGCAGGAATCGCTCAAGAGCAAGTTTCAATTTA
CCAATACTACTGGCATTGTAACACCGCAGCAGTTCCACCGTTTGACTAAAACCTGGACTAG
GCACCCCAACCAACAAGTCAGTGTAACAAATATAGTTAGTCTTAAGCTCTCTCTGCTAA
AAGACAATCGTTTCAAAATTTAAGATAAATGAGGAGAAAAAGAAGTCTGATGCTTACGATT
TTCCACTGGAAATTAATTCAGAAAGTTCCAAGAAAGGTCACGCAAGCCGGTTGCCGTTT
CTACTCAAACGTTTCGCTTACGCAATTTCTTTTAGTTCTTTCCACAAACCAATTCACAGA
GCAGGAAAGGCTCTAATAACTCAAATAGGCCACCCCTGATCCCATTTGCCGACCCACCCAC
CTCGATCTTCGAGAACTAATCAGCGATCTCGCAATCTCCCGTTAATTAATGCTTTCCCTA
ACCCATACAAAATTCACCAACTACAACAGGCTCCTATCCAATCAGGTATGCCTTTTACCAA
ATACCAACATACCTCCCCAGCATTAAGAGTGAAAACACCGTTTTCTGCTCCTCCAATTC
GGGCAAGAGGGGTACGCAATGCTCCGTGGGAAAGTTACGCTCTTTTGGTGCTAGACATG
CAACACAGTACGGCTCAATAACGGGGTACCTCCGTTTCCGCCATATGTCAGCTACCA
TAAATTTCCCAACTCGGAATAACTATCCCCCGTCTCTCTCTACAGTTACGCAGAAGCAAT
ATCCATCAGTTGTGCAAAACCTTGGCGCTTCCGGCTGAAATACCCCCAATTTTGTAAAGA
CCCATAGAGGCCATACAAGCTCTATTAGTTGATATACACCAACCCAGAATGAACAGGCT
CTAGATACGCACCCAACTATTAACAATCTTATCAGGTGCCATATACCTCACAACCTGTGTG
GTCTGTAGCTGGGAATTCAGCTATCAAGGCCAAACCCGAAGTCTTATGCAGTCTCTA
TGATGCCCCAGGCTCAAACCTTCAGCAAGTATTCAGGCTCACGCGAACAATTCACCCGCTA
CTGGCAATTTTACCTTTAGCCCTTACGACCTCTAGACCCCTTACAAGCCGCTACGAAC
TGCAACCCCGTGCAAGCAACATAACGGCTGCAAAATTCATACCTCTTTGCAAAATTTGCCAC
TTGCTGAAAACATACTGCUAGAAATTATCAGGCATCGAGCTACAAGTAGTGTGCAACAC

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CACGACAGGAAAATAATCCAAATTAAAATAGACAACGAGGCTTTATTACGCCGTCAATTTTC
CGATTTTTCATTTGGAGTGCTGCAAAATAAGGTCTGTGTACGCAGTCCUUUCTATCCCTGACC
AATCCGACGTACATGATTTTCATCAACCATTTGTACACGAAATAAAAGTGACACCAATTGACC
AGATAATTAACCCGAACGATATGCTCAAAAGCTTTCCAGGTCCCTTTGGGTAGTGCCAAAT
TAAAAAAGGATTTAACCAAATGGATGGAAACCACTATTAAATCCATATCTGAAAATG
AATCATCCACTGATATGACTATATGGCAACTATTGGAAATGAAACTAAACGATAAAGTTA
ACTGGAAAAATATTTCAAAACTACTATACAAATCTGACGAACCTTTAATGTACCTATCTC
AGCCCTTTTCAAACGGTGACATGATTTCCAAATGCATATAGACTGGATATAAATTTGTCAGA
TGAGAGTCCCTGGCGTTCTTACAAACGGGAAATCAGGATGAGGCACTTCGCTTAGCTTTAA
GCAAGAGGGATTATGCCATTGCACTATTGGTTGGCAGITTAATGGGTAAAGACAGATGGT
CTGACTCATTCAGAAATATTTATATGAAGGGTTTACTGCGGGGCCAAACGACCAAAAG
AAATGGGCACACTTTCTGCTCCTTATCTTTCAAGTATTTGTTGGTAACCTCCAAATGGCCA
TAAAAAGTTTCTACACTAATPAATGAGAUCACTCAATGGGCACTCCGAAAACCTGGAAGAGTA
TCGTTGCGAGCTCTTCTGATTAATATCCCAGAAAATAATGAAGATCCACTACTTTATACCAC
CTGTTGTCCCTTGATTTTGTGATAGAGTTGGTATATTTCTCACCAAAAAGGGCTTGACAG
CCGCAGCTACTACATTTACTTATTATTGGTAACGTACCCTTTCTAATCAGCCAGTAATGC
CAGATTCAGACCTTATATTTGAAAGTATTTGGAAACATCAATACTTTTGAAGCCATTCTAT
GGGATGAAATCTACGAGTATATATTCTCTATGACUCTAAATTCAAAGGATTTTTCATCTA
TTTTGCCCCAGAGATATACCATGCATCTCTTTTACAAGAACGAGGTTTGAACAGCCTGG
GGACAAAGTATACTGATTAACCTCAGTTTCCAGTTTCGAAAACCTGCCAAGAAAGATATTT
TAACAATAAACCTCAGTCTGTGAATTGAGTGAGGTGGCTAGTAGGCTTTCCGAGTCTAATA
CAGGATGGCTTTGCAAAAACCAAACTAAGCAGCTATTTGGGTCAATAGATAAATCTCTCA
ATPAAATATATTTGGTGGCGAGTATTTGATGCAATGAATPAAAAAAATGATAAAAAAG
TTTTTGATGGGTTCCACACCGGATCTTCTGCCAATTCGTCAACTGTGGATCTCACCCAAA
CATTCACACCTTTCCACCTCACTTACTTCGCAACCTATCTGCATACCTACACCTCTTT
TGCAATAATGCCATAATGTACCAAGCCATAGTGTGCTGCATTCAAAGCCTTCCAATGGT
CAAAGGGGTTAGTTGAAGCAAACTTACCGTATACGCATAGGATCGGTGATAGTTTGCAGG
GATCTCCTCAGCGCATTCATAATACACAGTTTCGCTGCTGCTGAGCCTCAAATGGCTTCTT
TGAGAAGAGTTAGAACAGACCCAGCATACAAAAGGAAAGGCTTTGAAGAGTCAGCAGATTT
TAGAGAAAAGTCTACCGCCCTACACTCCACAAATTTGGACAGAACCATAGCGTTCCAATGG
AAAAGCTTAATTGGAATGTGCGCATCTTTATTTGCCGACTTCCTCTGCTCCACCCAAACTTG
GATCAGTGGCGTCTAATTATGTCTCTACTCCTGACTTAGTAACAAGGCAGTCTATCATA
CTACCGGATCAGAAATTTCTTCTCTCTCCCAAAATTTGGGTACCTACTAAAGCTAATTCC
CGCAGGGATCGCTTATGTACTCACCAAGTGTGGAAGCTTTGCCATATCGACCTGTCTGCTC
CGCAAGTTCTAGAGACGGGATACAAATGATTTTGGTAACAAACATTTCTCAAAAAGTATGC
CTGATGATGAATCTCACACATCACATGATAATAGCAATGCTGATCAAAATACATTAAAAG
ACTCTGCAGATGTTACAGATGAACAATGGATATTGAAGGACCTGGCTTCAAAGATGTGA
AGAATCTTCTTCTATGGAGCCCAACCACUAGCCTACGCTACAGTAATCTCTACAAA
CTATTTAGTGACGATATCCAAACGATTTCTTCAAACTAACGTGGAGGTCCGGGCTACTGATG
CATCGAAAATGGAAAATTTCACTTCCCTCCATTTGAAAATGAAGAAGTAGCGAGGAGCAGC
CAGAAAACATTTCAAATCAGCACTCATCAGCATATCTTACCATCAACTCTGTGGATTTGTAC
TCGAAAACAGACCGCTAACTCAGGATGAAAACAGTATCTCAGAGACAGTTCAATCCACAT
ACTTGCCAGCGGAAGTATTTCAATGGAAGCTTAAACCAATTTCTCAAGTGCAAGATGTTT
CAAGAANTGTTAATAATAAAGCATCCAACTTGTGGAGCAACATATGGCACCACCAAGC
CAAAAAGTACTGACGCAACCAAAATGAACCTACTCACCATAACGTGCTCAATCAACTGCCG
CTAGTGCAGATGGCGATGAATCAACGATTTCTGAAAACATGCCCTGCTATATATGCAAGAA
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AAATTTCAAAACCTTCGGCTCAATAAGGACGCAACCGAAGAGCAAAAACAAAATATTTG
AAAGTTCCGGCACCAACCTCTCTCAATCGTGAACGTAAGATGGCGGCCCAAGACAA

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 TACAATAA

>YPL085W, 2195 aa (SEQ ID NO 384)

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 GNSFSSLDKPIFQSRKGSNNNSNRPPVPLGTQEPSSRTNSAISQSPVNYATPNPYKIQQ
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 PPPKIGVPTKANSSQGSIMYSPSVEALPIDPVVPQVHETGYNDFCNKHSQKSMPEDESHT
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 PTLQTNVFEVRGTDASKYENS LPSIENERSSEEQPENISKSASSAYLPSTGGLSLENRPLT
 QDENSISEFTVQSTYLFAGSISMEAKPIISQVQVPRNVNWKASKLVEQHRAPPKPKSTDAT
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>YPL190C, 2909 bp, CDS: 501-2909 (SEQ ID NO 387)

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>YPLI90C, 802 aa (SEQ ID NO 388)
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DDDDDDDEERKEEEEREGNINSSVGSDSAAEDGEDDEDKKOKTKDKKEVELRRRETLEKQK
DYDEAIKKITREENDNTHFTTNMERVXYDLLQKQVKYIMDSNMLNLQFQHLTQEEKMSA
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>YPL201C, 1886 bp, CDS: 501-1886 (SEQ ID NO 389)

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 TCTTCTTCTGCAATATTGCCCTTTTGGGAAGAAAGATCGAAAGTAGCCATTTCGAGACACG
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>YPL201C, 461 aa (SEQ ID NO 390)

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 WIFYSNQAEDKKLLLYDFNGQHLLFIKQQFYGLNLLSDAIIICMDCNFGYNSNTIQILV
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 ASTLNKEINFMLKIDEDVQKIDYLLKCNHLLLETNMRVLSIPTRDPIENSNSPPVSDSE
 VYPIFYKTQELHVHASGTGRQLANNGKYIFITEQHLYGTALSVYKYSISFKRWLFVGYSD
 IRAKYGIRSVKDLFVGNCPVNSPVLITLTDNNIQTILLK

>YPR028W, 1176 bp, exon1: 501-551, intron1: 552-684, exon2: 685-1176 (SEQ ID NO 393)

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 AATTCGATATCGTATGTAAGATGGTTTTATTGGTTCCATCGTCATCATGGTTCAAACAGC

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CAAAATGACCCGACACACCGTAACCGAAGCAGTTATACTAACAAAGAAAGCTAATTTTCACCC
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>YPR028W, 180 aa (SEQ ID NO 394)

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 KTVFLIYIALPQITGGARMIYQKLVAFLTDRYILRDVSKTEKDEIRASVMEASKATGASVH

YDR145W, 2120 bp, CDS: 5C1-2120 (SEQ ID NO 99)

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 GCATTCCAAATCATAACCGAATCTTTCCCGTCTCTGTATATAAATACGACA
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 GCTTGAATACAAAAAATAA

YDR145W, 539 aa (SEQ ID NO 100)

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 KSAIFKQTEPAIPISENI STKTPAPVAYRSNRPTITGGSAMNASALATPA
 TTKLPPEYEMDTQRVMSKRKILRELAKTVGTBEGDGRTVFDGQVRELIILDLA
 DDFVTVNTAFSCRLAKHRKSDNLEARDIQLHLERNWNIRIPGYSADETR
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YDR216W, 4472bp, CDS: 501-4472 (SEQ ID NO 109)

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 TCGTACTGGATAAAAGCCTATAATGATCATTTGPTTTTCAGTATCTGAAAG
 TGATGAAACTTCTCCAATGAACCTCTGAATTAACGACACTAAATTAATCG
 TCCCAGACTTTAAATCGACTATACATCATTTCAAGCATTAACGTCCTCC
 TCTTGGACTGTTTGCTATAGATAATAATAGCAATAACAATAAGCTATCAGA
 CAACCAACCTGATTTCTGTCATTTTCAAGAACTGCTGGATAATGATACTTT
 TAGGTAAATGATTTCTTACACACCACTGCCGTTTTAAAGAAATTTGAACTT

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TTACATGATGATAGCGTAAGTGCTACCGCCACCTCAAAATGAGATTGACCT
 TTCCCATTGTAACCTATCAAACTCTCCAAATTTCTCCACATAAGTTAATTT
 ATAAGATAAAGAGGGGAUCCAATGACGATATGTTGATTTCTTTGGGACTC
 GATCATCTCTCCAATCCCGAAGATGATCTGGATAAGCTATGTAATATGAC
 CAGAGATGTTCAAGCCATATTCAGTCAATATTTGAAAGGAGAACAGTCTA
 AACGATCCCTGGGAAGACTTTTTATCAACGTCAAAACAGGAAAAGAAAAGCCA
 GATAGCGGCAACTATACCTTTTTATGGGTTAGATTGTTAACCTTATCGAA
 AATATCAAGAGCTCTGCGCGCCCTCCACTGTGAACAACAAATCAGCCATCGC
 ATTCATAGAAATCAAAGCTATTTAATGAACCAATGAGAAATATGTGCATT
 AAAGTACTATGATACTATGAAAAGTTTCACTCATGATAGTAGTGAGAGTGT
 CATGGACTCTTAATCCAAACTTTGCTGTCCAAAGAAATTGTTAATGCCAGCTG
 TGAGTGAATGGAACGAATATTTAGATCTTTTCAAGAAATAATTTCCCTCCC
 CATTTCCCTATTTATTCACCCAAAGCTTCCTTCATTTCGATTTGGATAGCTT
 GCACCGATATACCTAATGAGGATGGGTATGATGACGCTGAAAACGGCGAGT
 TGTTTATCGATTAGTCAAGGGACAGATAAAGAATATGATACGAGCAC
 TATCAAAATCTTGTCATTTTCAAAAATCGTTTGTPTACCTTTATTTATCCC
 CACATTTGGTTCTTTGCATAAGTTTGGGTACAAATCTCAAACAATAGAAT
 TGTATGAGATGAGTAGAAGATTCTACATTTCTTTTTTGGAGACTAAAAGA
 AGGTGTCGCACTACAACAGTAAATGACACTTATCAGAACATTTGGTTGAT
 GCAATCCCTAATATTGAGCTTCATGTTCTGCTCTAGTTGCTGATTATTTGG
 AGAAAATGACTCCCTCTTGATGAAAAGGCAATTGTCCGCATTATGTTCA
 ACGATCAGATCAAACTGTTTACCGACAATTTCTGCAAATTCGAGAGAG
 TATCAATANTAACANTCAACCTTTAACATTTGGTTCTCTCTTCAATACA
 TCATTTTGTAGTCAAAAATTAGATGCACCTTAATGGCTTATGATTTTGT
 CAGTTCTTGAATGTTTCTTUCATATTAATTTGATTTTGTCTATAAAGGA
 AAAAGATGTTGAAACCATTTATATTTCCCGACAAATGAGTCAAAATGCCCA
 GTGAATCGATAACATGTAATGGGCATGTTGTGCAAAAGCAAAATTTTAT
 GATTTTAGAACTTTTATTACAGTTTTCAGTATGGACACTTACACTCAAT
 ACCAGAAATTTTAGGCTCATCTATGATTTTATTATGAATACGATTTAAGAA
 AAGGAACCAATCACATGTGTTTTTGGATCGAATCGATACGAAAAGGCTA
 GAGAGGAGTCTTGACACTTCTTCCTATGGCAATGATAATATGCCAGCAAC
 CAATAAAAATATTGCGATCTTAATTTGATGACACCAATATTTTGAABAATA
 ATTTAATGTCAATGAGATTCTATCAAAACAGATTGATCGCTCGTTTACTGAG
 AAGGTTAGAAAAGGACAAATAGCAAAGATATATCATTCCTTTTTTGAACCTC
 TGTGAGGTTGAATTTTTTGAAGAATTATTCAGTTGAAGTATTGTGTGAAT
 TTTTAGTAGCGTTGAACTTTTCAATCCGTAATATTTCTGTCTTTATACGTA
 GAAGAAGAAAGTGATTGCTCCCAACAAATCAATTCTCCAGACCTGCCAAG
 GATCCACCTGAATAATCAAGCGCTTCTGTCTTCAATTTACAAGGCTATT
 ACTATTGCTTCATCCTAATATCAAAATTTTATTTGAAATTTTGAAGUAAC
 CCAATTTTAAAGTTACTGAGAATTTTATTTAGTTGAGAAGCCTTGCGAA
 TTCTATTTTACTTCCCACACTTCAAGATTGTATCCGCAAGAGTTTCTG
 GATTTCTGTGATCTTGTATTTACGCAACAATTTATRAATAAAGATAATGGT
 ATGCTTGTCTTCTGGTTTTATCCGCAAAATGAACACCATATTTGTCAGTGC
 AGCTGTTAAGACTAAGTTAGCCAAAAGATCAATGTTGAAGGGCTTTGCAA
 TGTTTTATTAATGAAATCCTAGTTAACTCTTTTAAAGGATACCCTTTTTTG
 AATATGGAGGATCCTATTGCAAAATGAATTTTCTTTGATAATGGGGACAG
 GCGAGTGACAGACTTGCTCTGTTTCAAGCACAATTTCTATCGGATACCGGCC
 TAGAAGGTATTAACCTTACGGGCTTAAATGATTCGCATCAAACTGTTTCT
 ACTTTGAATCTTTTACGTTACGGGAAAAATCATTCATCAAAACATAAAAA
 TGGTGGAAAGGGGCAAGGATTTGCCGAAAAGTACCAATTATCTCTGAAT
 ATGTTACTATTCCCAAGTTATTTTTTACCATACTTAAAGAAAACCTACATT
 CATTTGTCACATGTTAGATAAGATGGCAAGTGATTTCCACACTTTGGAAAA
 TCTATCTAAAGGGAACAGTTGA

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YDR216W, 1323 aa (SEQ ID NO 110)
 MANYEKPNDSCGFVVDLNSCFNNGFNNEKQEIEMETEDSPILLMSSSSAS
 RENSNTFSVIQRTPDCKIITTNMNMNSKINKQIDKLPENLRLNGRTPSGK
 LRSFVCEVCTFAFARQEILKRIYRSHNTNEKPYTCGLCNRCFTRRDLLIRH
 AQKIHSQNLGRTISHTKKVSRITTKARKNSASSVKFQIPTYGTPDNGNFL
 KRRTANTRRKASPEANVERKYLKKLTRRASFSQAQSASSYALPDQSSLEQH
 PKDRVKFSTPELVPLDLKNEPELDSSPDLMNMLDLNLNLDNPNFIALNRSD
 SSGSTMNLDYKLPESANNYTYSSGSPTRAYVGANTNSKNASFNDAADLLSS
 SYWTKAYNDHTFSVSRFSQFTSPMNSRINDTKLIVPDFKSTIMHLEDSRSS
 SWTVAIDMNSNNKVSQNPDFVDFQELLNDTLGNLLELTAVLKEFEL
 LHDDSVSATATSNEIDISHLNLNSMPISPHKLIYKNKEGTNDMLISFGL
 DHPKSNREDDLDKLCNMTREVOAIPSOYLKCEESKRSEDFLSTSNRKEKP
 DSGNYTFYGLDCLTLQKSRALPASTVNNNQPSHSISEKLFNEPMRNMCI
 KVLRYVKFSSHDSSESVMCSNPMLLSKELLMPAVSELNEYLDLDFKNNFLP
 HFPPIHPSLLDLDLDSLQRYTNEDGYDDAENAQLFDRI.SQGTDKKEYDYRH
 YQLLSISKIVCLPLFKATFGSLHKFGYKSOTIELYEMSRRILHSFLETKR
 RCRSTTVNDSYQNIWLMQSLILSFMFALVADYLEXIDSSLMKRQLSALCS
 TIRSNCLPTISANSEKSINNNNEPI.TFGSPLOYIIFESKTRCTLMAYDFC
 QFIKQFWH[KKIDLSIKKKQVETPIYPDNESKWASESIIICNGINVQKQNFY
 DFRNFYYSFTYGHLSIFEFLGSSMIYYEYDLRKGTKSHVFLDRIDTKRL
 ERSIDTSSYGNDNMAATNKNIAILLDDTILKNNLMSMRFIKQIDRSFTE
 KVRKGQIAKIYDSFLNSVRLNPLKNYSVEVLCEFLVALNFAIRNITSSLYV
 EEESDCSQRMNSPELPRHILNNQALSVPNLQGYCYCFILIIIFLLDFEAT
 PNFKLLRFIELRSLANSILLPTLSRLYPQEFSGFPDVVFTQJFINKDMG
 MLVPGLSANEHHNGASAAVKTKLAKKINVEGIAMFINETLVNSFNDTSFL
 NMEDPIRNEFSFDNGDRAVTDLPRSAHFLSDTGLEGINFSGLNDSHQTVS
 TLNLLRYGENHSSKHKNQGGKGGFAEKYQLSLXYVTIAKLEFTNVKENYI
 HCHMTDKMASDFHTLENHLKGN

YBR122C, 3401 bp, CDS: 501-3401 (SEQ ID NO 51)
 GGGTGCGGTATCGGCTCTAATTATTTTATCTCTCTATTTTCTTTCTTTTC
 TCTGCGCTACTCCTTTTCTCGATCGTTGCTACTCCCGTCGCTAGCCACTGG
 TCTCCCGCGGTACTGTACTCCATCTTTTGGCGTFFTTCCCTATCCAA
 CTGGAACAAGGTTTGTTTAAATTTAATTTTATTTTCTTTCTTCCGTCCG
 TCGTCTCTTTTCCCTTCCGATTATCAAAGCAAAGCCCATTTTCTCTTG
 TCTTTTGTGTTTTGTGTTCTCTGTTCTCTGTTTTTTACAAACCACGTCA
 GAGTTCAATTGAGAGAACTAGAATCAACAAAGCCAAATACGACAACGTCA
 CTAGTCTTTGAACCAGAGGCGTATTCCCGTTACCTCTTTTCCCATATTTT
 TGCTTTCTTTTCACTCCTATAAGCCTTTAGACTAGTACTACAACTACA
 ACAGCAACAACAACAACAACAACGAGCTGGAAAAAAAATTAGGAAAA
 AAGAATCCGGCGCGTGAACAACAATTAATCGAACAACCCGCTCAACAGCA
 ACAACAACAGCAACAACAACAGCAGCAACAGCAACAGCAGCCAGCTTC
 CTGAGCAGCCACTCGACCCATTACACAACTCAACTGCGGAAACTTCCCTC
 TCCATTGCTTCTTTGSCAGAAACCCCTGGGTGATGGCGACAGGGCCGCAAT
 GGCATATGACGCCACTTTACAGTTCAATCCCTCATCTGCAAAGGCTTTAA
 CATCTTTTGGCTCACTTGTACCGTTCCAGAGACATGTTCCAAAGAGCTGCA
 GAATTATATGAACAGGACTTTTGGTAATCCCGAATATCAGATGTGTG
 GGCTACTTTAGGTCAATTGTATCTGATGCTGGATGATCTGAAAGAGCTT
 ACAATGCCTATCAACAGGCTCTCTACCACCTCAGTAATCCCAAGCTACCG
 AAATTATGGCATGGAATCGGCATTCTTTATGACAGATAAGGTTCCGTCGA
 CTATGCGCAAGAAGCTTTTGCCAAAGTTTGGAAATGGACCCCAATTTG
 AAAAGGCAAAAGAAATTTACTTTCAGACTAGGTATATTTATAAACAACAG
 GGTAAATGGTCTUAAGCTTTGGAAATGCTTCAGATACATTTCCCTCAACC
 TCCCTGCTCCCTTGCAGGAGTGGGACATATGGTTTCAGTTGGGTAGTGTTF
 TGGAGAGTATGGGAGAGTGGCAAGGTGCGAAGGAAGCCTACGAGCATGTC
 TTGGCTCAAAATCAACATCATGCCAAAGTATTACAACAATTAGGTTGTCT

[illegible][illegible]

[illegible][illegible]

YPL089C, 2531 bp, CDS: 501-2531 (SEQ ID NO 385)
TTCCACGTTTCGCAAAAAATACTTCCACGGTGACGAAGTCTGTCTCAGTCG
TATATTAAATGCAGAAATCGTCTTATCATTTATTGGGCTCTCTTAACGGCG
CAGCATCACCGGGIGATGAATGCGAAGCCGCGAAGAAAGAAAAAATT
TACTTCAGATCTCTGNTAAAAATAAACCGAAGAGATGAAAGCTAATAAI
AGAAACAGCTCGATCTTCTCTGAACCAATATAATTAAAGGACAGACAA
AAGAAACGTAAGAAAGAACGAGCCCTGTCTTAAGTGTCTCAACGACTGAT
TCATTAGAAGTCCCTACICTGTGATGCCAACTCAACTTTTGACTCGTGA

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AAGTAATTGAAAGCTGGCAAGCAGAATTATTCTTTTTTTTTTTTCAAGGTT
 TCTATCACCATTGTGAGCTTAATATCCCCCGAGCAACAGGCTGAAGCGT
 GAAAAAACTTAAATATTAAAGTGTCCCAAACTATACTATAGATACABC
 ATVGGGTAGACCGAAGATTGAAATCCACAGAATTCTGTGATGACAGAAATAG
 GGCTGTACCGTTTATAAAAACCTAAAGCTGGCCTTTTTAAGAAGGCCCATG
 AACTATCCGTTCTTTGTCAAGTAGACATAGCCGTCATTATACTGGGGTCC
 AATAACACGTTTCTATGAGTTTCCCTCTGTGGATACGAATGATTTAATCTA
 TCACTACCAAAAATGACAAAAACTTGGCTTCACGAAGTGAAAGATCCTTCCG
 ATTATGGAGACTTTTACAAAAAGTGCAATCCGTTAAACATAAAATCAAGACCTA
 CTCAGGTGGTCTATGTCAAATAAGCCTTCGAAATCAATGTAAAGGAAT
 GAACCACTCAGAAATGATGATGATGASAACTATGATGAGGACGACCATG
 ATCATGGCAATTTTGAGAGGAATTCAAATATGCATTCCAATAAAAAACCC
 TCTGATAAAAAATATACCGAGTGACACATGAGGTGTATATCCCCGACCGC
 ACTCATTTGCAAAAGATGGATGGTAGTGACAAATAAAACGTCATCCTTGAGA
 ACCGCTTCCCGCCTTTTACAACATTTGAAAAGATTGAAACCGGATCCTTTG
 CAAAATAGTAGAACTCCGCAACAGCAACAGCAGCAAAATATATCGAGACC
 ATACCATAGTAGCATGTACAATCTTAACCAAGCCTTCATCCAGTTTATCTT
 CTCCCTCCACGATGGATTTTCCAAAATTACCAAGCCTTTCAAAACTCTTCC
 TTTAATGGTGGTCTTCCACCCATTTCCATTTTCAACCGAACAAGTTCAGTAA
 GCCATTTACAAATGCATCCTCAAGGACCCCTAAACAGGAGCAAAAATTA
 ACAATAGTGGCAGCAATAATAATGACAACAGCAACTACACTCAGTCCACCA
 TCTAATTTCTTTGGAAGACTCTATTCAGCAGACTCTCAAAACCAACAACCAA
 ATTGTCTGGCAGACCGGTACTTCTGTGAGAGAATTCGGAACAACAATTCA
 GCAGTAATTTCTCTATTCCCAAGTGAACCCCTCTCTGCTCTTCCACATCG
 GCAACCGCAATAGTATGGGCTCTTCGCAGATAATGAAAGAAAACAAAAC
 AAGTAGGTCTAGCAAAATTTCTCCACTATCCGCATCTGCTCAGGCCCTT
 TAACTCTCCPAAAAGGTAATAATGGCAGAAATGGTAATAAAATTCGCAAT
 GCAAAATGCGCCTAACGGTTCTAACAAATGGTAATGGCACTAACAAATAACAA
 TCACCCCTTATCCTTTTCGGAAAGTGGGTCTTCCACCTCTTTTTTCTGCAACAC
 AGCCATACATTGCCACTTCTTTGCAACCAATCGAATATTCTTGGCGGACCT
 TTCCAACAAAATACATCTTTTTTAGCTCAAAGACAAAACCCAGCAATACCA
 ACAAAATGTCTTTCAAAAACAGAGCCAAACAGTACCATTAACTACAACAT
 TAACCGGACGCCCCCTTCAACTTTTTCCGGCCCTGAAACCAAGCAATGGC
 CCTCCAACGTGTTCACTGCCATCGAAGTTGTTACATGATTTGATGAGTAA
 TTCTCCAAATGTTTCTTCTATATCGATGTTTCCAGACTGGTCAATGGGAC
 CCAACAGTGGCAAGCCGGGAACACAAACAATCCTGGTACTTTCCCTCCC
 GTACAGACGGCCGTAAACAACGGCAACTCCAGCAATATCAGCAGCACTAA
 CAACACTAACAAACAACAACAATAACAACAACAACAGCAGCAACAACA
 ACAGCAACAACGGCAACGACAATAACAGTAACAATAACCAATAACAGTTAC
 TATAGTAATAATGAAGATGCACCCGTAAATGGAGCTGCTATTTTCAAGACA
 TACTACCGAATGGTGACTCGAACAATCAGTCCAACTCAAGTACATATGATC
 CTGCTGCCACCGCATATAATGGAAATACCGGGCTGACTCCATACATAAAT
 ACTGTCTCAAACACCACATAGGCACTAAATTTCTTTAATTTTTCGACTCATAT
 TTTCAAGGAGAAAAAATTCAAGCAAAATATAA

YPL089C, 676 aa (SEQ ID NO 386)

MGRKIEIQRI SDDRNRVTFIKRKAGLFKKAHFI SVLCQVDIAVITILGS
 NNFFYEFSSVDITNDLIYHYONDKNLLHEVKDPSCYGDVFKHSASVNIINQDL
 LRSSMSNKP SXSNVKGMINQSENDDDENNDEDDDHGNNFERN SNMHSNKA
 SDKNI PSAINKLLSTAI TSKMDGSEQNK RHPENAL PPLQHLKRIKPDPL
 QISRTPQQQQQNI SRPYHSSMYNLNQPSSSSSSSFTMDFFKLPSPFQNSS
 FNGRPPPEI SISFNKFSKPFETNASSRTPKQEHKINSGSNNDNMSNYTQSP
 SNSLEDSIQCTVKARRKLSARFVLKVHIFNNNPSNSAIPSEPPSSASSVS
 ANGNMGGSSQIMKENKLSRSSKISPLSASASGPLTLQKGNNGRMVILKLPN
 ANAPNGSNMCGNSNNNNHPYPFGSGSSPLFSATQFYIATPLQPSNIPGGP
 FQQNTSFLAQRQTQQVQOMSFKKQSOTVPLITTLTGRPPSTFGPETSNQ

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PPTGSLPSKFWHDLMSNSPNVSSISMFPDWSMGPNSAKTGNTNNGTFFP
 VQTAVNNGNSSNISS'NNTNMMNNNNNNNNSSNNNSNNGNDMNSMNSNSY
 YSNNEADPVNGAAISEHTTEGESNMQENSSYDAAATAYNCNTGL'PYIN
 TAQTPLGTFKFFNFSTDISGEKNSSKI

YOR372C, 2165 bp, CDS: 501-2165 (SEQ ID NO 371)
 AAAATCGTGGTTACTTTTCATATTCCTTAAACACTTTACCCTGTTACTGT
 GCGCGTTTCGAGCGTAGCTTTTCGTGGTGAATTTATTTGTAAGATTCCTCCAGC
 TGGCTCGATAGTTCTGCTCTCTGCGTATCCATATCCATTTCCGGTATGCTT
 TTACTATTCAACCTAGTCTGGCAATTTTTCACCTGAAATTTGTTCAACAC
 TTCTGGCATUCTAGATACTCATCTGTATTTATTTCAATTTATCTGTTGTGCA
 CGTTAATAGCATTTCCAGTAAACAAGTTTAGGTCACCTACCCGCATAAGCCT
 TTTGGCGTTTGGCGTAACCTCTCTCGCGAAAAGAAACGGCACCCAAAAAA
 AAAAAACAACAAAACAAGAACAAACAAAACAAATAGGACAGAGCCTTAA
 GGAGCTGCAAGGATCTTCTCAATATTTTGGCATCGGCATTCGTGGTGGAAA
 AAGTGTGCCAATTTGGAATAAATTTGGTCAGAATAGAGCATTTGATTTCCAACT
 ATGGACAGAGATATAAGCTACCAGCAAAATTTATACCTCAACTTGGGGCAAC
 TGCNACTTCTTCAAGACAGCCTCTACGGACAATAATGCAGATACAAAT
 TTTTGAAGGTAATGTTCAGAAATTCAAATATAATTTTAACAGTCCGTTACCT
 ACAACGACTCAATTTCCCCACGCCCTATCTTCTTAATCAGTATCAACAGAC
 TCAAGATCAATTTTGGCAATACAGACGCTCACAACAGTTTCGAGCAACGAAT
 CGTCTGTTGGTAGAGAACAGTATATTTACCGCATCATCAGCAGATACAAACAG
 CAACAACAACAACAACAACAACAACAACAACAACAGCAACCTCTAGCTTC
 ACTTGTACCTCTGCTGTACAAAGGACAGATACAAGTGAGACTTTTGGACG
 ATATCAACCTTCAACCTTCTTCTGTTTTTGCAGTTTGGCAACTCTTTTACCC
 AGCGAATTTTGGTTGCATCCCCAGAGCAATTCAAAGAATTTTGTGTTGA
 CTCTCCGTCCACCAATTTCAATTTCTTTTCAAAAACCTCCGGCAAGACAC
 CACTTTCGATTTTGTAAACAGATTTCTAACGGTGCCTCAGCAAGCACCCACAGAG
 AACCCAGATCAACAACAGAATGTTTTTTAGCAATCTCGATTTGAACAATCT
 TTTGAAGAGTAATGGAAAAACACCCCTCATCTTCATGCCACCGCGCATTTT
 CACGCACCTCTGTAGTAAAGATTGACATGAATCTCATGTTCAACCAACCG
 CTGCCGACATCTCCATCAAAAAGGTTCTCTCTCCCTGTGGTTGACACCAATA
 TCGAAGAAAAATTTCTGAATGACGTCCGTACACCTTATGCAAAAGCATTGA
 TATCGTCTAACACGCGCTTAGTGGATTTTTCAGAAGCCCAAGAAAGGATATT
 ACCACTAATGCAACATCCATAGGGCTGGAAAAATGCCAACAACATCTTACA
 GAGAAGCCCGCTAAGATCTAACAATAAAAAATTTATTTATTAAAAACCCCC
 AGGATACCATCAATAGCACTAGCACACTAACTAAGGACAACGAAATATAA
 CAGGACATATACGGCTCTTTCACCGACTACCATCCATTTAAATTCATCAAT
 AACTAAATCTATCTCCAAATTTGATAAATCTAGAAATCCCTTGTATGCTT
 CGAGATCAGATAACAATTCCTGGATTTCCAATGTGGATGACCANTTGTTTGAT
 TTGGGGTTGACAAGATTACCTTTATCACCACACCAANTTGTAAATCTTT
 GCATAGTACAACCACAGGTACATCTGCCTTACAAATTCCTGAGCTACCCA
 AGATCGGGTCTTTTAGAAGTCTATACGGGAATCAATCCAATTTCAAGTTCA
 AACACAGATTTCTTTTAAAGACAAATCAGGCAATAATAATTCAAAGGGTCG
 AATCAAAAAAATGGGAAGAAACCTTCCAATTTTCAATTTATTGTGGCAA
 ATATTGATCAATTTAACCAAGGATACATCATCGTCATCTTTATCATCATCA
 TCTGAATCCAAGTTCCAGTGCACCGAATTCMAATTCAAACGTAACAAAGAA
 AAGAGCAAGTAAACTCAAAAGATCACAGTCTTTACTTTCTGATTCCGGAT
 CGAAATCACAAAGCAAGGAAAGCTGTAATTTCAAATCTAATGGAAATTTA
 TCAATTCACACTAA

YOR372C, 554 aa (SEQ ID NO 372)
 MDRDISYQQNYTSTGATATSSRQPSTDNNADTKFLKVMSEFKYNFNSPLP
 TTIQFPPTPYESNQYQQTQDKFANTDAHNSSSNESLSLVENSILPHHQIQQ
 QQQQQQQQQQQALGSLVFPFAVTRTDTSETLDDINVQFSSVLOFGNSLP
 SEFLVASPEQFKEFLLDSPSTNFWNFHKTPAKTFLRFVTDNMGACQQTTE

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NPGQQQNVPSNVBLNMLLKSNGKTPSSSCTGAFSRTPLSKIDMNLMFNQP
 LPTSPSKRFESLSLTPYGRKILNDVGTIFYAKALISSNSALVDFQKARKDI
 TTNATSTGLENNILQRTPLRSNMKKLFIKTPQDILNSTSTLTKDNENK
 QDIYSSPTTIQLNSSITKSISKLDNSRIPLLASRSDNILDENVDDQLFD
 IGIWRLPI/SPIFNQNSI/HSTTTGTSALQIPELPKNGSFREDTGINPISSS
 NTVSPKSKSGNNSKGRICKNGKKPSKFPQIIVANIDQFNQDTSSSSLSSS
 LNASSSAGNSNSNVTKKRASKLKRSQSLLSDSGSKSQARKSCNSKSNGL
 FNSQ

YDR224C, 896 bp, CDS: 501-896 (SEQ ID NO 111)

TTTCTTCAACAACGACGAGTTAACTPATTTGTGCTCTTTTCTTGAGCCACCA
 AATACACTCCCATTCCAATAGCTTCGCACAGTGAGGCGAAAACTTTGGAAC
 AGCGCTAATGAATTATTTGTGAGCTCCCGGAGTTCAAATTTCAAGAAAAC
 GCGGTTGCGTCGTAACTATGGTATAGACGCTCAATGTGCGCCGAAAGSGA
 AGGCTGTTCTCACTTTTTCGCGCGTTGCACCCCTTTCTCCCGCAAAAAAT
 GAGAACGATGGATTTAAATCAAGAGAAATGCCCCCTTACTAGTGGCAATA
 CTACCTTGGTTGGTTATCTTGTAAAGATTGGTAAGAAAGGGGCATCTCTG
 TTTTCTTGATGTATATAAACAACATGATTTGATCATCTCAGATGOTCAGA
 TTTATTAAAGACGCTTCTCTTTCCGCATTTTCCATTATTGTTATATTTAA
 TTTATTCCTATATATAGACAACTCAAACCACAAATAAAACCATACACACATACA
 ATGTCTGCTAAAGUUGAAAAAGAAACCAAGCTTCAAAGCCCCAGCTGAAAA
 GAAACCAGCCGCTAAAAAGACTTCCACTTCCACTGATCGTAAGAAGAGAA
 GCAAGGCTAGAAAGGAACATACTCTTCTTACMTTACAAAGTTTGAAG
 CAAACTCACCCGACACTGGTATTTCCCAAAAGTCCATGTCTATCTTGAA
 CTCTTTCTGTTAAGGATATCTTTGAAAGAAATCGCTACTGAAGCTTCTAAAT
 TGGCTGCGTATACAAAGAAGTCTACTATCTCTCTCTAGAGAAATTCAAACC
 GCTGTAGATTGATCTTACCAGGTGAATGGCTAAGCATGCTGTCTCTGA
 AAGTACTAGAGCTGTTACCAAGTACTCTTCTCTACTCAAGCATAA

YDR224C, 131 aa (SEQ ID NO 112)

MSAKAEKKPASKAPAEKKPAKKKTSTSTDGKKRSKARKETYSSYIYKVLK
 QTHPDGTGISQKMSILNSFVNDIFERLATEASKLAAYNKKSTISARELQT
 AVRLILPGELAKHAVSEGTAVTKYSSSTQA

YLR294C, 830 bp, CDS: 501-830 (SEQ ID NO 281)

ACCAACCAACTTCTTCTTTGTCTCTCAATATCAAAGAAAAAAAAAAAAAAC
 CCACTGCTCAGATGTTATAAGCAAGGGCTGTTAACTTATATACACCTTCA
 TCTACCAGTCACCAGTCCATACAAACTTGAACCGTCTGCGTACCAGTCTT
 AATCAAAATGTTCCCTATCGCTTCCAGAAGAATACTGCTTAATGCTTAAAG
 TTTCTCCCACTCAGACTGTGCAATAGAAATTTCACTACCACAAGAAATATCC
 TACAACGTCATACAAGATTTGTATTTGAGGGAACTAAAAGACACCAAACCT
 GGCCTCAAAGTAACTTCCAAGATGCTGAAGGTAATGTTAAGCCTTGGAAAC
 CACCACAAAAACCAAATCTACCAGAAATTGGAACTTCAAGGCCACAGAGGC
 TTAAGAGGCTTACACCGAGCAAAATGTAGAAACCTGCTCATGTTCCCTAAAGA
 GCTGTAAGAGGGGTGAGTCAGAGCCAAATTGAAGAGGATGGCTAGTTTTGG
 ATGATGCTGAGGAAACCAAGAAAGTCATTGAACCTTTTCATAGCATCCCTC
 CTTCTCGAAGAAAAACCAACAGAACCAAGCTGAACAAGATCATTTATTT
 TTTGGCTTTCTTCCCTCTATCTTTTATATTTGAAATCCAGTACAATAAAG
 AAAAAGCAAAATACACTAAGCACCTCTTTGTAATCAGCCACACAAAAATCA
 GAATTTATTTTTTAAACAAAAATACAATTGTACATAGACACGTCTTTAT
 CTTTCTTATTACTACTATCTTTTATTTCAATAACTATTACTTTCTAAGT
 ATGACCTACGCTTCTTTGGTAAATAAATAA

YLR294C, 169aa (SEQ ID NO 282)

MMLRKPKKVIELFIASSLSKKKQTEFQAEQDHYFWLSSSHLPIFESSYIK
 KKQNTLRITLCNQPHKMQNIFFKQKIQLYIDTSLSPLLLLFFYPNNVYPLS

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MTYASLVNK

YMR256C, 683 bp, CDS: 501-683 (SEQ ID NO 319)
CTTTTCAGTTATTTACCTTCCTTTCTCTCACGTGTAAATATTTGTGTGTC
ATACACACCCGCTAAAAACCTTTGCAATCAACTTATACCCCTACATTTCTATA
GACGCTATTTCGAAACAAGATGTAACCCCTTTTTCCTTTAGTTTTGAGA
TTTCTACTCGTAAAGAGTACGTTTATTTATTTATTCAAAATTTTATCTTC
ATACCATGTAAATATAAGCGCATATAATCACTACGATCTTAGTACAGCTA
GAATTGCTGACGCTTAUAATTGCTTTATTTGTTTGATTATATGCACGTATA
CATATAGTGTTCAGCAAAAAAAAAAAAAAGGCAGTACTTGATTGGCTACGCC
GCCCATCGTCCGAGAAATCCGGCCTGGTAGGGGCAGGTTTGAAAAGGGCG
ATAGAAATAAAAGATGATATTATTTATTCATCCCATGAATAGTAGAACTC
GATATAAGATTCTAAACCAACAAGTACAGAAAGCAAAACAATAATAAATA
ATGGCTAATAAAGTTTATTCAACTACAGAAATCTTCCAATCTTCCACTAA
ACCTCTATGGTGCAGACATCCAAGGTCAGCTTATACCTGTATCCATTTT
ATCCATATTTTTCGCTAGCCGTCGTTACACCACTTCTATACATTCCAAAT
GCATATAGAGGTATCAAAAGCCAAGAAGGCATAG

YMR256C, 60 aa (SEQ ID NO 320)
MANKVIQLQKIFQSSTKFLWWRHPRSAIYLYPHYAIFAVAVVTPLLYIFN
AIRGIKAKKA

YLR327C, 761 bp, CDS: 501-761 (SEQ ID NO 287)
TTCTCATACGTATGTTTCTTTTAGATTATGCACCTTCTTTGCCACAGTAAA
TGTGGCCGGCAAGATGTTTGAGCTAGCGCCGTGCACAGTGGAAAGAGACGGA
CCCCATTTGTGGGGTTTCATCGGATTGTGGCGGAAGAAGGCTACACCGTTC
TTGAGCCACCCCCCCCCCAGGAGTAAATTTACACAAACAGTGGTGGTCCC
TATGGTGGTATACGAGATAGTGATAGAAGCTGCTGGATTGGGGTAGAAAT
TTTGTAGGCGTTTATGGAATTCGGTATCGGATATGGTATGGCTTGAGGTAGG
TAATCCAGACACCACTCGAAATATATATAAGGAGAGAGTTCTGGCAGGTA
GATTTGCTACTCCTCTCTACCACTTTCTTTCTACTCCTTTTATTATGTAATG
TTTATTATATAAGCACACGCAAAACGTTAAATAAATCTAATAAGATTTCAAT
ATAACATAACATTAAAGCACACAAATTTCTAACACAAACACAATTCAAAC
ATGACCCAGAACTAGCAAAATGGACAGTCCACGAAGCAAAGTCTAACCCAAA
GTATTTCACCCATAACGGCAACTTTGGGGAGTCTCCCAACCACGTCAGA
GAGGAGGCTATGGGAAAGGCAATTGGGGCAAGGCTGGGATGAGATTAAAT
GACTTAATCGATTCTGGCGAAATTAAGACAGTCTTCAACAAGACCAGAAG
GGGCTCTAACTCCCAAAACAATGAAAGAAGGCTTTCTTGATTTGCAACAAT
ACCAATCTAA

YLR327C, 86 aa (SEQ ID NO 288)
MTRTSKWTIVHEAKSNPKYFTHNGNFGESPNHVKRCYGYKGNWKGKPCDEIN
DLJDSGEIKIVFNKTRRGSNSQNNERRLSDLQQYHI

YLR161C, 2414 bp, CDS: 501-2414 (SEQ ID NO 211)
GTTCATGCGCGCATAGGAAAGCGCACGAAACAAATGAGTAATTCGTAGGA
AACAATGCAGCCCCCAGGGTCAGCAACTGACGTGACTCAGCCTGGCTTTT
GTAGAAAAAGATGACGCCCTGGCAGAGAGCTGGGGGAATTCACCGGTCCT
CGCTACCCACCTTAAGTATGGAAGAATATGATGAAGAATATGATGATAAC
TCTTGGAAGCGAGCGCGGGTTCCATCACTTTTACGGATTGGTAACACA
GGGGCCTCAGTTGATACCTTGGTATTCAGGCTTCCAGCCTTGGTGAGTTT
AGTTAGCGGTATGGTATGCACATGGTGTGATGCTTGGTGGTAATCATTC
GTTAGGTGAATPGAGCAGTAGCGATATAGATAATATTTAGTATTTTATAG
CGTCTTTTGGTGGGGGAGGAAGGACAAAACCTGTCTCGTAAATATAAAG
GGACTGTTCGATATCGCAGATACTAGAGTATAAATTCGATTGAGGCGAG
ATGACAAATATTTCAAGTTGGTAAAAGGTGCTACCAAGATCAAGTCAGC

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CUCGCCCAACAGAAAGTATCTCGGATCCGACTACTGTTGGGGACCAGCAAATG
 AAGAGGATTTCTATGAGATCCGTGAAGGGTTTGGATTCCCGAATTAATGAC
 ACGGCGTGGACTATTGTGTATAAAATCGCTGTTGGTGGTTTCATTTGATGAT
 AAGGGAGGGTTCCAAAGATGTTGCATATCGGGTACTACTCTAGGAACCTGG
 AGTTTTTTTGACATTGAAAACATACGTGGCTCCAATGGCAGTGCGTCTGGA
 GACATGAGGGCACTTGATAGATAACGAATATTATCTGAAGGTGAGATGACAG
 GGAGTTTGGTAAATCAAAALGGACTATGTGACAGACCCCTATTCGAACAC
 TGAAGCTGAACAGTGGCAATTACGGAAGCTCCAGAAACAAGCAACACTCT
 ATCAATATAGCACTAGATCATGTGGAGTCCCTAGACGTACAAATACAAGC
 CCTCATTTAAACCAAGTATACACAATATGATTTGAGTAACGAATTGATCA
 TATTTGGTTTCAAGCTGCTATATTCAAGACCTGCTAGCGCTATATAATGCT
 CTCAACGAAGGTATCATAACTCTGCTGGAGTCTTTTTTCGAACATATCTCA
 TCATAATCCAGACAGAACTCTAGACCTCTACAAGACGTTTGTTCATTTGA
 CCGAGCACGTTTGTTCAGGTACTTGAAGAGCGGGAAGACTGCGGGCTTTGAAA
 ATACCCGTCATCAAGCATATCACTACCAAACCTGGTCAGATCGCTAGAAGA
 ACNTCTGATAGAGGATGATAAGACGCACAACACTTTTGTGCCCGTTGACA
 GTTCTCAAGGAAGTCTGCGGCGGTAGTACCCAAATCTACTGCACAGGAA
 AGGTTGGAGCAAAATCCGGGAACAAAAAAGGATACTAGAGGCACAATTGAA
 AAACGAACAAGTAGCGATTTCCCCCTGCTCTAACTACTCTCACGGCGGCTC
 AATCTTACAACCCCGTTTGGAAACAGACTCTTCTATGCATACTAAATTTCCA
 ATGGCTGTGGCTAATCAAACGCAACAGATCGCAAATAACCCATTTGTATC
 TCAAACCTCAGCCACAGGTCATGAAATACACCAACCCCTCATACAGAGCCCG
 CAAATTTAAACGTTCCCTGAATATGCAGCGGTCCAAACACACAGTGAACCTC
 AACCCCTGTACAAGATGCTGGCGTAAGTGCCCAACAAACGGGGTACTATTC
 GATTAACAACCAATTTAAACCCCACTTTACAGGTGACAGGGTTTGGAGGAT
 ACTCCGTTTTCACAGGATACAAGTGGCGCTTTCTAATCAACAAGTCTCTCAT
 TCACAAACTCGTTCTAACAACCCCGTTCCGATTGCACAACGCGCGAGGAT
 CGCAACAGGGGAATCTGCACACGAAATGTTCTTAAATAACCCATTTTCAC
 GACCAAACTTTGATGAACAAATACCAATATGCCCTACAACAACAGATA
 ATAAGTAACCCCTTTCAAACCAACCGTACAATCAACAACAATTTCAACA
 ACAAAAAATGCTTTGAGCTCGATCAATAGCGTTATGACAACCCCTACTA
 GCAATGACAGGGATCGATGAATATTCCTCAGCGTTTTTGATAAAATGGAATTT
 CAGGCTCACTACACTCAGAATCATCTCCAACAACAGCAACAACAGCAACA
 GCAACAACAGCAACAGCAACAACAGCAACCAACAACAGGTTATTATGTGC
 CTGCAACTGACAGGAGCCCAACCCCTGTTACAAATATAACTGGGACAGTTCAA
 CCTCAAAATTTCTCTTTCTATTCACAACAGCAACCAACAGGAAACAGTC
 TCAAAACACAGCAACAGGTTTATAGGAAACCAATATGCTAACAAACCTCAATT
 TAATTGATATGTAA

YHR161C, 637 aa (SEQ ID NO 212)

MTTYFKLVKGATKIKSAPPKQKYLDPILLGTSNEDFPYELVKGLDSKIMD
 TAWTIVYKSLLVVHLMIREGSKDVALRYYSKNLEFFDIENIRGSNGSASG
 DMRALDRYDNYLKVRCREFGKIKKDYVRDCYRTLKLNSGNVCSSFNKQHS
 INIALDHVESIFVQIQALTKNKYTQYQLSNELIIFGPKLLIQDLLALYNA
 LNEGIIITLLESFFELSHHNAERTLDLYKTFVDLIEHVVRYLKSGKTAGLK
 LPVIKINLTTKLVRSLEBHLIEDDKTHNTFVPVDSQGSAGAVVAKSTAQE
 RLEQIREQKRILFAQLKKTQVATSPALTTVTAQSYNPFQTESSMHTNIF
 MAVANQTQQIANNPFVSQTQPOVMNLTPTAHTEPANLNVIEYAAVQIITVNF
 NPVQDAGVSAQQYGYYSINHLTPFTGAGFGGYSVSODTTAASNQQVSH
 SOTGSKNPFALHNAATITATGNPAHENVLMNPFSPNFDQNTNMPIQQQI
 ISNPFQNTVYQQQFQQQKMPISSINSVMTPTSMQGSNNIFCRFDKMEF
 QAHYTTQNLQQQQQQQQQQQQQQQQQQQQQQGYVPATAGANFVINITGTVQ
 PQNFPPYPQQQPQPEQSQTQQPVLGNYANNLNITDM

YLR206W, 2342 bp, CDS: 501-2342 (SEQ ID NO 277)

TACACCCCTGACTTTTCCCATCATACGACGATGCTCTAGTAAACTTCCAC

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CGCACCTGTTAGATAAACAAAGTGCGCCCAAGATCACAATACCGAAGGGGC
 GATATCACCACCTCAGTATCTTACAGTCGAGCATAGCCTAGTCTGCCAGTA
 TCCCGCAGGATCCATTGCTATTGTTTGTCCAAACCGCATTTTATGTGTAACT
 GATTAAATCGTAAATACAAGGCCAACAGAAATTACCTTCGGGCGAAGGGT
 GAAAAAAAAGTAGTGGAAACTAAAGAAAGAAGAGTTTAGTTACGGACCC
 TTTCAAGGATTGACACACTCCCAATATTTTGCTACATTATTGACCTTTGT
 TGAAGGAGGGCTTCGTTTATTTAATTATTTTGTTCGTTTTGCTACAAC
 TCGGAATACGGTCACATCTTAGTTTCACCTTCACAAATTCTTATCATCTT
 CTTTGTGTTTATTTTGACACACCCCTATTAAAGTGTATTTGTTTTGTAAAGTA
 ATGCTTAAGCAGTTTGTTCGTTCTGCAAGAACATGATGAAGGGCTACTC
 ATCCACACAAGTGCCTTGTGAGAGATGCCACGGCGAACGACTCGAGCACTC
 CATCGATAGACACTCTCGACGATTTCGCACAGAGATCTTACGATTCCGGTG
 GACTTCTTCGAGATTATGGATATGTTAGACAAAGAGGCTGAACGATAAGGG
 CAAATACTTCGAGACACGTTCCCAANTCCCTGACCGTTTTCGACTATCTTG
 TTGTTTTCGGGAGTGAGAACCTGCTGCTGCTAAGGTCGACAGAGAAATTCTTAU
 GTAAATAAGACATTAAGGGATTCAGACACGAAAAATGAGTCCCGATTGGA
 CGAGGGACAAATTTATCAGACTAAAGGCTAAAGAACTCTCTCTCTTTGTTGA
 ATGATGAAGAAAGGCTACCGGAAGACAGGCTCTATGAATACAAGAAACAGA
 AGGGGGAACAGAGCTTATAGGCCAAGGCCAAGAAGACAAAGAACAGGAG
 CAAACACACAGATTCTTCTCCCTCTTACCAGGACGATTTCGAAAAGGCCC
 TAGAGGAGAGCAGAATTACTGCTCAAGAAGATGAACAACTAGAGAGAA
 CTGGCCACGTACGACGATGAAGATCCTGACTTCCAAGCTGCCCTTACAAC
 AAGTAAAGAAGAAGAGGAGTTGAAGCAATTGCAGGAACCTACAGAGATTAC
 AGAAGCAACAACAGTCTCTGTCTCAATTTCAAGCTCCCTTACAACAACA
 CAACCACAACAACAACCAGCGTACTACGACATTTTCGGTAATCCAATCTC
 CCAAGATGAATACTTACAGTATCAGTACCAACAGGACCAGGAACAAGCAA
 TGGCTCAGCAAAAGATCCCTGGACCAACAGCAACAACAACAGCAGCTTGCT
 GAACAACAATATTTTACCAAGCAACAACAAGCTGCGGCCGCCGCTTCTGCT
 CTTGCAACAGCAACAACAAGCCGCTAATATGCAACAACAACAACAACAGC
 CCGCTGATTTTCAACAACCTTTTGCTACAGGTTCTAATAATCCGTTTTC
 ATGGATAATCTTGAAAGACAAAGCAGGAGCAACAGCATGCTCAATTGCA
 AAGACAACAAGAAGAAGCTAGACAACAACAAGAACAATTGAAGCTACAAC
 AATTGCAAGACACAACAACAAGAGGCTCAATTACACCAAGAGAGGCAA
 GAAGAAGCCCAATTACAACAGCAGCAAGCCCAATTGCTACAACAGCAAGC
 CCAGTTCCAGCAACAACAACCCCTTGAGCAACAAGGACTGGGAACCACT
 CTATATCGGATAAATACAGCGACTTGAAATACCTTCGTTAGCAACTGGTACA
 GGGATAGATACTTTTGGTAACACTGGAGAGGCACGTATTCCTGCACAACA
 TACAAGACAGGCACATTTATAAATTTCTCAGGCTACAGGCTACAACAGG
 TTACTAATGAACCCAGAACAACCTTTCTTAAGCAACCAATACAATTGGT
 TTACCAAGCACAAATATCGTGCCCAAGCAACAGGGTACGGGTTTGGTAA
 CCAACCTCAAAAGTCTCTCTACTAATTTCTCTCAGCAAAATCCTACTGGTA
 TAAGCTACTCTCAGCCACAACAGCAACAACAGCCACAGCAACAACCCCAA
 TACATGCAAAATTTCCAACAACAGCAACCTCAATACGCCCAAAACTCCA
 ACAACAACCAACAATACACTCAAAATATCAACAACAACCAACAATACATTC
 AACCTCATCAACAACAACAGCAGCAGCAGCAGCAGCAACAGCAGCAACAG
 CGATATACTCTGACCAAGGCTAAGCTTAATTGATCTTTGA

YLR206W, 613 aa (SEQ ID NO 278)

MSKQFVRSKNNMMXGVSSQVLVRDATANDSRTPSIVTTECLAQREYDSV
 DFFEIMDMLDKRLNDKKGKYWRIVAKSLTVLDYLVRFSGSENCVLCWRENFY
 VIKTLREFRHNESGFDEGQIIIRVKAKELVSLNTEERLREPRSMNTRNR
 RANRAARPRPRRQTRSNPHDS\$PSYQDDLEKALEESRITAQEDQRRRE
 LAGYDDEDIDFOAALQLSKEEELKQLQELQRLQKQQQSLSCFQAPLQQQ
 QFQQQPAYYDIFGNPISQDEYLQYQYQQDQEQAMQQRWLEQQQBQQQLA
 EQQYFQQQQQAAAAASALQQQQTAAAMQQQQQQQPAQFQQFIPTGSNNPFS
 MDNLERQXQEQQLAQQLRQQQEEARQQQEQQLKLQQQLQQQQQBEAQLEHQKRO

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EEAQLQQQQAQLLQOCAQFQQQQPLKQTRTGNQSIISUKYSDLNFLLATGT
GIDTFGNTGEARIPACHTKTGTFINSQGTGYKQVTNEPKNNPFLSNQYTG
LESTNIVFTQGTGYGFGNQPSPTNSPQQNFTGISYSQPOQQQQPQQQPQ
YMQNFPQQQPPUYAQNFQQQPOYTQNYUQXPOYIQPHQOQQCQOQQQUQQQ
GYTPDQGVSLIDL

YDR342C, 2213 bp, CDS: 501-2213 (SEQ ID NO 119)

CACTTCTCAGAAATGCATGCACTGCCACCACGCTANTTCGAAAAAATTCT
CCAGAAAGGCAACGCAAAATTTTTTTTCCAGGGAATAAACTTTTATGAC
CCACTACTTCTCGTAGGAACAATTCGGGCCCCCTGGGTGTTCTTCTGAGG
TTCATCTTTTACATTTGCTTCTGCTCGATAATTTTCAGAGGCAACPAAGGA
AAAATTAGATGCCMAAANGTCCTCTTCAAGCAAAAATCCCCACCATCTT
TCGAGATCCCTGTAACTTATTGGCAACTGAAAGAATGAAAAGGAGGAAA
ATACAAAATATATACTAGAACTCAAAAAAAAAAAGTATAAATAGAGACGATA
TATGCCAATACTTCACAATGTTTGAATCTATTTCTTCATTTGCAGCTATTG
TAAATAATAAAACATCAAGAACAACAAGCTCAACTTGTCTTTTCTAAG
AACAAAGAATAAACACAAAAACAAGTTTTTTTAATTTTAATCAAAAA
ATGTCACAACACGCTCCTATTGCAGAGCAAACTCCTGTGGAGCATCTCTC
TGCTGTTGACTCAGCCTCCCACTCGGTTTTATCTACACCATCAAAACAAGG
CTGAAAGAGATGAAATAAAAGCTTATGGTGAAGGTGAAGAGCACGAACCT
GTCGTTGAAATTCCAAAGAGACCAGCTTCTGCTATGTCACCTCTCTCTAT
TATGTGTATCATGATCGCCTTTGGTGGTTTCGTTTTTCGGTTGGCATACTG
GTACCAATTTCTGGTTTCATCAATCAAACCGATTTTCATCAGAAAGATTTGGT
ATGAAGCATAAAGATGGTAATAATTATTTGTCTAAGGTTAGAAGCTGGTTT
GATTCTCTCCATTTTCAACATTGGTTGTGOCATTGGTGGTATTATTTCTTT
CCAAATTGGGTGATATGTACGGTCCTAAGGTGGGTTTGATTGTCGTTGTT
GTCATCTACATCATCGGTATTATTATTCAAATTGCATCTATCAACAAATG
GTACCAATATTTCATCGGTAGCAATTATTTCCGGTTTCGGTGTGTGGTGGTA
TTGCCGTTTTATCTCTATGTTGATTTCTGAAGTATCCCCAAAGCAATTA
AGGGGTACTTTAGTCTCTTGCTACCAATTGAAGATTACTGCCGGTATTTT
CTTGGCTTACTGTACCAACTTCGGTACTAAGAATACTTCCAACCTCTGTGC
AATGGAGAGTTCCATTAGGTTTGTGTTTTGCCCTGGGCTTTGTTTTATGATT
CCTGCTATGACATTTGTTCCAGAGTCTCCACGTTAFTTGGCTGAAGTCGG
TAAGATCGAAGAAGCCAAACGTTCTATTCGCCCTTCTAACAAGGTTGCTG
TTGATGATCCATCTGTTTTGCTGAAGTCCAAGCTGTCTTGGCTGGTGTGTA
GAGGCAGAGAAATTAGCTGCTAATGCATCTCTGGGTCAATTGTTTTAGTAG
CAAGACAAAGGTCTTTCAGCGTTTGATCATGGGTGCTATGAATCAATCTC
TACAACAAATTGACAGGTGATAACTAETTTCTTCTACTATGGTACTACTATT
TTCAAGGCTGTTGGTTTGAGTGACTCTTTTGAACCTCTATCTCTCTCGG
TATTTGTTAACTTTGCTTCCACCTTTGTTGGTAATTAAGTTGTTGAGAGAT
ATGGTGGTGGTACTTGTGTTGCTATGGGTGCTTCCATCCATGACTGCTTGT
ATGGTTGCTATGCTTCCGTGGGTGTCACCAAGATTATGGCCAAATGGTCA
AGACCAACCAATCTTCCAAGGGTGCTGGTAAGTATGATTGCTTTGCCCT
GTTTCTATATTTCTGTTTTGCTACTACATGGGCTCCAATTCCTTACGTC
GTTGTTTTCTGAAACTTTCCTATTGAGAGTCAAGTCTAAGGCTACGTCAT
TGCTACAGCTGCTAATTTGGTTGTGGGGTTTCTTGATTGGTTTCTTCACTC
CATTTATTACTGGTGGTATTAACCTTCTACCTACGGTTAAGTTTTTCATGGGC
TGTTTTGCTCTTCATGTTCTCTATGTTTTGTTAGTTGTTCCAGAAACTAA
CGGTTTGACTTTTGAAGAAGTCAACACCATGTGGAAGAAGGTGTTCTAC
CATCGAAGTCTCCCTCATGCCCTCCACCATCCAGAACAGGTGCCAACTAC
GACGCTGAAGAAATGACTCACGATGACAAGCCATTTGTACAAGAGAAATGTT
CAGCACCAAAATAA

YDR342C, 570 aa (SEQ ID NO 120)

MSQDAALAEQTPVEHLSAVDSASHSVLSTPSNKAERDEIKAYGEGZEHEP
VVEIPKRPAAYVTVSIMCIMIAFGGPFVFGWDTGTISGFINQTFJRRFG

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MKHKDGTNYLSKVRTGLIVSIFNIGCAIGGLILSKLGDMYGRKVGLIVVV
 VIYIIGI I I Q I A S I N K W Y Q Y F I G R I I S G L G V G G I A V L S P M L I S E V S P K H L
 R G T L V S C Y Q L M I T A G T F I G Y C T N R G T K N Y S N S V Q W R V P L G T C F A W A I F M I
 G G M T F Y P K S P R Y L A E V G K I B B A K R S I A V S N K V A V D D P S V L A E V E A V L A G V
 E A E K L A G N A S W G E L F S S K T K V L Q R L I M G A M I Q S L Q Q L T G D N Y F F Y Y G T T I
 P K A V G L S D S F E T S I V L G I V N F A S T F V G I Y V V E R Y G R R T C L L W G A A S M T A C
 M V V Y A S V G V T R L W P N G O D Q P S S X G A G N C M I V F A C F Y I P C P M T T W A P I P Y V
 V V S F F F P L R V K S K A M S I A T A A N W L W G F L I G F F T P F I T G A I N F Y Y G Y V F M G
 C L V F M F F Y V L L V P E T K G L T L E E V N T M W E E G V L P W K S A S W V P P S R R G A N Y
 D A E E M T H D E K P L Y K R M F S T K

YDR343C, 2213 bp, CDS: 501-2213 (SEQ ID NO 121)

AAAAAATGTTTTTTAGGCAACGGAGATTCTGTTTATCCACGTTTACCC
 ACAAAAAGTGCAGGTACATTGTGGGGCCCCGGCATCGAAAATCACTTTT
 TTCCCTTAACCGCTCGA/AAAAACCGAGAAATTATTGGAACCTTGCCAGAGA
 ATAGTCCGTAGGCAAAATTGAAANTGTTCCCTTAAAAAATTTCTGTTTCTTAC
 TCATTGAGATTATTTCAGATCCCCCTCCGTGCCCTTCATTGAAAAAATCCAA
 GAGATGCTCTGGATCTCTATGCCAGATTTTCCGCTTGCAGACAATGGAGAGC
 AAA/CGGTATACAAATATAGAAAGCACAGAAACATATAAAAAGAGCTCGAG
 AAAAGACATATGGTTTGTAACTATCTTCTTCTTTTTCGAATTATTCTGT
 TTTAAATAA/AAAAAACAAGAACAAACAAGCTCAACTTGTCTTTTCTAAG
 AACAAAGAATAAACACAAAAACAAAAGTTTTTTTAATTTTAATCMAAAA
 ATCTCACAAAGACGCTGCTATTGCGAGAGCAAACTCCTGTGGAGCATCTCTC
 TGCTGTTGACTCAGCCCTCCUACCTCGGTTTTTA/TTACACCAATCAAAACAGG
 CTGAAGAGATCAATAAAAGCTTATCGGTGAAGGTGAAGAGACCGAACCT
 GTCTGTTGAAATTCCAAAGAGACCAGCTTCTGCTTATGTCACTGTCTCTAT
 TATGTGTATCATGATCGCCTTTGGTGCTTTTCGTTTTTCGGTTGGGATACTG
 GTACCACTTCTGGTTTTCATCAATCAAAACCGATTTCATCAGAAGATTTCCT
 ATGAAGCATAAAGATGGTACTAATTTATTTCTCTAAGCTTACAAC/CG/TT
 CATGTCTTCCATTTTCAACATTGGTTGTGCTTGGTGGTATTATTCTTT
 CCAANTGGGGTATATGTACGGTCTGAAGGTGGGTTTGATTGTCTGTTGTT
 GTUATCTACATCATCGGTATTATTATTCAAATTCGATCTATCAACAAATG
 GTACCAATATTTCAATCGGTACAATTTATTTCCGTTTTGGGTGTTGGTGGTA
 TTGCCGTTTTTATCTCCTATGTTGATTTC/CAAGTA/CCCCAAAGCATTTA
 AGGGGTACTTTTAGTCTCTTGC/TAACCA/TTGA/TAATTACTGCCGGTATTTT
 CT/TTGGGTACTGTACCA/ACTTCCCTACTAAGAACTACTCCAACCTCTGTGC
 AATTGGAGAGTTCCATTAGGTTTGTGTTTTTGCCTGGGC/TTGT/TTAAGATT
 GGTGGTATGAUA/TT/TTTCCAGAGTCTCCACGTTATTTGGCTGAAGTCCG
 TAAGATCGAAGAAGCCAAACGTTCTATTGCCGTTTCTAACCAAGCTTGCCTG
 TTGATCATTCATCTGTTTTTGCTGAAGTCGAAGCTGTCTTGGCTGGTGTGA
 GACGCAGAGAAAATTAGCTGGTAATGCATCCTGGGGTGAATTCCTTACTAG
 CAAGACAAAGGTCCCTCAGCG/TT/CGA/TCATGGGTGCTATGATTCAATCTC
 TACAACCAATTGACAGGTGATAAC/PA/TT/CTTCTACTATGGTACTACTATT
 TTCAAGGCTGTTGGTTTGAGTGACTC/TTTCGAAACCTCTATTGTCTTGGG
 TATTGTAACTTTGCTTCCACC/TTTG/TTGGTA/TTTACGTTGTTGAGAGAT
 ATGGTCTGCTACTTGTTTGCTATGGGGTGCTGCATCCATGACTGCTTGT
 ATGCTTGTCTATGCTTCCGTGGGTGTCACCAGATTATGGCCAAATGGTCA
 AGACCAACCATCT/TTCAAAGGT/TC/TTGTAAC/TTATGATTGTCTTTGCCCT
 GTTCTATATTTCTGTTTTGCTACTACATGGGCTCCAATTCCTTATCTC
 GTTGT/TTCTGAACCTTTCCCATTCAGAGTCAAGTCTAAGGCTATGTCTAT
 TGCTACAGCTGCTAATTTGGTTGTGGGGTTTTCTTGA/TTGG/TTCTCACTC
 CAT/TTA/TTA/CTGCTGCTATTAACTTCTACTACGGTTACGTTTTCATGGCC
 TGTTTGGTCTTCATGTTCTTCTATGTTCTTGTAGTTGT/TTCAAGAACTAA
 GGGTTTGACTTTTGAAGAAGTCAACACCATGTGGGAAGAAGG/TTTCTAC
 CATCGAAG/TT/TTCCCTCATGCTTCCACCATCTAGAAGAGGTGCCAACTAC
 GACGCTG/TA/TA/ATGCTTCAAGATGATAAGCCA/TTGTACAAGAGAAATGTT

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CACCACCAAATAA

YDR343C, 570 aa (SEQ ID NO 122)

MSQDAATAEQTPVEHLSAVDSASHSVLSTPSNKAERDEIKAYGEGGKHEP
 VVETPKRPASAYVTVSIMCIMIAFGGFVFGWDTGTISGFINQTDPIRREG
 MKHKUGTNYLSKVRTGLIVSIFNIGCAIGGIILSKLGDMYGRKVGITVVV
 VIYIIIGIITQIASINKWYQYPIGRIISGLGVGGIAVLSPMLISEVSPKHL
 RGTPLVSCYQLMITAGIFLGYCTNFGTKNYSNSVQWRVPLGICFAWALFMI
 GGMTFVPESPRLAEVVGKIEEAKRSIAVSNKVAVDPSVLAEVEAVLAGV
 EAEKLAGNASWGELFSSKTKVLRQLINGAMTQSLQQLTGDNFFYYGTIT
 EKAVGLSDSPETSIVLGIYNFASFTFVGIYVVERKGRRTCLLWGAASMTAC
 KVVYASVGVTRLWPNQDQPSKKGAGNCMIVFACFYIFCFATTWAPIPYV
 VVSETFPLRVKSKAMSTATANWLMGFIJGFPTPTGTATNFYGYVFMG
 CLVFMFFYVLLVVPETKGLLLEEVNTMWEEGVLPWKSASWVPSRRGANY
 DAEEMAHDDKPLYKRMFSTK

YGR192C, 1499 bp, CDS: 501-1499 (SEQ ID NO 183)

ACAGTTTATTCTCGGCATCCACTAAATATATATGGAGCCUGCTTTTTTAAGC
 TGGCATCCAGAAAAAAGAATCCCAGCACCAAAATATTGTTTTCTTCA
 CCAACCATCAGTTTCATAGGTCCATTCTCTTAGCGCAACTACAGAGAACAG
 GGGCACAACAGGCCAAAAACGGGCACAACCTCAATGGAGTGATGCAACC
 TGGCTGGAGTAAATGATGACACAAGGCAATTCACCCACGCATGTATCTAT
 CTCATTTCTTACACCTTCTATTACCTTCTGCTCTCTCTGATTTGAAAA
 AGCTGAAAAAAGGTTGAAACCAGTTCCCTGAAATATATCCCCTACTTG
 ACTAATAAGTATATAAAGACGGTAGGTATTGATTGTAAATTCTGTAAATCT
 ATTTCTTAAACTTCTTAAATTCTACTTTTATAGTTAGTCTTTTTTTTAGT
 TTTTAAACACCAACAACCTTACTTTTGAATAAACAACATAAACAACAAA
 ATGCTTAGAGTTGCTATTAACGGTTTCGGTAGAATCGGTAGATTGCTCAT
 GAGAATTGCTTTGTCTAGACCAAACCTCGAAGTTGTGTGCTTTGAACGACC
 CATTCATCACCAACGACTACGCTGCTTACATGTTCAAGTACGACTCCACT
 CACGCTAGATACGCTGGTGAAGTTTCCACGATGACAAGCACATCATTTGT
 CGATGGTAAGAAGATTGCTACTTACCAAGAAGAGACCCAGCTAACTTGC
 CATGGGGTTCTTCCAACGTTGACATCGCCATTGACTCCACTGCTGTTTTT
 AAGGAATTAGACACTGCTCAAAACACATTCAGCTCTGGTGCCAAGAAGGT
 TGTATTCACTGCTCCATCTTCCACCGCCCCAATGTTCTGTCATGGGTCTTA
 ACGAAGAAAAATACACTTCTGACTTGAAGATTGTTTCCAACGCTTCTTGT
 ACCAUCAACTGTTTGGCTCCATTGGCCAAAGGTTATCAACGATGCTTTCGG
 TATTGAAGAAGGTTTGTATGACCACTGTCCACTCTTTGACTGCTACTUAAA
 AGACTGTTGACGGTCCATCCCACAAGGACTGGAGAGGTGGTAGAACCGCT
 TCCGGTAACAATCATCCATCCTCCACCGCTGCTCTTAAGGCTGTGGGTAA
 GGTCTTGGCAGAATTGCAAGCTAAGTTGACCGGTATGGCTTTCAGAGTCC
 CAACCGTTCGATGTCTCGTTGTTGACTTGACTGTCAAGTTGAACAAGGAA
 ACCACCTACGATGAATCAAGAAGGTTGTTAAGGCTGCCGCTGAAGGTAA
 CTTGAAGGGTGTTTTCCGTTACACCGAAGACGCTGTGTCTCTCTGACT
 TCTTGGGTGACTCTCACTCTTCCATCTTCCNTGCTTCCGCTGGTATCCAA
 TTGTCTCCAAAGTTCTCAAGTTGGTCTCTTGGTACGACAACGAATACGG
 TTACTCTACCAGAGTTGTGACCTTGGTTGAACACCTTGCCAAGGCTTAA

YGR192C, 332 aa (SEQ ID NO 184)

MVRVALNGFGRIGRLVMRIALSRLPNVEVVALNDPFITNEYAAYMFKYDST
 HGRYAGEVSHDDKHIIIVDCKKIATYQERDPANLPWGSSNVDAIDSTGVF
 KEUDIAQKHIDAGAKKVVTAPSSATAPMFVMGVKHEKYTSULKIVENASC
 TFWCLAPLAKVINDAFGIEEGLMTTVHSLTATQKTVDGPPSHKIDWRCGRTA
 SGNITPSSGTAAKAVGKVLPELQGKLTGMAFRVPTVTVSVVDLTVKLNKE
 TTYDEIKKVVKAAAEGLKGVLYTEDAVVSSDFLGDSSHSSIFDASAGIQ
 LSPKFVKLVSWYDNEYGYSTRVVDLVEHVAKA

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YOR374W, 2060 bp, CDS: 501-2060 (SEQ ID NO 373)
CGACCCTCTGGTTAGATGACACTCCTGCCCCAACTGCCACGAATCTGTAA
CCCCATAACTATACCCGTACGCAGTACTAAAAATGTATGTAATTAGTAAA
TGTATGTAAACAATTTACCCGTTTTGTGTAAACAATTCATTCAATTCATTCTT
TTGATCCTTTAGTACCGTCCGCACATGATGTCAATTTCCCCCTCATTTTGTG
TTTTGCTGGTATGATTTCCCCGCCCGGGGACGGTACGGCTGTTATCCAGCG
ATGCGGGACTTCCGTCCACAGGTATCTTTTTTCTCCAACCTCCAACAGAGAT
GGAAAATGAGGGGGCGGGTGTAGGTAAGCAGAATGAGGAGAAATTTGTAAT
GAAAATGGAAGTTUGGGCGGTTATATAAATGGGGGGGGTTTGTGGGTGACA
ATTGACTTCACTCTCTTTTCTCAAAAATTTCTTGGGTCTTACGATTAGAA
GTATCTGGAAAACCAACCAAGAAAACACAAATAACAAAATAAATAAAGC
ATGTTCACTAGATCTACGCTCTGTTTAAAGACGCTCTGCACTCTCCATTTGG
GAGACTTCAATTTGAGATATTTCTCACACCTTCTTATCACAGTCCCTATCA
AGCTGCCCAATGGGTTGGAAATATGAGCAACCAACGGGGTGTTCATCAAC
AACAAGTTTGTTCCTTCTAAACAGAACAGACCTTCAAGTCAATTAACCC
TTCCACCGAAGAAAGAAATATCTCATATTTATCAAGCTAGAGACGACGATC
TGGAAAGAGCGCGTGCAGGCCGCCGACCGTGCCTTCTCTAATGGGTCTTGG
AACCGTATCGACCCCTATTGACAGGGGTAAAGGCTTTCTACAGCTTAGCCGA
ATTAATTGAACAGGACAAGGATGTCAATTTGCTTCCATCCAGACTTTGGATA
ACGGTAAAGCTATCTTTCTCGAGAGGAGATGTTGATTTAGTCATCAAC
TATTTGAAATCTTCTGCTGGCTTTGCTGATAAAATTGATGGTAGAATGAT
TGATACTGGTAGAACCAATTTTCTTACACTAAGAGACAGCCTTTGGGTG
TTTGTGGGCAGATTATTTCTTGGAAATTTCCCACTGTTGATCTGGGCCTGG
AAGATTGCCCTGCTTTGGTCCACCGGTAACACCGTCCGTGTTGAAGACTGC
CGAATCCACCCCATTTGTCGGCTTTGTATGTGTTCTAAATACATCCCACAGG
CGGCTATCCACCTGGTGTCAATCAACATTGTATCCGGGCTTTGGTAACATT
GTGGGTGAGGCCATTACAAACCATCCAAAATCAAAAAGGTTGCCTTCAC
AGGGTCCACCGCTACGGGTAGACACATTTACCAGTCCGCAGCCGCAGGCT
TGAAAAAAGTGACTTTGGAGCTGGGTGGTAAATCACCAACATTTGTCTTC
GCCGACGCCGAGTTGAAAAAAGCCGTGCAAAACATTATCCTTGGTATCTA
CTACAATTTCTCGTGAGCTCTCTTCTGCGGCTTCAAGCGTGATGTTGAAG
AATCTATTTACGACAAATTCATTGAACAGTTCAAAAGCCGCTTCTGAATCC
ATCAAGGTGGGCGACCCATTGATGAATCTACTTTCCAAGGTGCACAAAC
CTCTCAAATGCAACTAAACAAATCTTGAATACGTTGACATTGGTAACA
ATGAAGGTGCTACTTTGATTACCGGTGGTGAAAGATTAGGTAGCAAGCGT
TACTTCAATTAAGCCAACTCTCTTTGGTGACGTTAAGGAAGACATGAGAAI
TGTCAAAGAGCAAAATCTTTGCCCTCTTCTCACTGTAACCAATTCAAAT
CTGCCGACGAAGTCATTAAACATGGCGAACGATTTCTGAATACGGGTGGCT
GCTGGTATTTACACCTCTAATATTAATAUUGUUTTAAAAGTGGCTGATAG
AGTTAATGCGGGTACGGTCTGGATAAACACTTATAACGATTTCCACCACG
CAGTTCTCTTTCCGTGGGTCAATGCACCTGGTTTGGGCAGGGAAATGTCT
GTTGATGCTTTACAAAACACTTTGCAAGTTAAAGCGGTCCGTGCCAAATT
GGACGAGTAA

YOR374W, 519 aa (SEQ ID NO 374)

MFSRSTLCLKT3ASSIGRLQLKYFSHLPMTPVPIKLPNGLEYEQPTGLFIN
MKFVPSKQNKTFEVINPSTEEIICHIEGREDDVEEAVQAADFAFSNGSW
NGIDPIDRGKALYRIAFILPQDKDVIASTETLDNGKATSSSGDVILVIN
YLKSSAGFADKLDGRMLYGRTEFSYTKRQPLQVCGQIIFWNFPLLMWAW
KIAPALVTGNTVWLKTAESTPLSALYVSKYIPQAGIPPGVINIVSGFGKI
VGEAJTNHPKIKKVAFTGSTATGRHIYQSAAGUKKVTLELCKSPNIVF
ADAELKKAVQNIILGIYNSGEVCCAGSRVYVEESIYDKFIEEFKAASES
IKVGLPFDESTFQGAQTSQMQLNKILKYVDIGKNEGATLITGGERLGSKG
YFIKPTVFGDVKEDMRIVKEEIFGPVVIVTKFKSADEVINEMANDSEYGLA
AGIHTSNLNTALKVADRVNAGTVWINTYNDPHHAVPFGGFNASGLGRMS
VDALQNYLQVKAVRAKLDE

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VER177W, 1304 bp, CDS: 501-1304 (SEQ ID NO 151)
 AGATAGATAGATATAGATAGATAATGGACGTAGTATAGAAACAGAAAATC
 GGTAGATCCAAAACACAGGGGAAAAGGGGGGGGGGGGGGGGAGACAGCG
 CAGCCACGTGACGGGCTTCCTCTTTGGAAAGTGGAGCGAAGTTTGGCGGA
 AGCTACTTTTATTCGGCCTGGAGTCAAAAGAGGAAGCTUGGTGGUAAATA
 CCTTCTCTTTTGTGGCCGGGGCCGGGGGGGACGAGGCAAAAAGCAAAGAA
 AAGCAAAAATAAANAANAANCAAAAAACAGGGGTATGAGAAAAAG
 ACACGCTTTTCCACGCGCAGCAAAAAGCAAAAAGCAAAAGCAAACTCTTT
 ATTAATTGGACCTTAAACCTGAAAACGAGACGAACCGTAACATAAAACCGT
 GATGTTTCGCAAAAATCAACTTACTTTTTCCTACTTTTCAAAATTGAGAG
 UGCAAGCAAGTGAAGAAGAAAAGCAAGTTAAAGATAAATTAAGATAAABA
 ATGTCAACCAGTCCGTGAAGATTCTCTGTACCTAGCCAAAGTTGGCTGAACA
 GGGCGAACGTTATGAAGAAATGGTCCAAACATGAAGACTGTTGCCCTCCT
 CTGGCCAAAGAGTTGTCCGTGGAAGAGCGTAATTTGTGTGTCTGTTGCTTAT
 AAGAAGCTTATTGGTGTCTGTGTGCTCTTGGAGAATTGTTTCTTCTAT
 TGGCAAAAAGGAGGAGTCAAGGAGAAGTCCGAACACCCAGCTCCAGCTTGA
 TTTGTTCGTACCGTTCGAAGATTGAGACCGAACTAACTAAGATCTCCGAC
 GATATTTTGTCCGTGCTAGACTCCCACTTAATTTCCATCAGCCACCCTGG
 CGAGTCCAAGGCTTTCTACTATAAGATGAACGGTGACTACCACCGTTATT
 TGGCTGAATTTCTAGTGGCGATGCTAGAGAAAAGGCCACAAACGCCCTCT
 TTAGAAGCATACAAGACCGCTTCTGAAATTGCCACCACAGAGTTACCCCC
 AACTCACCCAATCCGTCTAGCTTTGGCTCTTAACCTCTCTGTCTTCTATT
 ATGAATTTCAAAACTCTCCAGACAAAGCCTGCCATTTGGCCAGCAAGCT
 TTTGACGACGCTATTGCTGAGTTGGACACTCTGTCTGAAGAAATCATACAA
 AGATAGCACAUATTATCATGCAAU TGCTAAGGACAAATTTAACTTATGGA
 CTTTCAGACATGTCCGAGTCCGGTCAAGCTGAAGACCAACAACAACACAA
 CAACATCAGCAACAGCAGCCACCTGCTGCCGCCGAAGGTGAAGCACCAAA
 GTAA

YER177W, 267 aa (SEQ ID NO 152)
 MSTREDVSVYLAKLAEQAEERYEEMVENMKTVASSGOELSV EERNLLSVAY
 KNVIGARRASWRIVSSIEQKEESKEKSEHQVELICSYRSKTELTETKISL
 DILSVLDSHLIPSAATTGSKVFFYYKMGDYHRYLAEPSSGDAREKATNAS
 LEAYKTASEIATTELPTTIPIRLGLALNFSVPFYEIQNSPKACILAKQA
 FDDAIAELDTLSEESYKDSLIMQLLRDNLTLWTS DMSESQAEQQQQQ
 QHQQQQPPAAAEGEAPK

YOR26/C, 2780 bp, CDS: 501-2780 (SEQ ID NO 163)
 TAGTTCTATTTGGCTATATATTTCAGACAGCAATCTTTAAGAGAGACA
 AACTGAGAATTAGCATATAGAATCATTCTATCAACTGTTTACAAACAAGT
 AAGCCCAAGACAGTTCCTCAACCGCTTAAGAAGTTTTTCTAGAGGGAGC
 AAAGTTCGTTTACATTTTACACACACAGTTTTTTTTTCACTTTTTTGGGCC
 TCTTTCTTTTCCCGTTTTTTTCAAAAAGCTTAGAAATCTTCTTCACTTCC
 TATTTTTTTCTAGAATCGTGAAGAATTTCCAGATTTAACAGTTTTTCCACTTT
 TTCAATAAGGAAATAGTAGGAATAATAAAAAAGGATAGTAGTAACGATA
 TACGTGCACTTTCCAGACTGGTCTCGAGCCGGAATTAATTAACAATAGCAG
 CGTTTTCAGCTACCACATTTGTAGCTCCGCTAGAATTTGATCGAAAACAAAAAT
 AATAACACTAATAATTTATAATAATACGGTAGAACTATTTCTTGTATAAAG
 ATGCCATAATCTATTGTGAGCAACCCATTCCATGCTCATCATTAATGACCA
 TCATCATGACCGTGAAAATTCGTCTAATAACCCGCCACAGTTGATCAGAA
 GTTCTAAATCTTTCTTAAACTTCATTGGTAGAAAACAAAGTAATGACTCA
 CTAAGAAGCGAGAAATCTACAGATTCCATGAATCTACCACAACCACTAC
 AAAATTAACATAACAACAACTTAATAACAACACCCATAGCCATCTTAATG
 CAACCGATATCTCAACAACAACCTACAATAATAACATGAAACAACUAC
 CACCATAATATTTCTCATGGGCTCCATGACTATACTTCTCCCGCCTCTCC

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AAAACAAACCCACTCCATGGCAGAAATTGAAAAGGTTTTTCAGACCTTCCTG
 TAAATAAAAACTATCTATGTCTCAACTTCGTTCCAAGAAACATAGCACC
 CATTCCCCCCCCACCTTCRAAATCAACTTCTACAGTTAACTTAAATAACCA
 CTATCGTGCCUAGCATUUTCATGGUTTTAAGAGACCACTATGCTCATACCC
 AGTCTGCTATACCGCCAGTACCGATTCTATCCTATCTTTGTUCAATAAT
 ATTAATATATATACAGCATGATTGTATTCTGGCTCAAAAATACCGGAAAT
 GGGTAAGCTATTGGGTTCCGGTGCCGGTGGGTCCGTTAAAGTTCTTGTGA
 GACCAACTCATGGTCCTACTTTTGCCCGTCAAAGAATTCAGACCAAGGAAA
 CCGAATGAGAGTGTGAAAGAATATGCCAAGAAGTGCACCCGAGAAATTTTG
 TATTGGTTCGACTTTACATCACCCAAATGTTATCGAACTGTTGACGTTT
 TCTCTGATTCTAAACAAATAAATACTATGAAGTTATGGAGTACTGTCCG
 ATTGATTTTTTTTCTCTCTGTTATCACAGCCACATCTCTCCTGCCAGAT
 CAAGTCTTGCTTGAAGCAATGACTGAAGGTGTTAAATATTTACATTCTA
 TGGGATTGGCCACATAGAGATTTGAAATTGGATAATTGTGTCATGACTTCC
 CAGGGTATTTTTGAAATTAATTGATTTTTGGTAGTCTGTTGTGTTACATA
 TUCCTTTTGAAGATGGUGTACGATGGCTCATGGAATCGTGGGTAGTGACC
 CTTACTTAGCGCCGGAAGTGATTACCTCCACCAAATCTTATGATCCTCAG
 TGCGTCGATATATGGTCTATTGGGATCATATATTGTTGATGGTGCTTAA
 AAGGTTTCCATGGAAAGCCCCTAGAGATTCTGACGATAACTTTAGATTAT
 ATTGTATGCCGGATGATATAGAACACGACTATGTTGAATCTGCCAGGCAT
 CACGAAGAGTTACTGAAGGAAAGAAAAGAAAAGCGTCAAAGGTTTTTGAA
 TCACAGTGACTGTTCCGCCATCAATCAGCAACAACCAGCTCATGAATCAA
 ACTTGAAACAGTTCAAAATCAAGTTUCABAATACTCCAGCATCTATACAG
 GGTAAAGCGGATAACAAACCAGACATTGTGGAAGAGAAAACUGAAGAAAA
 TAAAGAAGATGATAGCAATAATGATAAAGAAAGCACGCCAGATATGACA
 AGGAAAGTACCATCGATATTAAATAAGCAAAAATGAGAATAAAAGCACG
 GTAGTTTCAGCTAACCOCAAAAGAAAGTAGATGCCGATGCCGACGCTGATTG
 CCATGCTAATGCTGACTCTAACCCAGACTGCTTCCAAGCCTAACAGTG
 ACTGCAANTGACAAAACGGATTGTAATGCTAACAAATGACTGCAGCAATGAA
 TCGGATTGTAACGCTAAAGTTGATACTAACGTCACACTGCTGCCAACGC
 TAACCCTGATATGATTCCCCAAAACAAATCCACAACAACAACAACAACA
 AACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACA
 CACCACCATCAAAATCAAGACAAGGCCCATAGTATCGCTTCCGATAATAA
 ATCGAGTCAACAGUACAGAGGACCTCACCATAAAAAAATTATTCATGGCC
 CATACCGTCTATTACGCTCTACTACCACATGCTTCAAGACCTATCATGTCC
 CGTATACCTGCAAGTAGATCCAAAGAAAAGAGCAACCTTAGATGATATTTT
 TAATGATGAATGGTTTGCCGCCATGTCTGCCTGTACCATGGATTCAAAAA
 ATAAAGTTATTAGAGCGCCTGGCCATCACCATAACATTGGTTAGGGAGGAA
 AATGCTCACTTAGAGACCTACAACGTTTTA

YOR267C, 759 aa (SEQ ID NO 364)

MPNLLSRNPFHGHNDHHHDRENSSNNPPQLRSSKSPFNFGRKQSNDS
 LRSEKSTDSMKSTTTTNTYTTMLNNNTHSHSNATSISTNNYNNTYFNH
 HENISHQLHDYTSFASPKQTHSMAELKRFPRPSVNKKLSMSQLRSKKHST
 HSPPPSKSTSTVNLNMHYRAQHFGFTDEHYAHTQSAIFPSTDSL LSLSN
 INIYHDDCTIAQKYGKLGKLLGSGAGGSVKVLVRPTDGATFAVKEFRPRK
 PMSVKKEYAKKQTAAPCIQSTLRHPNVIKTVDFVSUSKQNKXYEYMEYCP
 LDFFAVVVTGKMSRGEINCCCLKQLTEGVKYLHSMGLAHRDLKLDNCVNTS
 QGTLKLLIDFGSAVVFRYPFEDQVTMAHGTVGSDPYLAPEVITSTKSYDPQ
 CVDIWSIGIYYCCMVLKRFPWKAFRDSDDNFRLYCMPDDIEHDYVESARH
 HEELLKERKEKRORFLNHSDCSAINQOOPAHESNLKTVONQVPNTPASIQ
 CKSDNKPDIVEEETEEKEDDSMNDKESTPENDKESTIDIKISKKNENKST
 VVSANPKKVDAADADCDANGDSNGRVDCKANSDCNDKTDNCNANNDCSNE
 SDCNAKVDNTNVNTAANANPDMVPQNNPQQQQCQQQQQQQQQQQQQHHH
 HQHQHQDKAHSIASDNKSSQQHRGPHHKKIIGHGPYRLRLRLPHASRPIMS
 RILQVDPKKRATLDDIFNDEWFAAIAACTMDSXNKVIRAPGHHHTLVREE

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NAHLEYTKV

YLR110C, 902 bp, CDS: 501-902 (SEQ ID NO 275)

TATTCGGCGTCTGATTTCCGTTTTTGGGAATCCCTTTGCCGGCGCGCCCTCTC
 AAAACTCCGCACAAAGTCCCAGAAAGCGGAAAGAAATAAAACGCCAUCAA
 AAAAAAAAAATAAAACCCAAATCCTCCAGCGTGGCTGGTACCCCTTGA
 TTATCCCGTACAAAGTATTTCTCAGGAGTAAAAAACCGTTTGTTTTGGAA
 TTCCCCATTTTCGGGGCCACCTACGCCGCTATCTTTGCAACAACATCTGC
 GATAACTCAGCAAATTTTGCATATTCTGTTTGCAGTATTGCGATAATGGG
 AGTCTTACCTTCCAACATAACGGCAGAAAGAAATGAGAAAAATTTGCAT
 CCTTTGCCCTCCGTTCAAGTATATAAAGTCGGCATGCTTGAATAATCTTTCT
 TTCCATCCTACATTGTTCTAATTATTCTTATTCTCCTTATTTCTTCCCTA
 ACATACCAAGAAATTAATCTTCTGTCAATTCGCTTAAACACATATCAATA
 ATGCAATTTTCTACTGTCCCTTCTATCGCCGCTGTTCGCCGCTGTCCCTTC
 TGGCGCTGCTAAAGTTTACCAGTACTGTCTAGCCAAAGAACTTACCAGTT
 TGGTCACCATCACTTCTTGTGAAGACCACTCTGTCTTGAAACATGTCTCC
 CCAGCTTTTGGTTTCCACCGCTACCGTCAACGCTCGATGACGTTATCACTCA
 ATACACCACCTGGTGCCCATTTGACCAGTGAAGCCCCAAAGAACGGTACTT
 CTACTGCTGCTCCAGTTACCTCTACTGAAGCTCCAAAGAACACCACCTCT
 GCTGCTTCAACTCACTCTGTCACTCTTACACTGGTGGCTGCTGCTAAGGC
 TTTGCCAGCTGCAGGTGCTTTGTTCGGCTGGTGCCGCTGCTTTGTTGTTGT
 AA

YLR110C, 133 aa (SEQ ID NO 276)

MQFSTVASIAA VA AVASAA NVTTATVSQESTTLVTITSCEDHVCSETVS
 PALVSTATVTVDVITQYTTWCPLTTEAPKNGTSTAAPVTS TEAPKNITS
 AAPTHSVTSTYTGAAAKALFAAGALLAGAAALLL

YLR109W, 1031 bp, CDS: 501-1031 (SEQ ID NO 273)

TGTCTATTACTAATCAAGAAAAGAACCCATAATCATCGGCGTCCCTCTG
 GGGCTCTCGGAAAAACCGGTCCCTGACGTCACTGAAAAGATTTCCGGCACAT
 GGTCAATGGGACCAGAGAAAAATTAATCCGACATGTGGAAATATCTCCTTCC
 GTTAAGGTAGTGAGCGCGGATTTTCTGATTTGTAATTATACGGGGAGC
 TCTGGCCAAAAGGTCAGTATTTGGTGATGAAGTTGAATATCATCTTTTG
 ATTTTCTTCTGTATCATTCTTTTTCTTTTTCCACACCCCTTCCGGACGGT
 ATTCACATATTGTTGAGAGCTTAAATGAAAAATAAAGGGGTGGAAAATTA
 AGCAGCAGATCTAAGGGAAAAGCATAAACGAAACATTATATAAAGGAGCA
 CAATTTCCCTCTCCCTTGCCAATTGTGCATATACCGTTTCTTATTAACGAA
 ATTTCAACAAACCAGAACACACAAGTACTACCAATAACCACAAACAAAC
 ATGTCTGACTTACTTAACAAGAAATTCACACCTTGGCCACTACAAATTCOA
 ATACATTGCTATCAGCCAAAGTGATGCTGACAGTGAATCTTCTAAGAGGC
 CACAAACAGTTCAATGGTCCAAATTAATTTCTGAAPACAAGAAGGTTATC
 ATTACCGCTGCTCCAGCTGCTTTCTCCCCAACCTGTACTGTCAAGCATAAT
 TCCAGGTTACATCAACTACTTTGGATGAATTAGTTAAGGAAAAGGAAGTTG
 ACCAAGTGACCGTTGTTACTGTTGACAACCCGTTTGGCTAACCAAGCGTGG
 GCTAAGAGTTTAGGTGTTAAGGACACCACACACATCAAGTTTGCTCCGA
 CCCAGGCTGTGCTTTCAACCAATCCATTGGTTTCGAATTAGCCGTCGGTG
 ACGGTGTTTACTGGAGTGGTAGATGGGUCATGCTTGTGAAAACGGTATC
 GTTACTTACGCTGCCAAGGAAACCAACCCAGGTACCGATGTGACCGTTTC
 CTCAGTCCGAAAGTGTCTTGGCTCATTGTGTAG

YLR109W, 175 aa (SEQ ID NO 274)

MSDLVNKKKFPAGDYKFQYTAISQSDANSFSCKMPQTVWESKLTSENKKVT
 LTGAPAA/SPCTIVSHIPGYINYLDLVKKEVIXVIVVTVDN/PFANQAW
 AKSLGVKDTTHIKFASDPGCAFTKSIGFELAVGDGVYWSGRWAMVVENGI
 VTYAAKETNPGTDVTVSSVESVLAHL

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YBL081W, 1607 bp, CDS: 501-1607 (SEQ ID NO 29)
 TTGTTCCAACAATTTTGGGATGCTTCTCCGTCCTACGACCCCTGATTTTAC
 CTTCTCTAGCTCATCGCTTCCAGGGTCCACGCTAATTTTTCAATTTTTT
 CTTGCGTGTGGAAGATTCAGGTCTCGAGAAATTTGTCAAAAATTTTTTAC
 TAGATATTAAAGAACTATATACATCGAATAAGATGCCAGCACAGAAGAGAT
 AGGCAATCAGTTTAGATACTACAGACACTATCCAATAGTCGAAAGCAAAA
 GCAGCATAGAAAAAGAGAATCCCGTTTCAGCTTTTCTCTTTTCCCA
 TTGTTTTTTCCCGATCTTTTCTCTGCAATCGTGGCACCTAGAACAAGAGG
 TACCATTCCAATCCATGCGTTAATATTTGATACGACTTTTGTGATTTCCAAT
 ATTATTTATTTGTTACTATTATTTATTTATCATTTGGGTTTGGGTTTTTGT
 AATAATTTTCTTTTCTTTTCTTTTGGCTCTATTTCACTAAGACATCGTATAT
 ATGCCAGGCCAGATAATCAGCAATTCCTTTTGTGCGAGAACGAGGACAT
 GGATAAATACTTGTGTGGAGTACCGCAGTTTGAAGCTCTTCATCAGTCCA
 GTAAATTCCTCCAGTCTCACAATGCGCCCTCCCAACAGTCGAACATACCAC
 CCCCATTACAAATCAGATGAATAACAACAACACTGGTAGCTATTACTATT
 CAACAACAACAATAACAGCAGTGTAACCCACATAACCAAGCTGGTCTAC
 AATCCATTAAACAGATCTATTCCATCGCCCCCGTACGGGGCTTACAACCAG
 AACAGAGCTAATGACGTACCATATATGAATACCCAAAAGAAACACCACAG
 ATTTAGCGCTAAACAATAATTTGAACCAAGCAAAATACAAGCAATATCCCC
 AGTATACGTCCAATCCAATGGTTACTGCACATCTGAAGCAAACGTACCCCT
 CAACTCTACTACAATAGCAACCTCAATGCTCACAACAACAACAACAACAG
 CAACAACAACAACAACAACAACAACAACAACAACAACAACAACAATCTTT
 ACAACCAGACGCAGTTCTCCACGAGGTACTTCAACTCGAACTCCTCTCCC
 TCGTTCACTTCTTCCACTTCTAACTCATCCTCTCCATACAACCAAGCAC
 CTTCCGAATACATTTTGGCGTCAACTTCGGCAGCTTCCACAAATTTATCGT
 CGTCATCATCAACAACCTCTATGCACACCAACCCAAACCACTCAACATCG
 ACATCCGCGGATTTAATCAATGATTTACCCGTGGGCCCCACGTCCAGTTT
 GCTTATCTCGGATCTACATCTCCACCAACTGTATCTTTCCATACCAGCAA
 GCCAAACCCCTGCTCATGTCCTCCACCAATCTAGCTCTATTTGGACCAAC
 ATAAACCCACCGCAACATTCACCAATCCCATCGCAAAGGGACGATTTTTTC
 GACGGCACCAAGTGAACATGTCTTCGTCCGCATCACTCTTGATCAATGATT
 CTTCTTTAGGATGGGCGTCTAACCATGTAACGTATCTTCATCTCTCAA
 CCAGCATCATCAAGACCCCTTTGGCATTGTGAATACTGACATGACCGTTTG
 GAGTTGA

YBL081W, 368 aa (SFQ ID NO 33)
 MPGQLISIFPLSQNEEMKYLLEYRSLKLLHQSSMSFQSHNAPSHQSNYH
 PHYNHMKYNNNTGSYYYNNNNNSSVNPHNQAGLQSIINRSIPSAPYGAYNQ
 NRANDVPYMNITQKKHHRFSANNNLNQQKYQYPOYTSNPMVTAHLKQTYF
 QLYYNSNVNAIUNCNKNNNNNNNNNNGNMMNNLYNQTFSTRYPNSNSSP
 SLTSSSTNSSSPYNQSTFEYILPSTSAASTNLSSSSSNNSMHTNPTTATS
 TSADLINDLPVGPTSSSLISDLHSPPTVSFLPASQTLLMSSTTSSSIGTN
 INFPQHSPSPSQREDFETAPVNMSSSASLLMNDSSSLGWGSENMNVSSSSQ
 PASSRPFGIWNTDMSVWS

YDR366C, 899 bp, CDS: 501-899 (SEQ ID NO 125)
 CTGTGATATTTGGGTTACTTTGTAGTGTATTATTTCCATCAATATTAGCA
 CTGTCTTCCAAGGTGAACCAATTGCTGTGTAACCAATAGAGTAAAAACA
 AGTGGAAATGGTATCGATTGTATAAAGTACGCAGATTTGCGAAAATACCA
 GCAACTTTGGCTTATGAATCAAAATACAGCCCTTGTGAGAATACGATTAAAT
 GTAAATACCGACCAAAGATATGCTATCCATTCGATAAAATCCACGGATG
 ACCCGTGAACAATGCTAAATACCATAAAGCAACACTGCATTTGTTTTAGAA
 TGGAAATACCTAAGACATCTCAACTGCAAGGTATAGCGGCATAAACCUC
 AAAAAAGACTATGAAAAAAAATATGTTTGAGAACAGCTTAGTAAATTTG
 TGCTTTGCTTCGAATCCTTACAAGTTAACAAAAATTTATAGCGTTTGGCG
 GAACATACTTTTGGGAAGGTTAGAACAGATGATCTCATAACTAAGGTTA

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ATGGTTACAACITGGTAGTTCCCTCCCTGGTATTATTTCTTTTCTTCGTAGT
 TTTTGTACAGATCACTTATACAGCTTTACACAGATTTTCCCGCTTGTGT
 GCACITTTTTTTTUGAAGATTATTGAAGAGGGATGCGTTTGGTACAATAAA
 AAACATAGGTTCCCAAACCTATATAAATATATATATGTATATGTATATAT
 ACTACATATATGCTTTGAGAAATATGTGAATGTTGAGATAATTGTTGGGA
 TTCCATTGTTGATAAAGGCTATAATATTAGGTATACAGAATATACTAGAA
 GTTCTCCTCAAGGATTTACGAATCCATAAAAGGCAATCTCCAATTCTACA
 CAATTCTATAAATATTATTATCATCATTTTATATGTTTATATTCATTGA

YDR366C, 132 aa (SEQ ID NO 126)

MVTIGSSSLVLFVVFVQITYPALHRFSRLCTFFSKIIEEGCVWYNK
 KHRFPNLKYIYVYVYILHICFEKYVNVETIVGIPLLIKAILLGIONLLE
 VLLKELGIHKRESAILHNSINIIIIILYVYIH

YDR154C, 851 bp, CDS: 501-851 (SEQ ID NO 101)

TAGACGGGGCTTCCACGGCTTCCACTCATTTCGTCTCTGGTAATGGCCG
 TCGCCCTTCTCACTTTTGGTTGGGCTTACGCTGACAAGTGTCTGTTGATT
 CCGCTGATAAAATATAAAGCTATTCCTCTGAGCCCTCTATCCCTTTGCCAC
 TGTCTGTCATCATTGTTCCTCCTTTTTCGCTAGATAGGTTATATTAAGAT
 TTGCTTGAATTTAATATCTCAACTCAATCCAACTCAACCGCTAATACCT
 ACCATGTCCCAAGTCTATTTTGATGTGGAAGCTGATGGCCAACCAATTGG
 CCGTGTGCTTTTCAAGTTGTACAACGACATAGTCCCAAAGACTGCAGAAA
 ACTTCAGAGCTCTATGTACCGGTGAAAAGGGATTCCGCTACGCTGGCTCT
 CCATTTCCACAGAGTTATTCCAGACTTCATGTTGCAAGGTGGTGACTTCAC
 TGCTGGTAACGGTACCGGCGGTAAGTCTATCTACCGTGGCAAATTCCCAG
 ATGAAAACCTTCAAGAAGCACCACGACAGACCGAGGTCTGTGTGTCATGGCC
 AACCCCGCTCCAAACACCAACGGCTTCTCAATTCTTCATCACCAACCTTCC
 ATGCCCATGGTTGGACGGTAAGCATGTTGTCTTTGGTGAAGTTGTTGACC
 GTTACGACATCGTTAAGAAGGTTGAGTCCCTGGGTTCTCCTTCCGGTGGC
 ACCAAGGCTAGAAATTGTTGTTGCCAACTCCGGTGAATTATTAACCGCTCTG
 CCTGGAACAATAACAGCAAAATTTGAAACGAACTATTCTCTCTTAAATTAT
 ATGTATATGTATAAGGTATGTGTATGTATGACAATCAATTCTTATAACTA
 A

YDR154C, 116 aa (SEQ ID NO 102)

MKTSRSTTTDQVCCPWPTPVQTFVVLNSSSPFIIAIGWTVSMLSLVKLLT
 VTTSRLRLSPWVLLFVPPRELELLLPSPVNYNRSAMNNTAKIETNYSLNY
 MYMYKVCVCMTINSYN

YHR102W, 890 bp, CDS: 501-890 (SEQ ID NO 213)

CGCTCGCTTCCAAGAGTTATCATCATATCTTCATCATATTTCTTCCATAC
 TTAAGGTGGGTAGCGAGGACCCCTCAATCCCGCACCTCTCTGCCAGGGC
 GTCATCTTTCTCTACAAAAGCCAGGCTGAGTCACTGATGTTGCTGACCCCT
 GGGGGCTGCAATTGTTTCCCTAUGAATTACTTCACTTGTCTCGTGCGCTTTCC
 TATTGCGCGCATCACTAGGATGGAAAAAAGAAAGAAAAAGAAAGCGT
 TCAGTATATATAAGAAAGAAAGAAAAAGTCCGAGAGAAAAAGAACACAAA
 GGTTTTTCTCTGAGGAAACAGTAAAGTTTGATACGCACATCGTTGACAT
 CGCTCACTTCANTAGGAAACTGAAATAGACGGCAAAACCAATTAGTTCATT
 GAAAGAACGTATTGTGAGAAATTATCACTCACCATATCAGAAATTTGACA
 CACGAATTATATAAACGAAGTTATACAGAAAAAGATTAAAGAAAAAGAAA
 ATCTCTACATCTMTCCGTACGTTTTCCATTTAGCCCGGTTCTGCCAAAGTGA
 GACAGGGCCCCAAGACGGTGCATTTCTGGGCTCCTACTTGGAAATGGGGTC
 TGGTTTTCTGCTGGATTACGCGATATGAAGAGACCGGTGGAAAAAATTTCT
 GGTGCTCAAAATTTGTGCTGCTATCTACTGCGCTGATTTGACATCGTTG
 GTCTTTGTCACTCAAGCCNAGAAACATCTTGTGGCTTCTGTCAACTCGT
 TTCTTTCTCTNACCGCTGGCTATCAATTCCCTAGAATTGCCCAACTACAGG

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ATACGGAATGGCGAUTCCTATATCGCAALGKGTAGCTATATTTCTCAGCGG
CGCCGACGAAAGCAAAAAGGAAATTACTACGGGCAGATAA

YHR162W, 129 aa (SEQ ID NO 214)
MSTSSVRFAFRRFWQSETCPKTVHFWAPTLKNGLVFAGFSDMKRPVEKIS
GAQNLSLLSTALIWTRWSEFVIKPRNILLASVNSFLCLTAGYQLGHIANYR
IRNGDSISQLCSYILSGADESKKEITTGR

YGR243W, 941 bp, CDS: 501-941 (SEQ ID NO 189)
CCTCCACCAAAGCAAAATGAAAACAAAGCCATACTGGGAAAAATCTGAAA
AAAAAATCTTAGGACTAAAGAAAAGAAAAATAAAGGTTACCCCTGCAG
TTTGGATAGTCGGGTAACATTTGGCCCTTTTCCTCCTTGATTGGATATTA
TTACCCCGATTACCCCTCATCTTGGGAGTGGCCCGCTTTTATTTCTCCCG
CCAATCCGCTATTAAACCCCTTTAGCTCATTCGGTGGCGGGTCAAGCCAG
CCGCTCCCTGGTTTGGTCACGCAAAACCGAAAGGCTCAACAAAACCTAAG
GCCATCATATATATATATCGCGCTGCGTGGCTGTATTCTCCCGGATAATA
TGGTGGCTTGGCAATTGGAGTATTGGAGAAAAATTTCTTTTCCCTTTCATT
ACGCGCGAATACTTCTATATAAAAAAAGAATACAAATCAGTCTTTAAGA
CTATACGCATAAGCATTCAGACACATAGAACACAAACCTATACTTTTA
ATGTCAGCATCAGCTTTTAATTTTGCTTTAGAAAGATTTTGGAACTAGTGA
AACAGGCCCTAAACAGTACACTTCGGGCCCAACTTTGAAGTGGGGGC
TGGTCTTCGCAGGGCTAAATGATATTAAAGAGCCCTGTTGAGAAGGTATCA
GGAGCACAAAATTTATCTTTATTAGCGAUGGCAGTGAATTTGAGCGCGTTG
GTCTGTTTGTTCATCAAGCCCAAGAACTATCTGTTAGCTTCCGTCATTTT
TCTTGGGTTGCACTGCAGGCTACCATCTAACAAGAATTGCTAATTTAGG
ATACCGAAGCGGTGATTCCTTTAAACAGGTTATTCACATACAATAAAAGG
GGAGACTCCTGCAGCCGTGCGAGCAAAAGCAAACTGCATCCACATCGATGA
ACAAAGCTCTCATCCGTACTAATCCCCCAATAACGCACATGA

YGR243W, 146 aa (SEQ ID NO 190)
MSASAFNFAPRRFWSETGPKTVHFWAPTLKNGLVFAGLENDIKRPVEKVS
CAQNLSLLATALIWTRWSEFVIKPKNYLLASVNPFLCCTAGYHLTRIANFR
IRNGDSFKQVIHYIIKGETPAAVAAKQTASTSMNKGVIQTNPPITII

YER056C, 1517 bp, CDS: 501-1517 (SEQ ID NO 43)
AAGTACCNTATCTTATAACTCTAACATTGAAGCACTGAAGCACTCAAGCA
CTGAAGGACTATAGTCAAGGGCCAATGGGGAAGGTCCCTTCCAGGCCATT
TGCCCGATAGTTTGTCTTCTCTTGCTTTTCCGACGGCCCGATTGCATGT
CGCGGGGCGAGCACTGGATAAAAAACGTGGGGGGAGTGATTAAATTTATA
CGCTTACTGTGTCAACACGGAAACCTTATAGTTATCATTAATAACATCGC
AACAAGCTGCTTTTTTACTGTTTTTAGCCACACCAATACCCCTTTAATT
AACTAATAATGCATAAAATAGTTATTGCTTCTTGAGTTGCAGCTTCTTCC
TGGACGTACTGTTATATATAGGCATGTCTTCCGATGTCCGTCAAATTTAGC
GTGTCTTCGAAACTTAGGCTGTCTGTCTTGTCTTCTGTCTTCTGATAAAA
TATATATATTGGAATAAGAAAAAATAAGGAACAAGAAAGTGTGTGAGA
ATGACTTTGAGTAATTTGCGACTCTTTTGATAACTTATTCCAGGACCCCTCC
AGAGGAACAGAGAAAGTAGTAATTTGTTGAGGCGGTGAGAACCTTGATGA
ATAGAAACGATATGGGATATCCTCCCGCGCTGCAATGGTACGTATTGC
TTAAAAAAAATCAAGTCTTTCAATGCCAAACACTGCAAAATAAACAAGAA
AAGATCTGTCATGTTGCCAGCAGTAAAGAAGAAATTTGACTTTACCG
AGCAAGAAGTTTAATCTTGAATTTAAATTTATGGAAATTCATCAAGTTT
ATCAATTGTAGTAGTAAAAACAATTACAAATAAAATAAGCATCTGAG
AAGCTTCAACCAACTGTAAAAAATGAAAATGTTTTACCGTTACAAAAAC
ACAGAGAAAGTGGACAATGATCAAAGATTGGAGAACCTTTTTTGCACAAGC
TGGTTTAAAGCCACGCAAAAGGAGAGATATAATGGGCAAGCCACGAGAGAG
GCATATCAAAATTTAACGATAACCTTGAACAGTGTATTATAACTGATGAGC

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ATTTTCATACAAAGGCTTCCTTCTACACGGTTGAATTCGACTGATGAAACAG
CGCCCTTGTTCAAAGTCTGAACTAGATCCCTGTATTGGCAAACGACGCAAG
TAACCGAACTTTCTATCATTTATAACAGCGTTTACCTCGCCACTGACGCAA
TTATTACGACTGCCGCTGCCACTGCCATTATCAGTAGTAATAGTCCAGAC
TATCAGCGTGGGCAAGATGTTCCGGATGTTCCAAGAAATGTTTCTTACA
GCCAGGAGAAACAGATTTTCAGTAGTGTGCTTCCCTTGACTCCGATCTCA
AGTTATCCACATAGTCATCATTTCCCCCGTAAACCTTCGTCAACTTCA
AGTCATTGACCTTUATTTTTCGAGTCGGAAACTGACACTGATACTGATAC
TGACGCTGAAAACAGAAAATGACATTCACGCTTACATAGACACCAGTATAC
CCAACCTGCTCTTATAA

YBR050C, 338 aa (SEQ ID NO 14)

MTLSNCDSLINLFDQDPPEEESSKPFVEAVRTLMMRNDMGYPAAANGTYC
_KKIKSLNAKQWKINKKRMCLPAVKKKNFDFHEQRSLILNLLWKFIKF
INCSKKNYKKNKHVRSSNNTVKNENVLPLOKHKKVDNQCRLFNLFWR
WFKARKRRDIMGKPRERHIFNDNVEQCIITDEHFIQRLFSTRINSTDH
RPSKSELDPCIGNAASERSFYDYSVYVASDAIITTAAATAIISNSGD
YQRGHDVRDVPFVLLQAGETDFSSVLRVDSDLKLSNISHHSFVKPSST
SHSTFIPESETDTDTCDAETENDIDAYIDTSIPNLLL

YEL071W, 1991 bp, CDS: 501-1991 (SEQ ID NO 143)

TACCTTGACCTGCTCACATTAATCAGCTTCCAACGTTACTTCCCTTTTCGC
AACAATCTACCCAAAATCTCTCCAGCATCTTCATTAATTACACTATCCTTC
GTCCCGACTTGGCATTGTGTTAAATTTCTAAGATGCTTCCTATAGGAACA
TAATTTGTCAAGAAAGUACAACAAATTTGTCTGCAATGTCACAGGAGTGGC
GCATTTTATGTTTTTTTCATTTTTTTTTTTTTTTGTGCGTGATCATTAAGCGG
GATATTGTCCACAGTCATCTAAAAGAATGACCATTTCGACGACTTAGTTTC
GGAAAATATTTCCAGCGGATGACACCACTTGGCCACAGTTGCTGACCGCCA
AATCTAAGCTCACGCGCGGAACTGAAAGGTTGTGAGTATATAAGTGATCA
CTCGCTTATATAAAGTACGAGGACAGAACAGGCTGCCAAAATGCTCCTCAA
TATTTTATTTCATTTGAGATTCAAGGCTTAAAGACAGCATATATAAGAATT
ATGACGGCCGCACATCCTGTTGCTCAGTTAACTGCCGAGGACATACCCATA
AGTCAAGAGAAACCCAAATTTCAAAGTTCTCGACTCGGAAGATTGCGGT
ACTTTTCGTTCCATTTTGTCAAATGATGAAATCTTAACTCTCAAGCTCCA
GAAGAGCTTGTCTCGTTTAACCAGGACTGGATGAAAAAATATAGAGGCCA
GTCCAATTTAATTCCTTTGCCAACTCCACTGATAAAGTGTCCAAGATTA
TGAAATACTGTAAAGATAAAAGTTGCCAGTAGTACCACAAGGTGGTAAC
ACCGACTTGGTCCGAGCCTCTGTTCCCGTATTTGATGAGATTGTTCTTTC
TCTAAGAAATATGAACAAAGTCAGAGATTTTGATCCAGTTAGCGGGACTT
TCAAGTGTGACCCGGGTCTCGTTATGCTCATGCGCATCAATTTTACAC
GACCATGACCATATCTTCCCATTTGGATCTGCCTTCTAGAAACAACGTCA
AGTGGCGGGTGACTTTCACCAAATGCAGGTGGTTTGAATTTTTAAGAT
ATGGGTCTCTACACCTTAATGTTTTGGGTTTGGAGTGGTGCTACCCAAC
GGTGAGATTTATCAGCAATATCAATGCCCTAAGGAAGGACAATACTGGTTA
TGACTTGAAACAATTAATCATCGGTGCAGAGGGTACTATCGGTGTCGTTA
CTGGTGTATUCATAGTTGCAGCAGCAAAGCCAAAAGCCTTGAATGCCGTA
TTTTTTGGTATTGACAAATTCGATACCGTTTCAGAAATTATTTGTCAAGGC
TAAAGTGAATTATCTGAGATTTTATCTGCTTTTGAATTCATGGACCGTG
GCTTCATTTGAATGTACGATAGAATACTTGAAGGAUTTGUUTTTCCCTCTG
GAGAACCAACACAACCTTTATGTTCTTATTGAAACGTCAGGGTCCATPA
GAGACACGACGATGAGAACTGACTGCTTTCCCTCAAAGATACCAAGATT
CTAAATTAATTTCCGAGGGTATGATGGCTAAGGACAAAGCCGATTTTGAT
AGACTTTGGACCTGGAGAAAATCTGTTCCAAACAGCTTGTAATTCCTACGG
TGCTATCTACAACTATGACATGTCACCTCAATTGAAAGACTTATATTTCCG
TATCTTGGGCTGTGACGGAGAGATTAACCGCAGCCGGTTTGATTGGTGAT
GCACCAAAACACAGTTGTAAATCATGTGGTTATGGTCATGTCGGTGACGG

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AAACATCCATTTAAAATATCCCGGTAAGAGAATTTACAAAACAGATTGAGG
 ACTTACTAGAACCATTTCGTTTATGAATATATTGCATCAAAGAAAGGTTCC
 ATCAGTGCCTGAGCATGGGATCGGTTTCCATAAGAAAGCTAAGTTACACTA
 CACCAGAAGTGATATTGAAATTAGATTATGAAGGATATCAAAAATCACT
 ACGATCCAAATGGATCTTAAACCCATACAAGTACATTGGA

YEL071W, 496 aa (SEQ ID NO 144)

NTAAIFVAQLTAEEYPKVKRNPFPKVLDSEDLAYFRSILSNDEILNSQAP
 EELASFNQDWMKKYRCQSNLILLPNSTDKVSIMKYCNDEKILAVVPQGGN
 TDLVGASVZVTFDEIVLSLRNMNKVRDFDFVSGTFKCDAGVVMRDHQAFTLH
 EHDHIFPLDLPSRMNCQVGGVVSTNAGGLNFLRYGSLHGNVVLGLEVVLPN
 GEIISNINLALRKDNTGYDLKQLFIGAEGTIGVVVTGVSIVAAAKPKALNAV
 PFGIENFDIVQKLFVKAKSELSEILSAFEFMDRGSIECTIEYLKDLPPFL
 ENQHNFPVLIETSCSNKRHDDEKLTAFLKDTTESKLISEGMMAKUKADFD
 RLWYWRKSVPTACNSYGGMYKYDMSLQLKDLYSVSAAVTERLNAAGLICD
 APKPVVKSCGYGHVGDGNIHLNIAVREPTKQIEDLLEPPVYVEYIASKKGS
 ISAEHGIGFPHKKGLHYTRSDIEIRPFMKDIKNHYDPNGILNPYKYI

YDR133C, 836 bp, CDS: 501-836 (SEQ ID NO 95)

GTGCAGAGGGTGAATCAACGGCCCCCTCAGAGAAACCGGCAGGAATTTT
 TCTGGTGTGTTGTTATTTTTTTTCTTGTACTTATCTCACTTTTCTTTT
 CTAAGTATTTTTTTTGCATTTTTTTTGTGTACACTTTCCACAACATATAG
 GATGGTTTAGTCATCTCTCGAAGTATATAAACCGTTGCTGGATCGTGGTT
 GTTCTTCATCGACTTCTCTCTGCTAGACTCTCTTTTTTAAATTTTTTCA
 TAGAATAAAAAACCAAGCATAACAAACATCTTCTTTTCGTTTCGCTTCAAAA
 TAACTACAAATTAATAATGCAATCTCTACCGTCGCTTCTATCGCTGCTA
 TTGCCGCTGTTCCTCCCGCGCTTCTAACATTACCACTGCTACTGTACA
 GATGAATCTACCACTTTTCTCACTATUACTTCTTGTGAGGACCAAGTTTG
 TTCTGAACAGTTTCCCCAGCTTTGGTTTCCACTGCTACCGTCACCGTAA
 ATGACGTTATUACTTAATACACCACCTGGTGTCCATTTGCCAACCACCTGAA
 GCACCAAGGAATAACCACTTCTCCAGCTCCCACTGAAAAGCCAAACCGAAAA
 GCCAAGTCAAAAAGCCAAACCAAGGTTCTAGCACTCAAACTGTTACCT
 CCTAGACTGCTGCCGCTTTAAGGCTTTGCCAGCTGCCGCTGCTTTTGTG
 GCTGGTGCCTGCCGCTTTATTGTTGTAAATTTACTCAACCTTTCTTTAATA
 TATTTTTTAGAAAAATGCTTAAGTACTTTTCCGTCAATACAGCTTCCACAA
 AATCGTTTTATTTCAAATTAATACATATCTCGGTAA

YDR133C, 111 aa (SEQ ID NO 96)

MTLSLNTPPGVHCQPLKHQRIPLIQLQIKSQPKSOLKSQPNKVLALKLLP
 PTLVPLIRLCQLPVLCLWLVLPLVCCNTLNLFPNIPLEKMLSTPPSIQLEQ
 NRFISINKIFW

YHL021C, 1898 bp, CDS: 501-1898 (SEQ ID NO 193)

GGTAAAGAAATGATCAGGGAGCGTTTCTTGCAACAGCAGCAACACTACA
 GGCAGCAACAGCAGGAAGGATGGCAATTACGTAAAGCCCTCTCAGGACAAC
 GTGGATAGCAAGGACTAACCGAGACAGATTGAGGTCTTTTCATGCATTACC
 ACCAGTAATATATATTATACCGAATAATATAGTTTATATAATATCCATAAT
 CATATATCATATCATATATCATATATCATATATCGTGATATTGTACCAGCCCC
 GCTTCTCCCCCTTTTGAAGTACCATTATTATCGGACCCCTTTTACCTTTGA
 ATGGCTCAGTAAGGACCTTTGCGCAGCCGTAAGGGGGTCGGGAATACATT
 TCCGGGGTTGATCCTCGAGGAAAAGTGCTATCTATATAAGGAGAGCCCT
 TCTAGATCCAAATATCAGGGGTAACTCTTCACAACTGGCCAGGAACATAT
 TCCAGCTTAAAAAGAAAAAATAATTATTAGAAACCAATTACCAACACCAAG
 ATGCTAAGATCAAATTTATGCAGAGGAATCTCGAATCTTTGCAAGACTGAU
 CACTACACCAAGGACATACACATCTGCGGCGACAGCTGCGGCTGCCTAATC
 GGGGACATATCATCAAAACATACCTTCATAGACATTCTACGACAATTACC

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TTCTCCATGGAGGAGTCCAGCAAGCCGGTTTCCGTTTGCTTTAACAAACGT
 TTTTCTTAGAGATGCCTCCCATAGTGCCAAGCTGGTGACCACGGGAGAAC
 TGTATCATAAACAGAAATTGACCGCTCCTCAGGACATTCAANTTTCTGAG
 GACGGAAATCTCTAGTGGTGAAATGGAAAGATCCCGGTCTTCACCACTT
 CCGTTTACAATTCCTTATCGACTATAAAGGTTCCAGTTTGTGTTCCGCCAG
 CAACAAGAAAACAAGAATCCAGATATAGACCCCACTTATCGAATAAGCGC
 ATCCTGAAAGATAACGTCAGGACTTACTTTCTGTGAGCTACAACGAGTT
 TATTGATCCTAAGGATGACTCCAAGCTTTTCCAAACGCTGGTCAACCTAC
 AAAAGTTTGGTATCGCTTTCATTTCCGGTACTCCTTCATCCCTCCTCTGAA
 GGCCTTACCATACAAAAGATCTGTGAAAGGATCGGACCCATAAGATCGAC
 TGTACATGGTGAAGGTACATTGACGTGAATGCAATCCCAAGCGACAAGTG
 TTAATGCCCATTTATGCCAATAAAGACTTGCCGCTACATACGGATTTACCA
 TTTTATAGAAAATGTGCCAGGTTTCCAGATTCTACAATCTCTACCTCCTAC
 AGAAGGGGAAAGATCCCAATACTAGACCCATGAATTACTTCGTGGACGCAT
 TTTTACTCTACCCCTAATGTGTAGAGAAATCGGATTTTGAAGGCTTATGAGGCT
 TTACAAAATTGTCTCTGTAAATATATATATGAAAACGGCGATTAAGAGGTA
 CTACCAATCCAAACCTTTAATCGAATCATCAGACATTATCGAGGACAATA
 CTCTTCTGGGTAATTATGAGGCCTTGATTAAATGCATTAATACTACTCTCCA
 CCATACCAAGCACCTTTCACTTTCCGGAATTATGATAAGCCCTCAGATCT
 AAATAATAATCTGGACCTTGAATTTAATTACCACCCCAAGCAAACTAACAG
 AGAGATTTTTGTTTAAAGTCTTTTCAATTAGGCGGTGAACTTGTTCCGAGAGT
 CATATCAATGACTTCAACAATCAATTTAGATTGCAGTTGCCCGAAAACCTG
 TTGTGTTATCTTTAACAACAGGAGAAATTTCCATCCTAACTCTTTAACAA
 GCTCAAAACCAAGCAATGGTTAAAGGGTTGCTATTTGATTCTGATACTTTC
 AAGACTAAATTAAGTTCTTGAAGAGAAAGTTTCCTCATGACAAATAA

YHL021C, 465 aa (SEQ ID NO 194)

MLRSNLRCGRSLRLRTTTPRTYTSAAATAAAANRGHIIKTYFNKRDSTTIT
 FSMERSSKPVSVCFNNVFLRDASHSAKLVTTCELYHNEKLTAPQDIQISE
 DGKSLVVKWKDGGRHQFPLQKFLIDYKGSFVSPATRKQESRYRPQLWNKR
 ILKDNVKKLLSVSYNEFLIDPKDDSKLFQTLVNLQKFGIAFISGTPSSSSE
 GLTIQKICERIGPIRSTVHGEGTFDVNASQATSVNAHYANKDLPLHTDLF
 FLENVPGFQILQSLPATEGEDPNTRPMNYFVDAFYATRNVRRESDFEAYEA
 LQJVTVNYTYRNQOKRVYQSKPLTFHHDTNEDNTLLGNVEALIKCINYSF
 PYQAPFTFGIYDKPSDLNNNLDLNLITTFAKLTERFLPKSFIRGLNLFES
 HINDFNNQFRLQLPENCCVIFNNRRILHANSLTSSNQQLKGCYFDSDTF
 KSKLKLFLSEKFPMDK

YKL054C, 2717 bp, CDS: 501-2717 (SEQ ID NO 237)

CCTGCTCTAGACGAAGCTACCGAAGGCGCCGTTTCAAATCGCGGCAG
 ACTAAAAGAAAGTTGACAAATGAAGTATATATTTTAGCACAGAATGTGCAT
 TATTCAACATGTAAATACTAATACTGCANTATCCACTTATAATATGTAT
 AGTCATCCGTATATTAATAGATCTGTTTCAATTCTTTACCTTTTATAGGAT
 ATCCGTACCCGTGATTCGGTCGGAGGTGAGCACTCGCCCAAAATAAATAA
 CGGGAAATGGTGGCAAAAAGTAGTGGCGGGAAAAGGAAAAATTTTCGTTT
 TCTCCCATATAAACGTTTCATTCCCTTTCCCTAAGTCITTTACAGTAATTT
 CAGAACATTCGTATTTTATATTTGATCTTTTGAAAGCTACAAAGAAAACCT
 CTTACCAATTACCCCAAAAATCACCATCATAAAGTACTTACATATTTA
 TTTTGTGTTGGTGGTCTCTCAATATAATCTACATCATCATATATATATA
 ATGTCTACACAATTTAGGAAGTCTAATCATAATAGTCATAGTAGTAAAAA
 ACTAAATCCTGCGCTAAAGTCCAAAATAGATACGCTTACAGAATTGTTCC
 CTGACTGGACGAGTGATGATTTAATTGAATATAGTTCAAGAATATGATGAT
 TTGGAAACTATAATTCATAAAATTACTTCCGGCGCAGTGACAAGATGGGA
 TGAAGTAAAGAAAACCTGCTAACGAAGGAAAATATCAAAAAAAGGAGCAAC
 AACACTCATATGTCCCTCAACAACAATTTGCCAAAATCCAGAAGATGATATT
 ACATATAAGAGTTCTAATAATAGCAATCTTTTACTTCTACAAAGCATAA

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CAGTAATTAACCAATTATACCTCAAGCCAGAAATAAGAAAGGTACAAACAC
 CACGAGCTCCTACAAACCGGAACCATGTTAATCTCGACAAAGGCAACAC
 GTACCCTCCAAAGCCTGTTTCAAACACTACATCGTGGGCAGCAGCTGTTTC
 TGTAGATACTAAACATGACGTTCTCAAGATTCAAAATGATAACAATAATG
 AAGAATTAGAAGCACAAGGGCAACAAGCGCAGGAGAAAAATCAAGAAAAA
 GAGCAAGAAGAGCAACAACAGCAGGAAGGGCATAATACAAAGAAGAACA
 CAAACAAATAGAGCAACCTTCTTTATCTTCAAAGAAAACTTCTAGGA
 CATCTGCTTCCACAACCAAGAAATGTCTGCTGGGCTGCAATTGCTACACCA
 AAGCCAAAGGCTGTTAAAAAGACCGAGTCTCTCTTTGAAAAAGTTGCTGA
 ATTGAAGAAAGAAATRAAGCATATTAAGAAGGATGACCAAAAGTCTGAAG
 CTAGTGAACAAAAAATTAATGAACAAGAAACATCTGCACAAAGAACAGAG
 GAGGAGACTGCTGAACCTTCTGAAGAAAATGAAGACAGAGTCCCTGAAGT
 GGACGGAGAAAGAAATCCAAGAAGAAGCTGAAAAAAGGAACAGTAAAG
 AAGACAACACAGACACCGCAACAGCTCGAACAAAGAACAGATATGTTGCT
 GCTCCAGAAGAAGAAGTTACAGTTGTTTGAAGAAAAGGTTGAAATTAAGTGC
 TGTATTATTTCAAGAGCTCCAGAAGATCAAGCTAATACTGTACCTCAACCCAC
 AACAAANTCCCAACAACCCACAGCAACCCACAGCAACCCACAGCAACCCACAG
 CAACCCACAGCAACCCACAGCAACAACAACCAACCCACAGCAACCCACAAACCC
 ACAACAACAACCTACAACAGCAACAGCAACAGCAACAACAACCAAGTACAAG
 CTCAAGCTCAAGCCCAAGAAGAACAATTATCTCAAAACTACTATACTCAA
 CAACAGCAGCAACAATACGCTCAACAACAGCATCAGTTACAGCAACAGTA
 TTTGTCCCAACAACAACAATATGCTCAGCAACAGCAACAGCATCCACAAC
 CTCAATCACAACAACCTCAATCAGCAAAAGTCCACAAGTCAAAAAACA
 GGGAAACAAGTGGGCTGCCCAACAGTACTACATGTATCAAAACCAATTTCC
 TGGATATTTCTTATCCAGGTACGTTTGATTACAAAGGATACGCTTACGGTC
 AACAAATATCAGCAACTTGCTCAAAACAACGCTCAAACTAGTGCTAATGCT
 AACCANTATATATTTCCAACAAGCTTATGGTCAGCAGGCGCAACACTGC
 TGCTGCTAATTTGACTAGTGTGCTGCCGCTGCTGCTGCCGCTTCTCCAGCTA
 CAGCTCAGGCCCAACCTCAACAACAACAGCCATACGGTGGCTCATTCATG
 CCATACTACGCCCACTTTTACCAACAGTCATGCCATACGGTCAACCTCA
 ATACGGTGTAGCTGGTCAATATCCATACCACTTACCAAGAACAAATACAA
 ACTATTACCAAACTCAAAACGGTCAAGGAACAGCAAACTCCAAATCAAGGT
 GTTCCCAAGCATTCTGAAGACTCTCAACAGAAGCAATCACAACAGCAACA
 GCAACAGCAACCTCAAGGTCAACCCCAACCTGAAGTTCAAATGCAAAATG
 GCCAACCTGTTAACCCACAACAACAATCCAGTTCCAACAATACTATCAA
 TTCCAAACAACAACAGCAACAAGCTGCTGCCGCTGCCGCTGCTGCTGCCCA
 ACAAGGTGTACCATATGGCTACAACGGTTATGATTACAATTCTAAAAATT
 CAAGAGGTTTCTACTAA

YKL054C, 738 aa (SEQ ID NO 238)

MSTQPRKSNHNSHSKKLNPAKSKLDTL/TELEPPIWTSDDLIDIVQEYDD
 LETIIDKITSQAVTRWDEVKKPAKKEKYEKKEQQHSYVPQQHLPNPEDDI
 TYKSSNNNSNFTSTKINSNNYTQARNKKKVQTPRAHTTGKRVNLDKGRH
 VPSKPVSNITSRAAAVSVDTKHQVPQDSNDNMNEELEAQGGCAQEKNOEK
 EQEEQQQQQEGHNNKEEHKQIEQPSLSKKTTSTRTSASQPKMSWAAIATP
 KPKAVKKTESPLENVAEKKEISDIKKDDQKSEASEEKVNEQETSQEQE
 EETAEPSEBENEORVPEVDGEEVQEEAEKKEQVKEEEQTAELEQEQDNVA
 APREEVTVVEEKVEISAVISEPFEDQANTVPQPQQQSQQPQQPQQPQQ
 QPQQPQQQQQPQQPQQPQQQLQQQQQQQQQPQVQAQAQAQEEQLSQNYTQ
 QQQQQYAQQQHQLQQQYLSQQQQYAQQQDHPQDQSQQSQSQSQSQSQKQ
 GNNVAAQQYYMYQNQFPQYSYPMFDSQGYAYGQQYQQLAQNNAQTSQNA
 NQYNFQQQYEQAGANTAAANITSAAAAAAASPATAHAQPCQQQPYGCSFM
 PYYAHFYQCFEPYGQFPQYGVAGQYFYOLFKNYNYQYQYNGQEQQSPNCG
 VAQHSSEDSQQKQSQQQQQQQPQQQPOPEVQMQNQGPVNPQQQMDFQCYC
 FQQQQQAAAAAAAQQGVFYGYNGYDYKSKNSRCFY

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YLR311C, 848 bp, CDS: 501-848 (SEQ ID NO 283)
ACAAAACAGACTTAGTTCATTTATCGGTATACAAACAAAGCTCGAATGAAA
GACGGTTGGCACAAGAGAATTAAACAAAATAAACGGAGGAAGAATAAAGTT
ACACCTTATTTCTCAAGAACTCTTTTAAATCCGGCTCAAGAAAGTTTAAGGG
TATTGCATARAAGAACAGAAACGCCGGCTGGAAAAGGCTCTTTGTGCTACTT
CATATAAATACAGGCAACTTTCTCCACATATTAAAAGGTATTTCCATCA
TTCTTGCCAAAAGCAAAACAATGTTGGTCTGGGATCCAGATTGCACTTGC
GCAACCTTCGTTTCAAGTCAATGAAACCATTCGGAGTTTTTCAGTTTAAG
GTTTCGCAAAGATACCAACTGGTTTGTAAAGCAGCTGAAACGGTTCCGATT
GAAATTACAGCATTCCAGGATGTATAAAGCGATGTGAGAATGCAAGGAAAA
AAATTTATTTTAAGTGCAAACACTAGATCATCCAAACCCAGCATGAAGA
ATGAAATTAACAAAAGAAAAAAAACGACTGCTTAGTAGGAGTGTCTTA
TATCCCTCCTTTAAATTTTTTTACACTTACTTTCTTTTTTTTATTTGAGAA
TAGAAAAGCTGCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTTAAGG
TTTTATTACTTTTCATAACGATATGCTATCCATCTCTTTTCCCTTTTTTTGT
TTTTGTTATTCCTTTTTTTACTCAGTTAGATTTCATACTACTATATTTAC
ATATTCTTCCGAGCTTTTATGAGTTAAATATTTTCTTGCTTTATGGGGCA
GAAAATAGTCGACGTCAGTCACCTCCAGGTTATTTATGTAATTCGGCTAA

YLR311C, 115 aa (SEQ ID NO 284)
MKLTKEKKNDCLVGVSYIPPLNFFTHTELFILRIEKVHLSLSLSLSLSIR
FYYFHNVCYPSLFLFFCFVIFPFYSVRFILLYLHILRSFYELNILLLYGA
ENSRRRQSPPGYVYLR

YMR107W, 848 bp, CDS: 501-848 (SEQ ID NO 309)
AGAGCAGAAATGATGAAGGGTGTTAGCGCCGTCCACTGATGTGCCTGGTA
GFCATGATTTAGGTATACTAACACATCATGAGGACGGCGGCTCACCCC
AAGCGCAAAAGAGTGACTTCCCTGCGCTTTGCCAAAACCCCATACATCGCC
ATCTGGCTCTCTGGCAGGGCGGTTGATGGACATCAGCCGCCCTCCCTTAAAT
GCTAAAGCCTCCACAAGGCACAATTAAGCAATATTTCCGGGAAAGTACACC
AGTCAGTTTGGCTTTTTATGACTGGGTTCCTAAGGTACTAGATGTGAAGTA
GTGGTGACAGAATCAGCGAGATAACAGCGACCCAGGGTGGGGTAATGATGT
GCCATAACAATCTTGCTTGGCTAATCACCCCCATATCTTGTAGTGAGTAT
ATAAATAGGAGCCTCCCTTCCCTATTGCAACTCCATAAAATTTTTTTTGT
AGCCACTTCTGTAAACAGATAAATAAAACCAACTAATCGAGATATCAAAT
ATGGGGTAGTTTTTGGGACGCATTTCGCAGTATACGACAAGGAAAAGCACGC
AGATCCAAGTGTATATGGAGGAAACCATAACAACACAGGAGACAGTAAAA
CGCAGGTTATGTTTTCGAAAGAGTACCGTCAACCTAGGACACATCAGCAA
GAGAAGTTGCAGAGCATGGAAGATCTTCCATAGGATCACAGGACACTTC
CGATGTTGAGGACGTTAAGGAAGGGAGATTACCCCGCAAGTAGAAATAC
CAAAGAATGTTGACATCTCTAACATGTCCGAAGGTGAGTTTTTAAAGACTT
TACGAAAGTTTGAGGAGGGGGGAACCCGACAATAAAGTAAATAGATAA

YMR107W, 115 aa (SEQ ID NO 310)
MGSFWDFAFVYDKKKHADPSVYGGNHNNNTGDSKTQVMFSKEYRQPRTHQQ
ENLQSMRRSSICQDSSDVEDVKECRLEAEVEIPKNVDISNMSQGEPLRL
YESLRRGEPDNKVMNR

YKL066W, 944 bp, CDS: 501-944 (SEQ ID NO 243)
GAAAAACATCTCATAAATCATCCCTGGAAAAATGCTAGTCAAPCAGAAA
GAACTTTTATTTCGGTAAAACAGATGGTGTCCAGAGGGGCTTACTATCT
CAAAATTCATCTCGTTTTTGAIAAAAAAGGTACAAACTAGTTTCTATTAA
ATTAAGTTAAGCGGATGATAAATTAATAAGCAACATTACGCAGAGCATG
TTGGTAABACCATTTTTCCCAAAGATGGTATCCCTTATGAAGTCTGGTCCC
ATTTTGGCCACGGTCTGGGAGGGAAAGATGTGGTTAGACAAGGAGAAC
TATCTCTGGTGTACTAATCTCTTTGGGCAGTGCACCAGGTACCATTAGAG

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GTEATTTGGTATTGACCTAGGCAGAAACGTCCTGTCACGGCAGTGATTCT
 GTTGATAGCGCTGAACCTCAAAACAATTGGTGGTTTAAGAAGCAAGACTT
 AGTTGATTGGGAATCTAATCARGCTAAGTCGATTATGAATGAATAACTT
 AFIGGCATGGGAGGGTACATATGAGCGCCCTTTTTTTCTTCGCTTTGGGCAG
 CTCATATCATGTTCCCTCACTAGCTAATAATATAATGAATTTTTTAGAAG
 GAGCACGATTATATAAAAAAATACCACTTATGTTGCTACCCCTATATAC
 GAATTTATAATACCTAATGACGCTTCAATGACGCCCTGATGTCAAAATGCTT
 TTGGCTCCGAGTGAAATGCCACACTCCCTTCTCTTTCCGAACTTTATA
 GTATCATCGAAAAATACAAGTTGGCAAGGTCATTTACAATCCGGGAACG
 TACGATGTTTCATACGGTTTCAGCGAATAGTCCTGTAATATCCGGGAAGCAT
 GCGTACCGGCATTATTTACAGGTAGTTTCATCGCCCTTGGACTATGTAGGGG
 TACAAGTAATAGGCAACTTGAAATGGATCTCCCTATTGAATGA

YKL056W, 147 aa (SEQ ID NO 244)

MAWEGTYERLFFLAIGSSYHVPISLANNIMNFLEGARLYKKNITTYVATLIY
 EFIIILNDASMTDPVKCFWLPVKLPHPFLLLSELYSIIERYKLAQVYVNRGT
 YDVHTVSANSLVISGSMPTGIIIGSSSPLDYVGVQVNRQLEMDLPIE

YML053C, 1139 bp, CDS: 501-1139 (SEQ ID NO 295)

GAGGCGACACCTGCTAATGTTTACAATTTTCCCGATTGGGGTGCTAGAGG
 CATACAGTGGGCTACATGGCACAGCACGGCAGTGCAGAGTGAGAAAATAT
 GACTTCACGCTCGAGGCGAGGCCACGCTTTCGAAGCTTCGAATGCCACTA
 CCTAGACCATTTGCTGTTTGTACCTTCACGGTCCCATTTAGAGACATTTTA
 CTTAATGCAAGATTGCCATATCCGTTGTCATGGTACCAACAGCGTAATA
 ATTTCTAGAAATCATGATACACGTATGACATCTGGGTAACTAATCCATC
 TGGGTAACCGATTTTTCTCTCCCTTTGCTTTCTCTTTACCACTCAGCTGA
 CTTTATATTTTTTTTTATATTTTTTCATTTTGACAAAATTATATAGTTAGG
 AAGATACAAATAGGACTGGGACAGAAACAGATAAGGGGCTCTTTTTCCTTG
 GGGTGGGCTGCTTTTATTCAATTAATTTAAGACTCAAGTGTGCTGGGTGAA
 ATGCTCTCATACTATGAACACAACTACTGCGTTCCAAACAAAACAAATGCCAA
 TTCCGGTAGCAATGCCGCCACTACATACAACAGCGACGCCAATAATGATA
 CGATCATGANTAAAAGAAAAAATCACCATTTCCAGTTTGATACACACACT
 TTCTACCAAGATCGAAGAGAACAAAACGAGATTCCTGTAAGTACAAAGTT
 TTCGGTCCGTTCCGGGTGTGCTAATCTTAATAACAACACACACACATCA
 TCATCAACAACAACAACAACAACAATAATAATAATAAACCATAATCAT
 AATAACAGCAATAATACTGCAACCTACAATATAATTCATTATAAAAAAA
 TATCGAAATATGTCCCTGAAACCGGTTAGTATGCAACACACTATGAACA
 GCCGCTTACTGAACGAATCTGAATCTTATCTGAAACAGAAGAGTACATG
 ATTCTATGCTTATCTCGGTAACTAATCGCCACATAACAGGCACGAGTCC
 TACTGGAAGTGCCTAGTATTATACAACACCGATATCATCTTCTACCATCCC
 AAAGTATAATTCATCACAAACACCCGGTACTGCCATGCCCGCGTTGACT
 AACAACAATATCGCTACGACTACATGGATATAGATTAA

YML053C, 212 aa (SEQ ID NO 296)

MLSYYEHNTAFQTNNCNSGNAATTYNEDANNDTIMNKRKNDIIEFDTHIT
 FYQRSKRTRKDSVSTKFSVSGCANLNNNNNNNIIINNNNNNNNNNNNNH
 NNSNTATYNNIIHYKKNIEICPLKPVSMENITMNSLLNESEFYSETEEYM
 IHGYFGNTNRDITGTSPTGSASIIIOHYHLLFSOSIIASCAPGTAMAALT
 NNNIANDYMDID

YOR121C, 806 bp, CDS: 501-806 (SEQ ID NO 355)

GGTGACGCTGTTTGGGCTACTTCTGGTGGGCTATCTTTGCAACCAAAACGA
 AATTTGGTGAATTTGTTCAAGGCTTTCGACAAATACAGCTGGTCTTCGCAAGCA
 ATGGTTTCATATTTCAAGGCCAAAAGTTCAATGTTGTTGAGAGCTGACGAT
 AGAAGTATCTACGGTAGACATGATGCTGAGGGTGTGTTTGTGTAGAAGC
 TAAGCAAAACCGTTATTATTGCTCATTTATCCACCAACCGTCAAGCCGGTG

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AGCCACCAAGATTGTGAGCAATTGGCTGACTACTTGATTGGTCTTCAA
TACTAATTTATGCAGGTAAAGTTTCTTGCCCTTATACACCACCTATTCTG
GCACTCTGCGGGATTTGCGCTTCTATTTTACAAATATTATTATTGATTGACG
CTAATTATCACTGTAAAAGGCGCACCTTTTATATGTAGTCACATCCGGTA
TTTAACATATTTACGAAACAGTCTTAAGAATATCGACATTTGATATACCT
ATGTTTAAATTTATCTACATATTACAAATCATACGAGAAACACGCAAAAACA
ATTACTTGAATACTTCGAAAGGAGACCAATTTGGATGTACAACCCTTTT
TCGCCCCTTTTCCCTTCGATATGTTATTTGATAGCTTCAAAGTCCTCAGTAGA
CAAAGTAAATATTTTCCCTGTTCCGTTTTCGATTTCGATCCGGATTACAGATT
TTCCCAAGACAAACATAACCTCTTTGGACCTGCCAGCTAATAACAACGCTGT
CCGGTTCGAACGTTATTTTCTTCGCAATTTCAAGGATAACCGGTTCTTT
CAATAG

YORL21C, 101 aa (SEQ ID NO 356)

MFNLSTYYNHTNTQKQLLEYFERRPIWMYNPFFALFLRYVIDSFKVLRS
QSKYFPVRPDSIGIHRPWQDNCTSLDVPANNVNSQLNVTFLRNFKDNRFL
Q

YOL106W, 854 bp, CDS: 501-854 (SEQ ID NO 341)

ATATGGTTTTCATCATTTTCTCTCAATTGTTCTCCATTTGGGTTACCTTTT
TGCCAGTTGGTCTGACTTGAGGTTTTTCCAGAACTTGCAACCTTGAATT
GTCCCTCTCTTSCCAACAACTAATTCTCAAGGTGGTCAGGAAATATTGGTC
GGCGATGCATCTGATACTTTTCAATTGATTACTTCTTTCTGATCTAAT
TAAGCCGATTTTGAGGCCGATTTTCAATTTTATTAATGTAGTCTGTTG
TAAATTTAAAGTCACTAAACCTTTTCATGATATTGATATAGATACTGGG
AACACCATCCGACAACTAGAGCCGCCAAAAAAATTATCACTGTAGAAGA
AAGACCAACACACTTACCTTTACAAGTTTTGGAAGAGCGTATGGTAAACC
CTTGATATATGGATCTATATAACTTGAABTATGCTCTATTATATCGTGAT
TTAATGACGGCTGTTGGCATTTCCGTCCTTACCAAGGTAGTAGCACTTGT
ATGCTGAATGTGCGCCAGTACTATCGAACCATAGAAACCATATATTTCCC
CAATATTAATPAATTCTACTGAGAAATGGGTGAATTTTGAATAAATGTTG
GGATTCATCGTTGATAAAGGCTATAAATATTAGGTATACAGAACTGACTA
GAAGTCTCTCGATGATATAGGAATCCCCATAATGGAACTATATTTCT
ATGTACCAATATTACGATTATTCCTCATTCCTATTTCATATCTTTTCAATTAT
CCTATTCATTTATCGATCCTTCGATTTTCAGCTTCTCTTACTTCCGGTGAC
AGCTTCTATAATAACTTATGTCACTATCTAACACCGTATATGATATATATA
TTGA

YOL106W, 117 aa (SEQ ID NO 342)

MLNVRQYYFTLETHIFPNINNSTEKWVNEELIVGIPSLIKAILLCIQNVL
EVLDDIGIPIMESIFLCTNTTIIPHSTSYVSLSYIIDPCISASSNFGD
SFYNNLCXYLPPYMIIV

>YAL003W, 1487 bp, exon1: 501-580, intron1: 581-946, exon2:
947-1487 (SEQ ID NO 17)

CCGATGGAACGTTCTGGAAAAAGAAGATAATTAAATTAAGTTTCTCAACTAAAATCTCCA
GAAAAACGCAATGACACCTTCTAAACCTTCCGCTGTGCTTTCTTTCTAGAATGCTCTGG
AAAGTTTACAAACAATCCACAAGAACGAAAAATGCCGTTCGACAATGATGAAACCATCCCA
CACACCGCGCACACGCTGCTTTATTTCTTTTTCTGAATTTTTTTTTTCCGCCATTTTCAAC
CAAGGAATTTTTTTTCTTAGGGCTCAGAACCTGCAGCTGAAGAAGCGCTTTAGAAATCA
AAGCACAACGTAACAAATTTGTCGACAACCGAGCCTTTGAAGAAAAAATTTTTCACATTTG
CGCTTCATAAATAAATAGTTTAAAGTTATCTACCCACTATATTTAGTTGGTTCTTTTCTCT
TTCTTTCTACTCTTTATCTTTTTACCTCATGCTTTCTACCTTTTCAGCACTGAAGAGTCCA
ACCGAATATATACACACATAATGGCATCCACCGATTTCTCCAAGATGAAACTTTGAAAC
AATTAAACGCTTCTTTGGCTGACAAGTCATACATGAAAGGCTATGTTCCGATTTACTTTA

CTTTATAGATCGTTGTTTTCCTTCTTTTPTTTTTCCTATGTTACATGTAAGGGAA
GTTAACTAATAATGATTACTTTTTTTTCGCTTATGTGGAATGATGAATTTAATTCCTTTGGTC
CGTGTTTTATGATGGGAAGTAAGACCCCCGATATGAGTGACAAAAGAGATGTGGTTGACTA
TCACAGTATCTGACGATATGACACAGACAGAGTATTCATTAATTAGTTATCTGTTATTTTTTTT
TTCCCTTTTTCGTTCAAAAAAAGAAAGACAGAGTCTAAAGATTGCAATTACAAGAAAAAAGT
TCTCATTACTAACAAGCABAATGTTTGTGTTCTCCTTTTAAAAAGTACTGCTGTTTCTC
AAGCTGACGTCACGTCTCTCAAGGCTTTCCAATCTGCTTAACCCAGAATTCCTCAGATGGT
TCAACCACATCGCTTTCCAAGGCGGATGAATTCGACTCTTTCCAGCTGCCCTCTGCTGCCG
CTGCCGAAGAAGAAGAAGATGACGATGTGCGATTATTCGGTTCCGACGATGAAGAAGCTC
ACGCTGAAGCTGAAAAGTTGAAGGCTGAAAGAATTGCCGCATACAACGCTAAGAAGGCTG
CTAAGCCAGCTAAGCCAGCTGCTAAGTCCATTGTCACTCTAGATGTCAAAGCCATGGGATG
ATGAAACCAATTTGGAAGAAATGGTTGCTAACGTCAGGSCCATCGAANTGGAAGCTTCA
CTTGGGGTGCCTACCAATTTATCCCAATTTGGTTCTCGGTCAAGAAGATTGCAAAATTAAT
GTGTTGTCGAAGATGACAAGGTTTCTTTGATGATCTGCAACAAAGCAATTGGAAGAAGACG
AAGACACGTCCTCAATCTACCGATATTGCTGCTATGCTCAAAAATTAATA

MASTDFSKIETLTKQLNASLADKSYIEGTAVSQADVTVFKAQFSAYPEFSRWFNHIASKAD
EFDSFPAASAAAAEEEEEDDDVDLFGSDDEFANJASAEKIKAEERIAAYNAKKAAPAKPAAK
SIVTLDDVKPWDDETNLEEMVANVKAIEMEGLTWGAHQFPIPIGFGIKKLQINCWVEDDKVS
LDDLOQSLEEDEDHVOSTDIAAMOKL

AAGAGCTACGAGAATCAATAAACGAGGCTAAACTGCTTACACATGATTTGTGATTGAUTA
 CTCACGTTCTCGTGTTAATCCCGCGGTCTTCTTGTTTTACTAACTTTTCTTCTCTCATA
 GCATTCTCTTGACAGTGTTTTATATACATCATATGTACATTTATCGAGCCAATCGAGGGC
 AGCAGTTTAAACATCAAGCCGGATTTCGCTCAGGCTACTTTGACCCCTTTTCGTTTCGACGS
 AGAGAAGAAACCGGTGT'TTTCCTATCCCTTGCCATTCTTTCCTTCTTACGGGGTCTTAGC
 CTGTTTCTCTTGATATGATAATAGGTGGAAACGTAGAAAAAAAATCGACATATAAAAGT
 GGGGCAGATACATTCCGTGTGACATGCCCCAATCAAGCCCTTTGGCGAGATGTTGCCCTCT
 TTCTTTCTTAAAAAGTCTTTAGTACCATGTGACCAACTCAGAAAAAATAAAAGGAACT
 AAAAAAAGTTTTTAATTATTAGGAGAGCTTTGGCATATTTCAAGAAGGGTGATATTCACT
 TCACCTAATGATATCCCTAGGCCAGAAATCCAAACCGACGATGAGGTATTATCCACCTCT
 CTTCGTGTGGGATTTGTGGCTCGGATCTTCACGAGTACTTGGATGGTCCAATCTTCATGC
 CTAAGGATGGAGAGTGCCTAAATTAACCAACGCTGCTTTACCTCTGGCAATGGGCCATG
 AGATGTCAGGAATTCCTTCCAGGCTGGCCCTAAGTGACAAAGGTCAACGTTGCCGACC
 ACGTGGTCGTTGATGCTGCCAGCAGTCTGTCGGGACCTGCATTGCTGGCCACACTCCAAAT
 TTTACCAATTCAAAAATATGTGATGCTGTCAGAGGGGCACTGAAAAATCTATGTACCCACG
 CCGGTTTCTAGGACTAGGTGTGATCAGTGGTGGCTTTGCTGAACCAAGTCGTAGTCTCTC
 ATCATCATATTTCTCCCTTCCAAAGCAATTCCTCTAGATGTGGCTGCTTTAGTTGAGC
 CTCTTTCTGTCTACCTGGCATCTGTTTAAGATTCTGTTTTCAAAAAAGGCAGTTGACGCT
 TGGTTCTTGGTGCAGGTCCCATTTGGGTTGTTGATACCATTTTGGTACTTAAGGGAATGGG
 CTAGTAAAAATTGTAGTGTCTGAAATTGCAGAGAGAGAATAGAAATGGCCAAGAAACTGG
 GCGTTGAGGTGTTCAATCCCTCCAAGCACGGTCAFAAATCTATAGAGATACTACGTGGTT
 TGACCAAGAGCCATGATCCGTTTGATTACAGTTATGATTCTTCTGGTATTCAGGTACTT
 TCGAAACCTCTTTGAAGGCATTAACATTCAAGGGGACAGCCACCAACATTGCAGTTTGGG
 GTCCAAAACCTGTCCCATTCCAACCAATCGATGTGACTCTCCAAAGAGAAAGTTATGACTG
 GTTCGATCGGCTATGTTGTGGAAGCCTTCGAAGAAGTTGTTTCTGCCATCCACAACGGAG
 ACATCGCCATGGAAGATTGTAGCAACTAATCACTGGTAAGCAAAGGATTGAGGACGGTT
 GGGAAAAGGGAATCCAGAGTTGATGGATCACAAGGAATCCAACTTAAGATTCTATTCA
 CGCTTAACCAATCAGGGGGAATGAGTAA

NRALAYFKKCDIHFTNDI PRPFTQTDDFVTTDVSWCGICGSDLHEYLDGEPIFMPKDGEC
KLSNAALPLAMGHEMSGIVSKVGPVKVTKVKVGLHVVDAASSCADLHCWPHSKFYNSKPC
DACORIGSENLTTHAGFVGLGVISGGFAEYVWVSOHHITPVZKEIPLDVAALVEPLSVTH

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AVKISGFYKCSSALVLCAGPIGLCTILVLKMGASKIVVSEIAERRIEMAKKLGVEVFN
SKIHGKSIIEILRLTKSHDGFDSYDCSGIQVTFETSLKALTFKGTATNIAVWGPKPVTF
QPMDDVTLQEKVMTGSIGYVVEAFEEVVRAIHNGDIAMEDCKQLITGKQRIEDGWEKGFQE
LMDHKESNVKJLLTPNNHGEMK

>YBL058W, 1772 bp, CDS: 501-1772 (SEQ ID NO 23)

TTATTTACATAGTGCCATTGAACACTTTTCAAGCAAACACCCAGCCCGACCCACACAA
TAACACACACACAAAAGAGTCTTGCAGGTCTCTTTTAGCGGCAACGGGCATGACACTAG
GTATATTTGGTATGGGCATCACAGGGACATGTTGGAGCTGGGAATGTTTCATCATTTTCAGG
AACTAAACCAACCTCTGCAAAAGGCGTGCUAAACGAATTTGTAGTACAAAACATGCCTC
TGGATAAAAGAGCCAGCAAGTAGTGGACAGCTTAGTTAAGACACACAATTCATCTCTTT
GTAAATAGTGTTATACCATAGTAGTAGTTTCAATAATATATTTCCACTACTTATATGTGT
ACCCGCATTAGAACTCTTATTTGGTGGCGAAAATCGATGSCAATAAGAACGGAGGGGTT
TAATAGTTGTATGCTTAACATATTTTGATTAAATATATAAGAAACCTCCGTAGCACAA
AATTAATCATTTATTTAGGTATGGCGGAAATACUUGATGAAACUATCCAGUAGTTCAATGG
CATTACACCAATCTCTCGCATACATAGCCGTTCAATATCTCTCTGAATTTGGAGATTAA
ATGAAGCACTAAATTCCTATCTATGCTTCTCAAACGGATGACCAAAAGGATAGAAGAGAGG
AAGCACATTCGAACACACAGCAGGAGAAAGCCCTCAAGCAAGAAAGUUTCTCCACCAACT
CTTCGAATAAAGCCATAAATACGGAGCACGTTGGTGGGTATGTCCAAAACCCAGGATCCT
CACAAAGGTAGCAACGAGTACTTGAAGAGGAAAGGTTCTACCTCTCTCTGAACCAACCAAGG
GTAGTAGCCGCTCTGGAAGTGGTAACAACCTCCAGGTTTATGAGCTTPTCGGATATGGTAA
GAGGTCAAGCTGATGATGACGATGAAGATCAACCGAGAAATACTTTTGCTGGTGGTGAAA
CATCCGGCTTAGAGGTTACAGATCCTTCAGATCCTAATTCATTACTGAAGGATTTGCTGG
AAAAAGCGAGAAGGGGTGGTCAATGGGCGCTGAAAACGGATTCCGTGATGACGAAGACC
ATGAAATGGGTGCCAATAGGTTTACTGGAAGAGGTTTTAGATTAGGSTCAACCATCGACG
CAGCAGATGAAGTCGTAGAAGACAACACTTCACAATCACAAACGTAGACCAGAAAAAGTCA
CAAGAGAAATTACATTTTGGAAAGGAAGGTTTTCAAGTGGCCGATGGTCCGCTTTATCGCT
ATGATGATCTCTGCGAACAGTTTCTATTTGAGCGAGTTAATCAAGGAGGGCTCCATTAA
AGCTCTTAGATGTGCAATTTGGACAAGAAGTTGAAGTTAATGTATATAAAAAAATTAGATG
AGTCTTATAAAGCTCCGACGAGAAAACCTGGGCGGTTTTCAGGCCAGGGCCAAAGACTAG
CATCTCTATCCCGCTCAATCTCTACCTGCCGAGGTTCCAAAGAATGAGACACCCGCTG
CTCAGGAACAACCCATCCCGGACATGAGCCAAAACAAGGCGACACCTCCATCCAAATTA
GATACGCAAAATGGCAAAAGAGAAGTTTTGCACGTCAATTCACAGATACAGTAAAGTTTT
TGTATGAGCATGTGACATCAAAATCGAACACTGACCCATCGAGGAATTTCAACCTGAATTT
ATGCCCTTTCTATCAAAACCAATAAGCAACGATGAGACAACATTGAAGGACGCTGATCTGC
TGAACCTCGTTGTCTGCAAGATGGGCATGA

>YBL058W, 423 aa (SEQ ID NO 24)

MAEIPDETQQFWALTNVSHNLAVQYLSEFGULNEALNSYYASQTDQKDRREEAHWNKQ
QEKALKQEAFFSTNSSNKALNTEHVGLCPKFGSSQGSNEYLRKGSFSPEPTKGSRSKSS
GKNSRFMSFSFDMVRGQADDDDEDQPRNTFACGETSELEVTDPSDPNSLLKDLLEKARRGG
QMGAEANGFRDDEHEMGANRFTGRGFRLGSTIDAADDEVVEDNTSQSQRRPEKVTREITFW
KEGFQVADGPLYRYDDPANSFYLSELNQGRAPLEKLLDVQFGQEVENVVYKLDSEYKAPT
RKLGGFSGQGQRLGSPFPGESSPAEVPKNETPAAQEQPMPDXEPKOGDTSIQIRYANGKR
EVLHCNSTDTVKFLYEHVTSNANTDPSRNFTLNYPPIKPISENDETTLKDADLLNSVVVQ
RNA

>YBR039W, 1436 bp, CDS: 501-1436 (SEQ ID NO 41)

TDEAGATTTTCCAAGTAGTAACATCATCTTTCTGAGTGTGCTATCAAATACATACTAAGGA
GAATAAACTCTTGTTATTACGTATCTTTCATCCTTATGGGTAGAGAGCGCACTGTTTTAG
TACATTTTCTAGACGTGAAACGTAGAGCAATTGTGATAAAACAAAAAAGTAAGAA
GATATATGAATAGGACGTGTCCCTAGAACCTAGTAAGTATATGATGGAGATATAATAAGTG
AATTATTCGATATTTAATGAACGTTCTCATTTATTTGGAAGAAATGTTATCACGTGAATG
GAGAACCAATGAGCGGCGAGTAACCTACGCGAGGAACCCGGACCGCAATAACGATTAAGA
AGGCCCGGAAGGGAGATGCTTAATGATTATCACTCAGTTAAAAAGACAAATAAGAAAC
TATTGAGACTGAACCGTTTGGTTAATTTTCAGGTGGAACAATGAAGACGAGCAGTAA

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CATTATTTTATTAGTAGTCATGTGNTCAAQAATTGTATCAAACAAATGCAACACGCTCCG
 CAATGTGCCACCAAGCGCAAGTGGGTATTCTTTATAAGACTAACCCAGTGAGAACTTATG
 CTACTTTGAAACAAGTGGAAATGCGTTTGAAATCTATCAAAAATATTGAGAAGATCACAA
 AAACATATGAAGATGTTGCCATCTACAAGATTGAGTAAAGCTGAAAAGGCTAAAATTTCCG
 CAAAGAAGATGGATGAAGCAGAGCAGTTGTTTTACAAGAAGCGCCGAAACCAAAAATTTGG
 ATGTTGAGGCTACTGAAACAGGTGCTCCTAAAGAGTTGATTGTTGCTATCACCTCTGATA
 AGGGGTTGTGTGGTTCTATCCACTCTCAATTGGCTAAAGCTGTGAGAAGACATTTGAATG
 ATCAACCAAAACGCCGATATAGTCACATATTOCTGATAAAATTAAAATGCAGCTATTGAGAA
 CCCATCCTAACCAACATTAAAATTGTCTATTAAATGGAATTGGTAAAGATGCCCCAACTTTUC
 AAGAACTCGCTTTGATTGCTGATAAATTAATGAGTCTCATGAAGGCCCGCACTTACUCAA
 AGATTTTCUATTTTCTACAAATGACCCAGTGTCTTCCCTATCTTTTGAACCATCTGAAAAAC
 CGATCTTTAAAGCCCAAGACCATTTGAACAATCCCATCATTCGGCAAATTTGAGATCGACA
 CGGACGCCAAACGTTCCAAGACATTTCTTTGAATATACTTTGGCTAACCAATGTTGACAC
 CAATGGCTCAAGGTTATGCTGCTGAAATTTCCGCCAGAAGAAAGGCTATGGATAACGCTT
 CCAAGAATGCCCGTGATATGATCAATCGTTACTCTATCTTGTACAACAGAACAAGACAAG
 CTGTCAATTACCTAACTGAACCTGGTCTGATATTATTACTGGTCTCTCTCTTTGGGATGA

>YBR039W, 311 aa (SEQ ID NO 42)

MLSRIVSMNATESVMCHQAQVGILYKTNFVRTYATLKEZVEMRLKSIKNIEKITKTNKIVA
 STRLSKAKKAKISAKKMCEAEQLFYKNAETKNLDVEATETGAPKELIVAITSDKGLCGSI
 HSQAKAVRRRLNDQPNADIVTIGDKIKMQLLRTHPNNIKLSINGIGKDAFTPOESALIA
 DXLLSVMKAGTYPKISIFYNPVSLSFEPSEKPIFNAKTIEQSPSPGKFEIDTDANVPR
 DLFVYTLANQMLTIAMAGQYAAEISARRNAMDNASKNAGDMINRYSLYNRTRQAVITNEL
 VDIITGASSLG

>YBR062C, 848 bp, CDS: 501-848 (SEQ ID NO 45)

CCATTTTGGGTGACCAACTCTCCTACCCGAATTACTGTGATGATATATACTCTTCGTTTTC
 TAGTAATGGCTTCATTTTGCCCTAAGTTGGTCAAAATTTGTTGTGGGCGGCTTTTGTTTGCA
 CCGAGGACCGCTCAGTTCGTTATAATAACAGTTTTTGCCACTCCTAAACTACCTAAAGAAAT
 AATAGAAAGATATATTTCATCAAAACATAATCACAATCAAAAAAATGTCTACATATGAAGGT
 ATGTAATGATAATATTATCAAGTAAGTTCCCTCAAAGCCCAATTAACCTAACCGAATTTTAATC
 TGCACCTCATCATTAAGATTAGAGGAACATGCAATACAAACAATACTCAAGCGATTACCAAGA
 AGTAGGAGGAACCTCACAGGAGGAGCAGAGAAGACAGGTCAAGATCCCAACTGCAAGGTC
 TATTTCAAAACTTTTGTAACACCAGTCTGCTGAGGCTGATGCACATTCAGATTCAACACTAC
 ITTTACGATTATTATCGCAAATGCTTCAGAAATCATTAACGGAAGAATGGTTGCAAGAAA
 TGGATAAAGGCAAGAGTGCCTGCTGCTGATACCTTTGCAGCCTCTTTTACCACGAATCA
 ATAAAAAAAGCTCAAAACCACTGCAAACTGCTCCATTTGTTTACACTAATTATTTCACAAAC
 ATGAGTACCCCTTAGTAGTTGAATTACCTCAATTGCCATCATTAAGTTCCGACTTAGAGTGTT
 TGTCTGTCTGGCTATCTCGAAGTACAACATGTTUATTAATGAGAGATAATGTTATGCGGUC
 ACCGAATCATTAATGAGATTGATACAACTGAAGCAGAACTGGAAGAAGATTGGGGTATGT
 ACGGTTAA

>YBR062C, 115 aa (SEQ ID NO 46)

MLPHSLQEEWLQEMDKGKSACCPDTFAASLPRINKKKLKATDNCSTCYTNYLEDEYPLVV
 ELPHICIMKFDLECLSVWLSRSTTCFLCRDVMGHRILINEIDTTAELEEDWGMVY

>YBR101C, 1373 bp, CDS: 501-1373 (SEQ ID NO 49)

AATGATCAAAATGTTATCCCCAGGGTCCATTAACTCATCCAGAAAACAGATAGATGGATTG
 AAGGCCGTAGGTTTGAATTTTGTCTACAAATTGGACGAGTTTATCAAAAAGCAACAGTGAT
 AAAATTCGCTAAACAAGATCACAGAAAATAAACCTCACTTCAATATATATGATGTGTAGG
 TAGGGTATATACCTTATACCACTGCTCTCGACAGTGTACTAACCTATTTCTTATTTGTAG
 GTAAGCTTTTCAGCTACTGGTTGGTCAAGTTGGGCCCTATTAAGGTTGTAATCAGCTTAT
 TCGTTTGAATGATATACCTCTTTGGACTGGAATCTTCTGGAAGTTTTTTGGAGGTTAGAA
 AAGAGGAAGGCATCTCGCGCTGACAGAAATTTGCTTATAAAACCAAGGATTGGCTACATCT
 AAAAGAGTACTCATCTCAGTCAGAAAGCCATTTACCTTTCAACGAAAGAGTAAAAAGAA
 AAAAAACACATACATAACTATGGAAAAGCTATTACAGTGGTCTATTGCGAATTTCTCAAG

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GGGACAAAGAAGCTATGGCTAGGGCCGGCCAAACCTGATUCTAAATTGCTACAGCAGTTAT
TCGGTGGTGGTGGTCTTGACGATCCAACTTAATGAAAGAATCCATGGCTGTTATTATGA
ATCCGGAGGTTGACTTAGAAACAAAACCTCGTTGCATTGACAACTTTGAAATGTTSATTTG
AGAACTTAGATAATGCTAATAATATCGAAATTTAAACTTGTGGAGCCATTGTTGGATG
TTCTTGTTCAGACGAAGGATGAAGAACTACGTCCTGCTGCTTTATCCATTATTCCGAACCG
CTGTGCAAAACAACCTTGGATTCGCAAAATAATTTGATGAAATACGACAATGGTCTGCGAA
GCCTTATCGAAATAGCTAGTCACAAGACAAAGCCACTCGACCTGAGAACAAGCTTTTTT
ACGCACATATCDAATCTAATAAGAAACCACAAAGATATCTCAGAAAAGTTMTTCAAAATTAA
ATGGGCTCGAATGCATAGCACCTGTAATAAGTGATAACACCCGCCAAACCAAACTGAAAA
TGAGAGCCATTGCUATTATTGACCGCATATTTGTCATCTGTTAAGATTGATGAAAATATAA
TCAGTGTGCTGAGAAAGGATGGAGTAATTGAAAGTACCATTGAGTGCCTGCTCTCAGGACA
GTAAATTGAACATCATAGATAGAGTTCTGTCTTTCTCTCTCACCTGATATCTTCCGGAA
TAAATTTAATGAACAGGAATTGCACAAATTGAACGAAGGTTACAAACATATCGAGCCTC
TAAAGGACAGACTTAAAGAAGACGATTATTTAGCCCTAAAGTATGTATTATGA

>YBR1D1C, 290 aa (SEQ ID NO 50)

MEKLLQWSIANSQGDKEAMARAGQPDPKLLQQLFGGGGPDPTIMKFSMAVIMNPFVDFE
TKLVAFDNFEMLIENLDNANNIENLKLWEPLLDVLVQTKDEELRAAALSIIGTAVQMNLD
SQNNFMKYDNGLRSLIEIASDKTKPLDVRTKAFYALSNLIRNHKDISEKFFKLNLGLDCA
PVLSDNTAKPKLKNRATALLTAVILSSVKIDENILSVLRKDCVIESTIECLSDENLNIID
RVLSTFLSHLISSGIFNEQELIKLNEGYKILIEPLKDRLNEDDYLAVKYVL

>YBR139W, 2027 bp, CDS: 501-2027 (SEQ ID NO 55)

GGAGGAGTCAAGGGCCTGGAAAGTACGGATCCTGTAGAAATATCACTGGCAATTATACTG
AGTTTATTGTTGGTGTGCTATTTCATATTTGAGCTGGTATTGGAAGGAAGCAAGCATAT
GAGTTTGTGTCTACTGACTCCAACACCCTAGGCTGGATTTGATCTTTCTCCATCCTTTAA
TTTTAACCTTTTAAATTAGTGGTTGGATCAAGTTTTCGAGACTATCCCAATCTGTGACTTG
TGGATAAATAGTTTTTACTCGTTTAGTATAATCCCTTTTTCTTAAAGTGTCTTAGAGTT
CTCTAAGATGTTCTTGTTTACAATCTGAGCGATTTAGGAAATTTCTTAAAAATGGCCGAG
GCCGGCCTAGCATTTCTACGAAAGGTGAGATAACGCTTCGTTATCGAAAAATGTCAGGGGA
CACGGGTTATATAAGAACGAAAATTGTCATCCTGCTATTTTTCTTTAAAAACAGCTATACA
AAAAGTGATACCGACATACAATGAAGTATCTAACTTAGTTTTCTGCTCAGCTTCTTA
TTAGCATCAAAATACGCCCTCATTTGGCCGAGCTTTTCTCTTTTTGAAGATGATACCACCT
TTGCCAATTTGGATAAACAGCTAAAGCTTCCACAGAATACACAGCAAACCTTAAATTGG
ACCGTTTGAATCAGGATGATCCGCTGTTTACAACCTTTATTTCTCTCTGTGGACACAGATT
ACAGTTTGGACTTAGAACAGTAGATCTTCTAAACTAGGAAATGACACCGTAAACCAAT
CGTCGGGTTACATGGACTATAAGGATTCCAAACACTTTTTTTACTGGTTTTTTTGAAGTA
GGAACGATCCTGCTAACGACCCAATTATTCTTTTGGTTAAATGGTGGACCTGGTTGTTCCT
CCTTTACTGGGTTGCTATTTGAACTAAGCCCTCATCAATTTGGCCCGATATGAAACCA
TCCACAATCCCTATTCTTGGAAATAACAACGCTCAATGATCTCTTTAGAACAGCCACTCG
GAGTCCCTTTTTCTATGGTCATGAAAAGTCTCCTCTACAAAATTAGCAGGCAAAGATG
CCTACATTTTTCTGCAATTGTTTTTGAAGCTTTTCTCTATTACGCTCCAAACGATTTCC
ACATATGCAGGCGAATCCTATGCAAGGACATATATCCCTCAAATTGCACATGAGATCGTTG
TCAAGAACCCTGAAGAAGCGTTCAATTTAACTTCAGTTATGATTGGTAATGGTATCACAG
ACCCTTTGATTCAAGCAGATTATTATGAACCAATGGCATGCCGGAAAGGGGGCTATCACCC
CTGTTCTCTCATCGAAGAATGTGAGAAAATGAGTAAAGCTGCAGGTCGTTGTCTGATGGT
TGAACAGTTATGTTATGCTTCTAATCAAGTTTACCATGUAATAGTCCGCACTGCTTACT
GTGACTCTGCACCTTTTCCAACCGTACATTAACACAGGACTCAACGCTCTATGACATTAGAG
GCCCCCTGTGAAGATAATAGTACTGATGGTATGTGTTATACAGGCTCCCGCTATGTCGACC
AGTATATGAATTTTTCTGAAATTCAGAAACGCTAGGGTCCGACGTGCATAATTAATCTG
GCTGTGATAATGACGTGTTACCCGATTTTTGTTTTACGGGCGATGGAAGTAAACCAATTC
AACAAATATATTGCTGAATTATTAATCACAAACATTCCTGATTAATATATGCCGCTGATA
AGGATTAATTTGTAATTTGGCTGGGAAACCATGCTTGGTCCAATGAGTTGGAATGGATCA
ATAAACGTAGGTATCAGAGAAGGATGTTAAGACCATGGCTCAGTAAAGAAACAGGTCAAG
AGTGGGACAAGTCAAGAAGTATGCCCTTTCAACCTTTTTCAGCAATATACGATGCCGGTC
ATATGGTTCCTATGATCAACCCGAGGCAAGTTTGGAAATGGTCAACAGTTGGAATTCGG

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GTAATCGTGCCTCTTTCGGATCTTTCCCACTTCGAAAATGCTAGTTAG

>YBR139W, 508 aa (SEQ ID NO 56)

MKYLNLVFVLQLLISIKYASFGRAFLFEDDTTFANLDKQLKLPQNTQQTLKLDRLNHDD
 PLFTTFIISVITDYSLR/RTVDFSKLGIDTVKQWSCYMDYKDSKHFFYWPFESEKNDPAND
 PIILWLNGGPGCSSFTGGLFELGPFESIGADMKPIHNPYSWMNNASMIFFLEQPLGVGF SYG
 DEKVSSTKLAKDAYIFLELFFFAFFHLRSNDPHIAGESYAGHYLPQIAHEIVVKNPERT
 FHLTSVMIGNGITDPLIQADYYEPKACGKGGYHPVLSSEBCEKMSKAACRCRRLNKL CYA
 SKSSLPCTVATAYCDSALLEPYINTGLNVYDIRCPCEDNSTDGMCTGLRYVDQYKMFPE
 VQFTIGSDVHNYSGCCNDVFTGFLFGDGSKFPQQYIAELLNHNIPVLIYAGDKDYTCNW
 LGNHAWSNELEWINKRRYQREMLRFVWSKETGEELGQVKNVGPFTFLRTYDAGHMVPYDQ
 PEASIFMVNSWISGNRAFSDLSTLENAS

>YCL052C, 1751 bp, CDS: 501-1751 (SEQ ID NO 67)

TGCACATGTTGAGTATCCCTATTGCGCATTTTCTCTATTCTGAGAAGGAGTGTGAATAAAT
 TGGCGAGGGTTTCAGAAATGCTCTTTTAGAAATAAAAAAGAAATGTAATGTAATAGTTGGAATGTAT
 CTCTTAAGTAGACAAATGCAGGTAAGTTTACTGCGCTTTTGGCGATTAAACAGTATGCTCTT
 AGTGCAAAACACGAAAGAGCTCCCAATCTTTGAAACACAATCGACCACGGAGGAACAATA
 CACGTAGAAGGGGATAACTAATACTTTGTGCTGCAAGAGTATTGGACGACACACTTAACAG
 CAGAACTTTGCCCTTCCTAATCTTTGTTTATGATTGCTTGAAGTATTACACATGTAATAAA
 AGATGATTTATTTTCTTTTCTTCTTAAABAAAGTTCTTTCTTTGAAATATCCCCCTGATAAAA
 AAGATCAAAATAATGGAACGCTAATCATAATCAAATCGGGAGGAGAAATAACGCCAAGAAG
 TCTCCCTTTCTACCTGAGTAATGGTGACAGACATAGAGTGAAGTACTCTTACAATGCCCT
 CTGAGGATATCGGTAAATCATATGCGCCAAAATGACACTCATTTGACTCTTCTCTGAGCCTT
 CTGGTGTGGTTTTTACAACAAAGCTGGCTATTAGAGAGGACTGGAAGCTTTGGATAAATCCT
 TTACGAGAATCACTTGGAGGCCACAGAGCGGACCTGGCTAGAAATTTAAGCGTTATAGAAA
 ATGAACTGAGTGTGGCTTTTTCAGTTTACTCAAAATCTTTGGATGTGCCGGAAAGGTTTA
 TTACTTAACCCAGTCTACAAATTCATTTACAGTGCACAACTTTGACATAGAGCAGTACTTGC
 CTCCCAGAGTAGATTGAAATCTGTCAATGGAATCCACAGAGATTTTACATATGATATATCAG
 TGGAGCCCCACACAAAATCCAAAATGTTGAATATGCTCTGTTGAAACAGGGTGAAGAATTTA
 CAATTGCAAGAGTGAAAGATGAGAAACCTCGAAGTAGGTGTATTCTTTGTGGATGCAAGTG
 ATGAAAGTGAATGTGATATTGGTGGAAATACCTTCTAATTTGGAGGATGGACGATGGTAAAA
 TGGAAAGATGTGAGAAACATCCTTATTTGATATAAACAGGGCCATATCGCATACAATCACT
 CGACGACTACGACATCACTATATCTGAATGAACCTATCGGTTTGCAATCCAAAATCATGA
 TTGATCTCACAGATTTGGAAGAACGCCCTAAATGCAATGTATCTAATGCACTGCAATTTGC
 CGTTAGAAATTTATTTATCGATAAATCCCAATCTCTCCCTTACTACTTTTTTGGAGAAGACG
 ACTTAGAAATTAACAGAAATCTCTCTTCGAGATAAGGCATGGGGTCTGAAAGTATCTTTG
 AATTGAAAGCCGGCACAAATGAATGAAGTGACATTTGCATACTAGATATATTGAGCCTTCTA
 ATAATAAAGGGGATAAATTAGAAGTTTCATTTGATCCAGAAAGTTATATTAGCCTGCGGACA
 CAGGTGACAAATAACTTTCCCGTAATCCATTTTATAAAAAAGGTCTAGGATATGAATCTTC
 CTTTACAGACGATACTACATTTCCGCCATTTGAACTCGACAACTCTTCTAGTACCAATTC
 CAGGCCCTGACACAAAGGATTATTTCCAAGATCAAAAATGGTACGTTACTATCCTTACTCA
 TCTCCATCATATACATTTTCTCCAAGGTATTTGCTAACAAACAAGAAGAAAGATCAGTAA
 AACGGGAATAA

>YCL052C, 416 aa (SEQ ID NO 68)

MTRHRVTVLYNAPEDIGNHMRQNDTHLTVRCGSCVVLQQRWLLERTGSLDKSFTRITWR
 PRADIARSLGVITENELGAGFSVYSNSSDVPERFITNPVYNSFHSEKFDIEQYLPPEVDLN
 LSWNPEDFTYDISVEPTQIQIVEYRLKQSEETIARVKDEXLRVGVFTYDASDESVDZ
 GGIRCNWRMDDGKMRRCQKTSLLYKQGHIAYNHSTTTTSLYLNEPIGLHPKTMIDLTFE
 ERPKCMYLMILQLPLELFDKFOSSPILLDFGEDDLPEYSLRDKAWGSESIFELKAGCM
 NEVTLHTRYIEPSNNKGDKLEVSFLFEVILACDTGDNKVSBNPPYKKGLCYRSLFTDDTT
 FRHLNSTTLVPTPRPDTKDYSKTKNGTILQGLTSLIYTFSEYFGNNKQKRSVKRE

>YCR009C, 1298 bp, CDS: 501-1298 (SEQ ID NO 73)

GTACAAAAATGATTACGAAAATATAGATGATGTAAGCAAGGTACGGTTATAAACAGTTAA

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CACATAAGTTTACTTTCACCTTTTTTGGCTGACTCCCTTTACTTGTCTTCCCTGCACITTTGATT
 TTACTTTCAGAAAAATAAGATATATGTTTCTGATAAAACTTTTAGGTTAGCGGAGAAGAT
 GTTCCCAUGAATATCAATGTAATTGAAAGGCAACGAAAGGTCTATCGTTTGCCATTTCATAA
 TGTGATTCCGACTTGTCTTTTTTCATTGTAACAGACATGAAACGTTTCCCTTTACGTCCCTAT
 GAATTTTTTGTGCTGAACTGGGCGCTGAGGGGCTGACGATCCAAATCCCCGATTTTT
 GAACAATTATGAGAATCCGAATTAAAAAGAAAGGGAAAAACAATTTAATAACAGGCAGACG
 TGAGAGAAAGAAAGGAAACGCTGTGATATAGAAAACATATACAAATCCTATTATAAGAAGC
 CAGAAGAAACCTGATACAAAGATGAGTTGGGAAGGTTTTAAGAAAGCTATCAACAGAGCTG
 GTCACAGTGTGATAAATTAGAAATGTCGACAGAGACCATTTGATAAAGAGTATGACATGGAG
 AACGTCGTTATAAAGTTCTTCAAGAGAGUAGTGGAGGCAATTACAAAAGGAAGCCAAAGGTT
 TCTTGGACTCATTGAGAGCTGTGACAGCATCACAGACTAACCATTTCCGAGGTTCATCTCTA
 ACCCTATGACGATTCAAAATATGTTTGCTGGTGGTGGTTACAACGTTGGTAACTATTATT
 TGCATCTGTTCAAGATTTTTCATAGCGAACTGTAAAGCAATTAGACGGGCCCCTTAAGAG
 AAACCGTACTAGATCCAATAACAAAGTTTTTCGACGTATTTCAAGAAATTGAGGAGGCCA
 TAAAAAAGAGAGACCATATAAGAAACAAGACTTCGATGCTGCGAAGGUAAGTTTCTGATAGT
 TACGCGACAAACCTCGCTAAAGATGCCCTCTAAACTGCCAAGGGCTGAAAAAGAATTGAGCT
 TAGCTAAAGATATTTTCGAAATCTTAATAACCAATGAAAACTGAACTACACAGTTAG
 TTTCAATTAAGAGTACCTTACTTTGACCCAGTTTTTGAAGCTTTAATCAAGATTGAGCTAA
 CGTTCTCTACTGATGGTTACACTCGTTTAGCGCAGATTCAACAATATTTGGACCAACAAT
 CAAGAGACGACTATGCCAATGGGTATTAGACACTAAAATCGAAGAACTATTACGACAAA
 TGACAAGCCTAGATATTGTGCGCTCGGGATAAAATAA

>YCR009C, 265 aa (SEQ ID NO 74)

MSWEGFKKAINRAGHSV.IIKNVDKTIDKEYDMEZRRYKVLQPRAGEALQKEAKGFIQSLRA
 VTASQITLAEVTSNLYDDSKYVAGGGYNVGNYYLQCVDFDSETFVQLDGLPLRETVLDPI
 TKFSTYFREIEEAIKKRDHKKQDFDAKAKVRRLLVDKPAKDASKLPRAEKELSLAKDIFE
 NLNNQLKTELPLVSLRVFYFDPSFEATIKIQLRFCITDGYTRLAQTQQYLDQQSRDDYAK
 GLLDTKIEELLGQMTSLDICALGIK

>YCR010C, 1352 bp, CDS: 501-1352 (SEQ ID NO 75)

GAGCTCCGTGCAATAGGCCACCGGCTCACTGGTTCTCCAAGCTACGGTTTTTTACGTGTAG
 CCCCATGTCAGCAAGCCAAACAGGGCCCCTTAAAGGCGTGACTACAAAAAGGGGCGGGTT
 GGAAGGTTCATCTGCAGCGAGATACGAAAGATTTTTTGGCCAGATTGGCGTTGGCGGCT
 ATTTCCGTATTGTTGGGGTAACAAACGTTGGGGAAGACTGCAATTTCTTTACAGCTTTTPT
 TCGTTATCGCGGTTGGGCGGCTATGGCGCCTTCTCCTCTGTACTCCAACCTGTCAGAGA
 CACCAAGCTGTATATAAAGCACCTTGGTTGGATCGTATTTCCTCGAGATCTTGCTATAGG
 TTCATTTTATATATCGTCCAAATAGCAATACAAATACAAACAGAACTACTAGCATCTGTTT
 ATAAGAAAAAGGCAAAATAGTCGACAGCTAACACAGATATAACTAAACAAACCAACAAACAA
 CTUATATACAAACAAATAATATGCTGACAAGGAACAAACAGCTGGAACACAGACTTGG
 AGAATGCACCAGCAGGATACTATAGTTTCUCATGATAACGACGTAAATGGCGTTGCAGAG
 ATGAACCTCCATCTCATGATTCCCTTCCCAAGATTTACACTGGAGGTGATAACCAATGAMT
 ATATCTATATTTGGGCGTCAAAAGTTTTTGAAGAGCCACTTATACCAAGCCTTTGGTGCTA
 CCTTGAATCTAGGGTTAGCTCCTGCTCCAGTGCACAAATTTGCTAATCTGCGCCCTTAG
 GTCCTTCAGCCTTCCCGTTGACGACATTTGTGCTGTCCATGTTCAATGCCAGAGGCSAAG
 GGATCACTGTTCCCTAATGTTGTGCTCGGTTGTGCTATGTTTTATGGTGGTTTGGTSCAAT
 TGATTGCTGGTACTTTGGGAGATAGCTTTGGAAAATACTTTTGGTGGTACCCTATTATGTT
 CTACGGTGGGTTTGGTTGAGTTTGGCTGCAATTTACATTCCTTGGTTTGGTATCTTGG
 AAGCTTACGAAGACAATGAATCTCATTTGAATAATGCTTTAGGATTTTATTTGTTGGGT
 GGGCCATCTTACGTTTGGTTTAACCGTTTGTACCATGAAATCCACTGTTATGTTCTTTT
 TGTTGTTCTTCTTACTAGCATTAACCTTCTACTGTTGTTCTATTTGGTCACTTTGCTAATA
 GACTTGGTCTCACAGAGCTGGTGGTGTCCCTGGGAGTTGTTGTTGGCTTTCATTGGTTGGT
 ACAACGCATATGCAGGTGTTGCTACAAAGCAGAAATTCATATGTACTGGCTCGTCCATTCC
 CATTACCATCTACTGAAAGGGTAATCTTTTAA

>YCR010C, 283 aa (SEQ ID NO 76)

MSDAEQTSQNTDLNENPAGYYSSHDKNVNGVAEDERPSHDSLGKIYTGDDNNEYIYIGRQ

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KFLKSDLYQAFGGTLNPG LAPAPVHK TANPAPLGLSAFALTTFVLSMFNARAQGITVENV
 VVGCA MFYGG LVQLIAGIWEIALENTFGGTALCSYGGFWLSFAAIYIPWFGILEAYEDNE
 SDINNALGFYILGWATFTFGLTVCTMKSTVMFFI LFFLLALTFILILSTGHFANRLGVTRA
 GGVLGWVTFIAFWYNAYAGVATKQNSYVLARPFPLPSTERVIF

>YCR021C, 1499 bp, CDS: 501-1499 (SEQ ID NO 79)

ATCGAAAGCGTGCTTTGTAGAATATTTGGTATGGCTAAAGTAAGCAAAGCCATATCCCC
 ATCCCGATCCCCGACTCTTACTCCGATCCCTTCGCCACATCCCTGCATGTTTATTCGAAATA
 CCAAATTAGCTCATCTTCTCTATTTTCATCATCCCTTTCTGCTATGGCAAGGACAAGTTT
 TTTCTAGCATCTCATCGAAAACTTTCCTCTCCCTAAATGGGCCAAAGTTTTCATATTCATC
 ATCAGTTAGAAAAGTATAATATCAATCCCTTACCTCATTACAAGTTGTATCACACTAAAAA
 AATCATATATAAGCTCTGTGACAGCTTCAATTATTTACCTAACACCTATTCACCTTCTA
 ATCTTGTCTTCTGTTTTTACATTTCTGCAATACAACACAACAATAATTAACCTCAATTA
 TTATTATTTATAATTACAAAAACAAAACAAGTTTGAGACTTTAATATCTTTTGATTA
 CTAAAAACAACAATTTCAAATGAACGATACCTTATCAAGCTTTTAAATCGTAACGAGG
 CTTTAGGGCTTAATCCACCACATGGCCTGGATATGCACATTACCAAGAGAGGTTCCGATT
 GGTATGGCGACTGTTTCCAGTCTTTGGCTTTATATGGCTATGCTATGTGTGATGTCT
 TCATTCCGGACAACAAGGCTCCAGATTGACTACATATGCCCTTAGCTCCCTGCATTTTGA
 TCACTTTCTTTGAATTTTTGCTTTCTTCACTTATGCTTCTGAATTAGGTGGAGCTGGTG
 TTCAGCTGAATTTAACCACGTCAAGGTTAGCAAGTCTATCACAGGTGAAGTTCCCGCTA
 TTAGACAAATCTTTTACTCGAAATATATTGCCTGGTCTTGTCTGGCCATGCTTTTAT
 TTTTAATCCAGTTAGCCCTAGTACTACTGGTGAGAAATGACGACATTCGGGCTTCGATA
 TGGTACATTCGCTGTTAATTCAAATCGTGGGTACCTTATCTGSGTGTGTTTCGCTATTAG
 TTGGTTTCATTGATCAAGTCCACCTACAAGTGGGTTATTAACACUATGGTTCCTGCTGCTA
 TSTTGGTTACCCAACTGTGCATATGCCAACCTCAATTCCTCAATTCGAAAACAGAGGGT
 TCAATGCACCTTATGCTGTGTACCTGCATGGTAATCGTTTGGTTGTACTTTATCTGTGGG
 GTCTAAGTATGTTGGTTAACCCTATTCAACCAGACGGTGAGGCTATCTTTATGGTGTAT
 TGGATTTATGTGTATTTGCCATTTATCCATGTTACTTGCTAATTGCAGTCAGCCTGTGATG
 GCAAATTGCCAAGGCTATCTTTGACAGGAGGATTCTCTCAACCATGCTACCGACGATG
 TCGAAGATGCGGCTCCTGAAACAAAAGAAGCTGTTCCAGAGAGCCCAAGAGCATCTGGAG
 AGACTGCCAATCCACCAACCCGAACCTGAAGCAGAGCAAGCTGTGGAAGATACTGCTTAG

>YCR021C, 332 aa (SEQ ID NO 80)

MNDTLSSFLNRNEALGLNPPHGLDMHITKRGSDMLWAVFAVFGFILLCYVVMFFIAENKG
 SRLTRYALAPAFLLTFEFEFAFTYASDLGWTGVQAEFNHVKVSKSTGGEVPGIRQIFYS
 KYIAWFLSWPCLLFLIELAASTTCENDDISALDMVHSELLIQIVCTLFWVSLLVGSLTKS
 TYKWKGVYTTGAVAMVVTQGVICQRQFFNLKTRGFNALMLCTCMVIVWL YFICWGLSDGGN
 RIQPDGEALFYGVLDLCVFAIYPUYLLIAVSRDGKLPRLSLTGGFSHHHATDDVEDAAPE
 TKEAVPESPRASGETAIHEPEPEAKQAVEDTA

>YDR073W, 1010 bp, CDS: 501-1010 (SEQ ID NO 91)

GTTAGCTTGCCCTTGCAATTTCCCATGGCGTCTCGAAAGGAATTATTCAAGATGGATTATT
 GGCATTTACGAGTAACCAAGGATAACCCCGCTGTGGGTGAACCAACCTCTTTTTCACCTT
 TCTTCAAGGCCAGTGCAAAACGCGAATAAACATATCTACGCTATATATAGATATGACGTTT
 CTCAGGCCAACAGAAATAGATAAAGCAGCCAGGAGGTAGAGAGTGTTCAAATTATAGCA
 AGCCTTCTTCTACCTGTTTTTTTTTGTATGATTGTTTTTGCCGGGTAAACAATCGACTTTCGG
 CCAAATTTTTTTTCCCTTTTTTCTCCTAACAGTATATACGGAGTGGAGAACAGACTTCCCA
 TAAAGCATATTACGTGGGGTCTGTAGTAAGATTGCCGTTTATGATAACCTCTATTTAGGG
 CTCAGAGCGCATCACGATCGGGAGTGTAATTCATGTGCATATAAGCAAACACACAGA
 TTTCCCTTTTTTCCAGAAAAATGAGCAGTCAAAATTGCCTACTCGAATACCAACACCAACA
 CTGAAAACGAGAACCGCAATACTGGCGCTGGCGTAGATGTAATACAAATGCAAAATGCAA
 ATGCAAAATGCAACTGCAAAATGCAACTGCAAAATGCAACTGCAAAATGCAACTGCAAGCTGA
 ACCTCCCCACGGTCGATGAGCAAAAGACAGTATAAGGTACAACTGCCTATTCGATATCAACA
 GCATATTACTTGCTAGAGTTATTACAGATGAATAATAGTTTACAAAACAATCTACAGAAACA
 ATATAAATAATAGCAATAACAATAACATCATCAGGATACAGCAACTTATATCTCAGTTCC
 TAAAAAGGGTTTCATGCCAATCTTCAATGCATATCTCAGATAAACCAAGGAGTGGCCCTCAG

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CGAAACCACTGATCCCTCAGCGCTCCCTCAGCTAGCCCAACCAGCAGCAACCTCCACAGGATA
TTCTTTCTAAACTCTATCTTCTCTTGGCAAGAGTGTTCGAGATATGGTAG

>YDR073W, 169 aa (SEQ ID NO 92)
MSSEIAYSNITNTNTENENPNTGAGVDVNTNANANANA'ANATANATANATAELNLPVDE
QRQYKVQLLLHINSILLARVIQMNNSLQNNLQNNINMSNNNNIIRIQQLISQFLKRVHAN
LQCISQ_LNQGVPSAKPLILTPPQLANQQOPPDILSKLYLLLARVFEIW

>YDR178W, 1046 bp, CDS: 501-1046 (SEQ ID NO 105)
ACGAATTAGGCGCTCAAGTCCTTAGACCCCCAATGACAAACAACACAGCCAAACCGTATCATCGA
GGAAATTGTTGAAGTGAATAGATATAAAAAAAAAACGCAUCAAAGTAACTAAATAAAGAA
TAAATAAACTATATCAGTAAACACCAAGCGAGGATGTTTTCATTGTGCATCCGTGTTCTT
GATGATCACATAACTGTAAAGAATAATACGGCACGTTAAATGTTTATTTTAGAATATATA
AACACCTTATCTGCCATAAGCATTGAGCCCAATCGCTGCTGTTTATTCTTATCCGGGGCAC
CTTCGGGAAGAACACAGCGCGCAATTTASTTATATAAGGAGAAGCCCTCGAGCGATCAGGGG
ACCGACTGCGGATCGCTTTAAGGCCAAGATAGAAGGATAAATATCTGCTTTTGGAGGATAG
TCGTATCTAATTTCCCATTTCTGTTGTTTCTTGTATCTTTCTACGCTTTTCGACTTTCTTC
CTACGGCGCTTTATAATAGCTATGATCTTTCCTCAAGATCCATGAAATTTATGACTGGAAGGA
GAATTTTCCATACTGCCACAGTAAGGGCTTTCAGTCTACCGCTAAGAAGAGCTTAACTA
TCCCATTTTTCGCGGTATTACCCCAAGAAACAGGTTGGTGTAGCGGCACTCCCAATGATG
CCTACGTCUCCCCCUUTGAGAA'AAATTAGAGGGCTTCATACCACTGGTATATGGAAAAAA
TCTTTGCCCTGTCCGTGCTTCCATGGCTACGACGGCTATCTCACAACCGGTCCCTTAT
CCACTGCAGCTGATTCTTTCTTTCTGTGTCATGCTTTTGGCATATTTTACATCGATTTA
ACTCTTGTATCACCGATTATATTTCTGAAAGAGTTTATGGTGTTTGGCACAAAGTACGCCA
TGTATATGTTGGGCGCTTCGTTCTCCGCTCTCCCTTTTGGGAATCTATAAACTAGMAACCG
AGAAATGATGGTGTGTTGCTTTATGTAAAGAGTCTATGGGATTTCTTCGAGAAAGACAACA
GTCAAAAAGATTGAAGCCAAAGAGTAG

>YDR178W, 181 aa (SEQ ID NO 106)
MMLPRSMKFMTGRRIFHTATVRAFQSTARKSLTIPFLPVL PQKPGGVKGTENDAYVFPPE
NKLEGSYHWMYMEKIFALSVVFLAIPFAMLTTHGFLSTAADSFPFVMLLGVCYMEFNSCIITDY
ISERVYGVWHKYAMYMLCLGSAVSLFGIYKLETENDGVVGLVKSLWDSSEKDNSQRIEAK
K

>YDR202C, 1556 bp, CDS: 501-1556 (SEQ ID NO 107)
GAATTCCAACCGGAAATTGCNAACAGCAGCAATTTCTCGTACCGATGAAGGGGAACATGG
CCGTGTGTACCGAGGTTCCATTGGCCGAGTATTAGCCAGGGCCCTAATACGTAACTCGGTA
CGCTCTTCAGCTTCTTTTCGCATAATCAACGTTCTTGTATATGTAAC'NCACCAAGTTCCATG
GCATCCGCCAAACCTTGCTTCCCTTACCAATATTAATGAGCCCTAAGGTGTACATTGCCGCC
GCAGGTAATATTAGCCCAAGCAGCTTGGCATTTCACTGGCAAGTAGCTGCTTGATCTCACT
AAAGATAACCTCAACATACTCTTTTACTTGTCTCTTTTGTAGCTAATTGCTTTCTCTCCC
CTTCTTTTCCACAAACUGCAACTATTTTCTCTCAAAAGTTATATGAAGTATATATACTC
AATGGAGCAATTCCGGGTTGAGTGAATTACAAAATTATAGTATCTTGATCAACCACACACT
GGAAGTGCCTCGAAAARCAATATGAGTGTGTGATTTGTTTCCAAATGATAGATTGGGTGCAG
AAGATAAA'ACGACAAC'ITTAAGGAAGCCGTAAAAGAAATGCTCCTGGCTCATCGAAGAAA
TCGTCAAACCGCAATTACCCCAACATTTATGACAACTTTTCTAAATCCCTAGAGATGCTAG
AGAGTGACCAAAATATTCAAAATGCCTGTATCTAATGGTATTCCCAACCGAAACTAACCAAC
AAAACGACTCTCCGACGGTAAGGGGTGTTATCACAAAGATAAGGCCAAATACATGTGTGACT
TTACATATTGTTGTGATGATTTCCACAAATTTCAAAGGGGTAAACAAGTTATGTTCCGAATGA
ATACGGGCACTGAATTTCTTACTTATTCATTTCAAGTAGATAATGACCCACTTGAAAAATA
TTTTTGGAAAT'ACTGAATCAACTTCAAGTAGCTACAGATGTGAGCGAATTGCTATCCAAAT
TTGGCGCTGCCCATGCAACTTTTGAACCACTCTCTAA'ACTTTTACAAAATCCTCTCTAGAG
ACCTGCTATCTCCAGAGATAACAACCTTGGCTATGAAGGAAATGTTCCAGGATTGTACT
CAGTCTGCGAATCCACAGCTCAGATCCTAGGACTGGAAC'ITACGCTTTGTAGGAATGAGC
TTTGCATAGAACTACGAAATCTAATTAAGGTGACTAAAAAACCTTGGTGCGAGATTGATA
GTAAAAC'TGGCAGGTCA'TTTTCGACCAAAATAGAAATCAAGTGACAAATCAAAAGAACAA

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AAACCTTTATCTAAGATCCTCTCAGAAAACGGTGTACAGTCCAGGATTCCACATTACTTA
 ACCACATAATTTCTTCTTTTCAAAGTGAAGCTATAACACTTCCAGAAGCTCAGCAATTAT
 TAAGAAGGGGGCGTTACTTTCCGATAATAGGGTAGTCATGGAATCTGAAAACCTTAATAGTAT
 CTACAAGTGAATCCAACTTTGATCAGTATAAGCGCCAAATTGAACAGTCTCAAAGCTTCGA
 TGGCGAACCATCAAGCAAATTTGGTAGCTAGCBAACAGTTAAGTACATATAAGTAA

>YDR202C, 351 aa (SEQ ID NO 108)

MSVDLFPNDRFGAEDKYDNFKDAVKESWLTERIVKPQLPNIIDNFSKCLEMLESDDQIEK
 MPVSNIGIPNESNKQNDSPYKGVITRCQQYIVDFHIVVRFPPQPRGKQVMFRMNTGILNFI,
 LIQFSKIMTHLKNILEILNQLQVATDVSEFVSXFGVAMELLNHSLLILLQNPFRDLVFPED
 NMFAMKEMFQDCYSVCESTAHILGLELTLCRNELCIELRNLIKVTKKPWCEIDSKTGRSF
 CDQIRNQVTNERNKTLSKILSENGVQVQDSTLLNHIISFQSEAITLPEAQEILRRGVTF
 DNRVVMCECKLIVSTSDPTLISISAKLNSLKASMANHQANLVASKQLSTYK

>YDR256C, 2048 bp, CDS: 501-2048 (SEQ ID NO 115)

GGGAAGAACCAAGAGATGTTATCGGCTCGGAGAGTTTGTAAAAAGCGAAATAGATTGCGTGC
 AAGTPTGTGAAGAAACCATCGACAGAATTACAAAGTTATTCTGTGATGAAAAGCTGCTAA
 CTAATATTTTAAAGAGAAAGTTGACAGAGGAAGAAAAAGCTCTGTCAAAAGCTCCTTGGG
 TGAAGAAGTGAGCGGTGTGTCTAACCACTATTTTAAAGCCGCAATTAGTAATGCAAAAAGT
 TGGCCGGAATTAGCCGCGCAAGTTGGTGGGGTCCCTTAATCCGAAAAAGGACCGGCTTTAA
 CAAATATAAACTCCGAAATCCCCACAGTGACAGAAATTGACAAAACAACCACTTTTGATA
 TCGCCATACATATAAAGAGATGTGAAAGCACTCTCTCACTGTAATGTCCAAATCGTACAT
 TTGAATTTCTTGTAGGTTTATTTTAAAGGTAAGTTAAATAAATATAATAGTACTTACAAA
 TAAATTTGCAACCTTAGAAGATGTCGAAATTCGGACAAGAAAAAATGAAGTAAATTACT
 CTGATGTAAGAGAGGATAGAGTTGTGACAACTCCACTGGTAATCCAATCAATGAACCAT
 TTGTCACCCCAACGTATTGGGGAACATGGCCCTTTGCTTTTGCAAGATTATAACTTAATTG
 ATTCCTTTGGCTCATTTCAACAGGGGAAATATTCCTTAAAGGAATCCACATGCTCATGGT
 CTGGTGCCTTCGGCTATCTTGAAGTAACCGATGACATTACTGATATCTCGCGCTCTGCTA
 TGTTTAGTAAAATTGGGAAAAGAACGAATGTTTAAACAAGATTTTCGACTGTGGGTGCTG
 ATAAAGGTAGTGGACACCGGTTGTTGATCCAAGGGGCTTTGCCACCAAAATCTACACAC
 AAGAAGGTAATTTAGATTGGGTCTACAATAATACACCGGTATTCTTTATCAGAGACCCCT
 CCAAGTTCCTCACTTTATCCACACACACAAGAGAAACCCACAAACCAACCTTACGGATG
 CTGACATGTTTTGGGATTTCTTCACTCCTGAAAATCAGGTGGCCATTCAATCAAGTAA
 TGATCCTTTTTTTCAGACCGTGGTACCCCTGCCAACTACCGTAGTATGCAAGGTATTCTG
 GTCATACCTATAAATCGTCCAATMAAACGGAGATTGGCATTATGTGCAAGTTCCATATCA
 AAACCGATCAAGGAATAAAGAACTTGACCATAGAAGAGGCTACCAAAATTCGGGATCCA
 ATCCAGATTACTGCCAGCAGGATTTATTTGAGGCTATTTCAGAAATGAAAACATCCCTTCC
 GGACAGTTTATATTCAAACAATGACCGAACCGATGCCAAAAAATPACCATTTTCAGTCT
 TTGAATTGACTAAAGTATGGCTCAGGGGCAATTCCTTTACGGCTGTGGGTAAAGATTG
 TTTTGAACGAGAATCCACTGAACCTCTTCGCACAGGTGGAACAAGCTGCCTTCGCCCCCA
 GTACCACCGTTCTTACCAAGAAGCAAGCGCTGATCCAGTATTACAGGCCCGTTTGTATT
 CATATGCGGATGCTCATAGATACAGGCTAGGTCTTAACCTCCATCAAATACCCGTAAACT
 GTCCATATGCATCTAAATTTTTCAATCCCGCTATCAGAGATCGACCGATGAATCTTAACC
 GCAACTTCGGCTCAGAACCTACATATTTGGCCAACGATAAATCGTACACGTATATCCAAC
 AGGACAGACCCATTCAACAAACACCAAGAGGTATGGAATGGGCCAGCTATCCCTTATCATT
 CGGCAACATCCCGAGCTGACTAGATTTCTGCAACCAAGAAATCTCTACCGGTTTTTGG
 GTAAACAACCTGGACAGCAAAAGAACTTGGCATATAACATCGGCATTCAATGTAGAAGCG
 CTTGTTCTCAAATACAGCAGCGGCTTTATGATATGTTTGTCTGTTGATAAGGGACTAT
 CTGAGGCAATTAAGTAGCTGAGGCAAAACATGCTTCAGAGCTTTGAGTAACCTCCA
 AATTTTGA

>YDR256C, 515 aa (SEQ ID NO 116)

MSKLGQEKNEVNYSVREDRVVENSTGNPINEPVTQRIGPHGPLLLQDYNLIDSLAHFN
 RENLPRNPHAHGSGAFGYFEVTDUUTDICGSAMFSKIGKRTKCLTRFSTVGGDKSSAIF
 VRDPRGFATKFYTEENLDWVYNNCFVFFIRDPKFPFHIFTQKRNPQTNLRDADMFWD
 LTTFENQVAIHQVMILFSDRGTPANYRSMHGYSGHTYKWSKNKNGDWIHYVQVHLKTDQGEK

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NLTIEEATKLAGSNPDYCCQDLFEALQNGNYZSWTVYIQMTTERDAKKLPFSVFBLTKVW
 PQGQFLRRVVGKIVLNENPLNFFAQVEQAAFPSTTVPYQEASADPVLQARLFSYADAHK
 YRLGPNFHQIPVNCOPYASKFFNPARDGPMNVNGMFGSEPTYLANDKSYTYIQDDRPIQQ
 HQEVWNGPAIPYHWATSPGDVDFVQARNLYKVLGKQPGQKNLAYNIGIHVEGACFQIQQ
 RVYDMFARVDEKCLSEAIKKVAEAKHASELSSNSKF

>YER103W, 2429 bp, CES: 501-2429 (SEQ ID NO 145)

ACCATTCGTCACTTCTCCATTGAGATTCCGAAAAACCCCTCGGCTCTTCTTAGAACTAAATT
 ACCTTCATAGGGGTGGGATTTATATTGTAATTCCGCGAGGTTTACACGAAAAGATATCTCA
 ACTCTAGCCGCACATCCATTCCGGTATGTAATCTCCACCATTGGGTATTATAGAATGTA
 ATTACGTTTCAAGCGGATATCTTTTGGCCCGTGAGTTCTTACTTTTTCATTTCGAGCAATG
 AAGTACATTCTAGAAGTTCTTAGAACCTTATGGAAGCACCAAGAAAAAAGGAAGTTAAAC
 AAAACATAAGATTCAATAAGCAAGGGGGGAAGCTCCTTAGTTTGACGACAGTAACAAAATG
 TTCTTATTAATGTAACGAAACTCAAGCCAATAAAGCACTTTTCAGAGGCCATATCTCTTCT
 TTTCTCCACAACTTTTCGAAATAAAAAACCACTAATAAAAAAGTAAATAACAAAAACAAGAAAA
 AAATAAACAAAAACAATAATCAATGTCAAAAAGCTGTTGGTATTGAACTTAGGTACAACTATT
 CATGTGTTGCTCATTTTGCACACGATACCGTTGAAATTATCGCTAACGATCAACCTAATA
 GAACGACGCCCTTTCTTATGTGGCTTTTACTGACACAGAAAGGCTAATTGGTGACGCTGCCA
 AGAATCAAGCTGCGATGAACCCACATAATACAGTATTCGATGCTAAGCGCTCTGATCGGAC
 CTAAATTCCTATGATCCACAAGTGACCAACGATGCTAAGCATTACCCATTCAAAGTGATTG
 ACAAGGGAGGTAACCGGTAGTGCAAGTGAATATAAAGGCGAGACAAAGACATTTACTC
 CAGAAGAAATTTCTCTCAATGATCTTGACAAAGATGAAGGAGACTGCTGAGAACTTTTATG
 GAACAGAAAGTGAAAGATGCTGTAGTAACGGTTCCAGCCTATTTCAACGATTCCACAAAGGC
 AAGCAACAAGATGCGGGTACAATCGCGGGCTTGAAAGTTCTTCTGTAATCATTAATGAAC
 CTACAGCTGCCGCTATTGCGTATGGGCTGGACAAGAAATCGCAGAAGGAGCACAAAGCTCT
 TGATCTTTGATTTAGGTGGTGCTTCTTGTATGTCCTCTCTGCTATCCATAGATGAAGGTG
 TCTTTCAAGTTAAACCTACTCTCTGCTGACACTCACTTCCCTGCTGAACATTTCCATACTA
 GCGTGGTTAATTTCTAGCCAGGAGTTCAAAACAAAAAATAAAACCATCTAACCACTA
 ACCAAAGGTCCCTAAGGAGGTTAAGGACCGCCGCTGAAAGGGCCAAGAGAACTCTGTCTT
 CGTCTGCTCAGACATCTATAGAAATAGATTCAATTATTTGAGGGTATCGATTCTTATACTT
 CCATTACAAGGGCAAGATTTGAAGAATTATGTGCTGATTTGTTTAGATCTACATTGGAGC
 CACTCGAAAAAGTTTGGCTGATTCAAAATTAGATAAGTCACAAATTGATGAAATTGTAC
 TTGTTGGTGGTTCAACAAGAATTCCAAAAGTACAAAAACTGGTTTCTGATTTTTCACACG
 GTAAAGAACCAAAACCGTTTCGATTAAACCTGATGAGGCCGTGGCTTATGGTGCTGCCGTAC
 AGGCTGCCATCTTAACGGGTGACCACTCGTCCAGCAACCAAGATTTACTGTTGCTGGATG
 TTGCACCATTATCTCTAGGTATTTGAAACTGCAAGTGGTATTATGACAAAGTTGATCCCAA
 GAAATTCGACTATCCCAACAAAAAATCGGAAGTGTTTTCCACCTACGCTGACAAACCAAC
 CTGGTGTGTTGATACAACTTTTTCAGCGTCAAAAGCAACAGACAAAACACAACTCTAC
 TGGGTAAATTTGAGTTGAGCGGTATTCCACCCGCTCCCAAGAGGCGTACCACAAATTGAAAG
 TTACATTTGATATCGATGCAATGGTATTCTGAACGTATCTGCCGTTGAAAAAGGTACTG
 GTAAATCTAACAAAGATTACAATTACTAACGATAAAGGAAAGATTATCGAAGGAAGATATCG
 ATAAAAATGGTTGCTGAGGCAGAAAGTTCAAGGCCAAGATGAACAAGAAAGCTCAACGTC
 TTCAAGCTAAGAATCAGCTAGAACTCGTACGCGTTTACTTTGAAAAATTCTGTGAGCGAAA
 ATTAATTTCAAGGAGAAGCTGGGTGAAGAGGATGCUAGGAAATTGGAAGCCGCCGCCCAAG
 ATGCTATAAATTGTTAGATGCTTCGCAAGCGCCCTCCACCCAGGAATACAAGGAAAGGC
 AAAAGCAACTACAAGCTCTTCCAAACCCCATTTATGAGTAAATTTTACGGAGCTCCAGGTG
 GTGCCCCAGGAGCAGGCCAGTTCCGGGTCCTGGAGCAGGCCCCACTGGAGCAACAGACA
 ACGGCCCCAACGGTTGAAGAGGTTGATTAG

>YER103W, 642 aa (SEQ ID NO 146)

MSKAVGIDLGTTYSCVAHFANDRVEIIANDQCNRTTPSYVAFEDTERLIGDAKNQAAMN
 PHNTVFDARKLTGRKFDDPEVTNDKEYPEKVTDXGGKPVVQVEYKGETKFTTPEELSSM
 ILTKMKETAENFLGTEVKDAVVTVFAYFNDSQRQATKDAGTIAGLNVLRINEPTAAALIA
 YGLDKKSQKEHNVLIIFDLGGGTFDVSLLSIDEGVFEVKATAGDTHLGGEDFDSPLEVNFLA
 EEFKRKNKKDLTTNQRLRLRTAABRAKRTLSSAQISIEIDSLFECIDPYTSTTRARF
 EELCADLPRSTLEPVEKVLADSKLDKSLQIDELVLVGGSTRIPKVQKLVSDFFNGKEPNRS

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INPDEAVAYGAAVCAALLTGDQSSTTQDLLLLLDVAPLSLGIETAGGTMTKLTFRNSTLPT
 KKSEVFSTYADNQPGVLQVFEGERTRTNDNNLLGKFELSGIPPAPRGVFPQIEVTFDIDA
 NGILNVSAVEKGTGKENKTITNDKGRLSKEDIDKMVAEAEKFKAEDEQEAFVQAKNQL
 ESYAFTLKNSVSENNFKEKVGEEDARKLEAAQCAINWLDASQAASTEYKERQKELEGV
 ANPIMSKPHYGAACGAPGAGPVPFGAGAGPTGAPDNGPTVEEVD

>YER150W, 947 bp, CDS: 501-947 (SEQ ID NO 149)

ATACCGCGGGAAGAAGAAATATCATATTCAAGCTAATTCATTGAAATTAGTGTCTGCTC
 ATCTAGCCTTTAGTCCCTAATCTCTCGAGCAGCACATATGCCCTTAAACCCATGCCCGGA
 CTGGGGGGCCCCATCGGGGCTCGAACCCTGAATCCCCGCGAGTATTTATTTGAAGGTCCGGG
 ACGCAAGTTACCTAATCTGGTTAATTGATATCCCATTTAGGCGATGAUGTTCCTTCCCT
 CACCCCTCGGCTTCTTACAAGATCTATTCTTATAGCCTCCCTCTGGAAGAATTTATGCCAG
 ATPAAAGAAAAAACTTCTCGAAGTTCCAGATGCCCAAATGAGGGCTTTCATCCCTGTT
 AGCTGCAAACTCTAAGTATATCTATATAAAAAGTCCGCTACTTTTGGCAGGTTCTGTCT
 TTCACCTTGCACCTCTCTTGATCTTACTTTCTACTCAAAAACAATCCAATACACAAAATAA
 AATCAGTACTATTACTAATAATGTTGTCTAACGCTAAGCTCCCTTCTATCATTGGCCATGG
 CCTCTACGGCTCTCGGATTGGTATCTAATTCTAGTTCCTCTGTAAATCGTGGTACCATCAA
 CGGATCTTACTATTCCCCGTAACGATACAGCCACCCCCAGCACCAGAGCCATCATCCGCCG
 CTCCAAATATTCTACAACCTCGACTGCTACTGCAACACAGTACGAAGTTGTCAGTGAATTCA
 CTACTTACTGCCCAGAACCAACGACTTTTCTAACGAATGGCGCTACATTCACCTGTTACTG
 CCCCCAATACCTTAACAATTACCAACTGTCTTGCCTATCGAGAAGCCTACTTTCAGAAA
 CATCGSTTTCTTCTACACATGATGTGGAGACAAATCTAATGCTGCTAACGCAAGAGCAA
 TCCAGGAGCCCTAGGTTTGGCTGGTGCAGTTATGATGCTTTTATGA

>YER150W, 148 aa (SEQ ID NO 150)

MLSNAKLLLLSLMASTALGLVSNSSSVIVVPSSDATIAGNDTATPAPEPSSAAPIFYNS
 TATATQYEVVSEFTTYCPEPTTFVCTNGATFTVTAPTTLTITNCPCTIEKPTSETSVSSTH
 DVETNSNAANARAIPCALCLAGAVMMLL

>YFR033C, 944 bp, CDS: 501-944 (SEQ ID NO 155)

ATCGAGCCATTGCGGCTCGCTGAGTAAGCGACGGTCATCGGGCGCGCTCGTGGACGATGA
 CAACCGCGGAATCACACAACCATCCACACCAAGCACGGCGTAATCGATTAGCGCTCGCGCT
 GCACGAACCTGGCTCTTTAATCCCCGCGGCACTGGAAACAGCAAAATCTGTGGCGCGCGCC
 GTCCAAAGCGATCACCGTGGAGGGCGGCTGCGGGTACATCCGTCACTACAGCAGAACGT
 GAGCAAGTTGACCGTTGCAUCAAATGGGAAGCACGTTCCCGGGCATATCGGACTGGGGCGCGCC
 TCCCCCTGCGCCCTGCTTCTTATAAGAGCGGCTTTGCTGGAAAGTGGCCACACCGGGTTT
 TCGAGATTAGGACCTACTCAGTCTTAAGGGCAGTATTGGTTGGCGCTTATTTGCACATAT
 TGTATACAGGCACTCACATTAACAGAAGCACACATATACACTTACACCTACACACACCGGA
 TAAAGAAAAAGAAATAGAAAATGGGCATGTTGGAAGTAGTTGGTGAGTACTGGGAACAAC
 TAAAGATAAACCGTTGTGCTGTGTGTGGCCGCGGCGGAAGATGACGATAACGAGCAGCATG
 AAGAAAAGGCAGCAGAGGGAGAAGAAAAAGAGAAGAAAATGGGGATGAAGATGAGGATG
 AAGACGAAGACGAAGATGATGATGATGATGACGACGAAGAAGAGGAAGAGAGGAAGAAG
 TCACTGATCAGTTGGAAGATTGAGAGAACATTTCAAGAACACGGAGGAGGGTAAGGCC
 TTGTGTACCACTACGAGGAGTGTGCTGAGAGACTCAAGATAACAGCAACAACAACCGGCT
 ACGGGATCTTGAAACAAAGGAGGACTGTGTGGAGGAGTTTTCATCTACAGCACTATT
 TGGACACTGCCACGGCACCTAGATTATTTGACAAATTAAAGTAG

>YFR033C, 147 aa (SEQ ID NO 156)

MQMLELVGEYWEQLKITVVPVVAADDDNEQHEEKAAGEEKEEENGDEDEDEDEDEDD
 DDDDEDEDEEEBEVTDQLEDLREHFKNTEGKALVHHYBBAERVKIQQQQPGYADLEHK
 EDCVEEFPHLQHYLDATAPRLFDKLX

>YCR086C, 1520 bp, CDS: 501-1520 (SEQ ID NO 175)

GTTGAATATTTACCAATTEGGAAAAAGAACTCGTATTTTCATTCCCCTTTTTTGAAGGGG
 TGGGGAGAGACTGTTGTTTACGCCACGTCAATTATTATTTTTTCTTTGGCCCTGCGCTTGT
 CTTATAAAATTCGGCAGCCCGCTCTTATTTTTTTTTTTTTCCATTTTGGCCCCACAGGTC

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ATATFGCAAAAACCGAATGGCCGCGCCCCCTCAGGCAUUGGACGGAAGAAAGGCGGCGT
 CCCCCTGTTTCTCTGCTTGGGCTCAGCTCTTGGGCTCCGACGGACGAAAGACGGGATCCCC
 CCTCCCGTGTCTTTTATAAATAACAAGTGCCTATTCTGCATCCTTCCTTGTTCCTCGTC
 GFTTGGGTACAATGCGTGTGATTATCCCAACCCAAAGAAAGAAAATTTGTCTCACATCTGCA
 TCTGCACATTTATTTACCTATACTTTTCCATTGTTACCAGCTATTGCAAAGTCAGAAATAT
 ATCAGCATCAAGTATATATCTATGCACAGAAGTTACTCTTTAAGAAATTCACGGGACCTTA
 CCGCTCTCAATTACAGAACCCACCGCCACCACCATCTACAACCAAAGGTAGATTCTTTTG
 GGAAGGGTGGTCTAGCTTACAGCTTTAGGACAAGTGCTGCTGGAGCTTTTGGCCCAAGAT
 TATCCAGAAAAGTTGCTCAATTGGTTAAGATTGAAAAGAAATGTTTGGAGTCCATGGAAAT
 TGACAGCCAAACGAAAGACGTGACGCTGCTAAGCAATTGCTCTATTGGGGGTTGGAAAACG
 ATCAGCATCTTTCCGACATCACTGATAAATTAGGTGCTCTTGATCTATGAAGTTAGTGAAT
 TAGACGACCAATTTATCGATCGTTATGACCAATACAGATTGACTCTTAAAGTCCATCAGAG
 ATATCGAAGGTTCTGTTCAACCATCTAGAGACCGTAAGGACAAGATCACCGACAAAATCG
 CCTACTTGAAAATACAAAGNTCCTCAATCACTAACATTGAGGCTCTGGAAACAAGPATTGG
 TCGTCTGAGGCTGAATCTTTGGTGGTGAAGCTCAATTATCTAATATCACAGGTCAA
 AGTTGAGAGCTGCTTTCAACTACCAATTGACTCCATCATCGAACATTCAGAGAAAATTG
 CTTTAATCGCTGGTTACGGTAAGGCTCTCTTGGAACTATTGGACGACTCTCTGTCTACTC
 CAGGTGAAACCAGGCTCTGCTTACGATGGGTATGAAGCCTCTAAACAAATCATTATTGATG
 CTGAAAGCGCACTGAATGAATGGACACTAGACTCTGCCCCAAGTCAAGCCTACTTTTAGTT
 TCAAGCAGGATTACGAAGACTTCGAACCTGAAGAGGCGAACAACAGGAAGAGGAAGACG
 GTCAAGGCAGGTGGTCCGAAGACCAACACACATCCACAAATTGAAGAACCTGAACAAG
 AAGAAGAAGGTGCTGTTGAAGAACATGAACAAGTCGGACACCAGCAAAGTGAGTCTCTTC
 CCCAACAAACAACAGUTTAA

>YGR086C, 339 aa (SEQ ID NO 176)

MIRTYSLRNSRAPASQLQNPPPPFSTTKGRIFGKGGLAYSFRRSAAGAFGPPELSRKLSQ
 LVKIEKNVLRSMELTANERRDAKQLSTINGLENNDDVSDITDXLGVLTYEVSELDQFCTD
 RYDQYRLTLKSIRDIEGSVQPSRDRKDKITDKIAYLKVKDFQSPKIEVLNQHGVRAEAEES
 LVAAEQLSNITRSKLRAAFNYQFDSIIHSEKIALIAGYGKALLELLDDSPVTPGETRPA
 YDGYEASKQILIDAESALNEWTLDSAQVKPTLSFKQDYEDFEPEEGEEEEEDGQGRWSE
 DEQEDGQIEEPQREZGAVEEHEQVGHQQSESLPQQTAA

>YGR197C, 2144 bp, CDS: 501-2144 (SEQ ID NO 185)

TCCAGTATGCCACACATTATGCCTTGACACCTAAAGCACATATTTTCGTTATTTTTTCAC
 CACAATAGGTGGATCTCGAAAAGGATGGAAAATCAGGAAAAGAAATGTTCCAGAAAAAAA
 TAAACCGATTCCCCTTTAGTTTTCTCCTATTTCCGCTGATATGCGTGGTTATTGCTTTTC
 GAATCCTTTTATGAATGTCCGAGGAGGTGATACAATCCGAAATAGACTAAAGAAAAGCGA
 AAGCCGTGAGTTTGTTTGATGATAGATGACTCCGAGCTTTGTCATCAACGGGCGACCCCTA
 TTCCAGAAGAGGAATGGAAAACGGACTGGCGTAGTCAATAAGCGTCTTCATATCTTAGCA
 TTGTTGAGAGATACATAGTGTACTCCATATCGTTCTTTTTTTTTTGTATATATCAAGCCAC
 ATATCCTGTTCCTTTAATCTTTTAACGCCGTAAAGAATCGGGTACTGACATAAGTGTAAAG
 TAGCCGTACAGAGAAACAATATGACTAATCGGTTGGTGTATGAAGACTCACAGTACATTTG
 AGGACCTTAGTTTTGCAGCAGCAGCTGCATTTACTGGCGGCAGGGACGGGGTTCTGTAQA
 CTAAATCAGCCATTTCTTGAGCGTTCCCGCCATTTCTTTCTGACTTAGCAAAGTCAATTGAAG
 ACTATCGGCCCTCTGATGAAAAGCCGTCCTCATTTGTCATCTGTGGCCGAAGCTGGCCCTA
 ATGAGGAAGACAAGCGCGGTAAAGACGGCGGTCCCTTGGCAAGAATTCAAACAGGGCTTT
 TTTCTCCAAGACTGCGAAATCATAGGAAAAGATTCTCTCGAAGTTTGTTTTGAACAACCT
 TCTTCATTGCTTGTGTGTGTATCGCTCATATCGATTACTGGGGTGCCCTCTTACGGAA
 CACATCCTTACTTTTTCAAAGTGAATAATATGTTGTATTGCAGGATGCGCCATCTAATA
 CTTCAGTTCAATCTATTTCCGCGATCATACCTCATTTGTTAGCGTCTGTCCCGGAGACAT
 GGCATATATACAACGCAACATCAATTTTCATAGGAAATTTGGTACGACGAATCCACCGAAA
 TTGACAGAAAGATAGTCGATTTAATTTACGATGAGAGATACTGGCTGGCGTTAAACGTPA
 AACCTAATGCTACAGACACTTTGTATAATTCTTTGATTAGCCAAGACGCAAACTCGGAGT
 TCAATTCATCAATTTTTTTTGAATCCGTCTTTGAAACTGGTGGTGACCCATCGAGTGTTA
 AATCGACATTTCTACCACCTCATGCAACAATTGAGGTCGGCTTCAGAAATATTACGTCA
 AGGAATATCTTCCCTCATTGATGAGCAACATCACTTCTAATGACAGAGATCTTAATATAA

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ACATGGGAGAACTGGGUGATTGCAGGACAGTTGTGTTCACCTACAACGATTATCGTCCCT
 TTGCTGATCGTATTCTAATGGCCCCCTCTGCAGGTCGGTCTGATTTATTGTATTTTGTAA
 CCGCTTTACAACTGTCATTATATGGTAAGCTGCACGGAGAAATGGCCAGAGTTCTGAAGC
 CAAAGCATATTTAATCTACAGGUTTCFAATTTCCCTGGGCAACTATTTTCTTCTTTCCA
 TTGGATTCTGTACCCTATCTGCAATTTTATAGGATCGATTTCACCCCCGCCCTTTGGCAGAG
 GAGGATTGCTAGTATATTGGATGTCTACGTGGTTGCTAATGATGGCTCTTGGTGGTGCCA
 ATGAAAACCTTCTCAGCTTAGTTATAGCTTACTGCCCTCCATACCTCAGTATTTGSETTGA
 TGACGTGGATCATATTTAAATATTTCTCTCTTCATTCTACCCAATGGTTTTGAACAACGAAT
 TTACAGGTTACGGCTACATAATGCCAATCCATAATGCCGTGGATATCTATAAAGTGAATTT
 TTTTGAATTTTAAACAAAAGAAAAATGGGAAGAAATTACGGTATTCTCGTGGCAATGGGTTG
 CCGTCAATACATCTTTGATGCCATTTTGTATGAAGTTTGCAGGTAAAAAATGCAAAAAA
 ATGCTATGCAAGCAGCAGAAGCCGCTGTGCGAGCAGCTACCCAGCGTGTAGTCCCCCGG
 CAGAGGCCAATACTGATAAAAAATAACAACCCGCCCGGAAATTAA

>YGR197C, 547 aa (SEQ ID NO 186)

MTKSVGDDEESQYLRPSFAAAAAFTGGRDGVSYSNQRFAEGSGHSSDLAKSLEDYRPPDE
 KPSSTSSVGEGCANEFKGCNDGGPLARIQTGLFSPLRLNHRKKILSKFVLNNFFIACVC
 VSLISLYWGACYGIDRYFFKVKNIIVVLQDAPSTSVQSSISAIIPSLLASVPGTWHIYNAT
 SFHRKFGTTNSTEIDRKIVDLIYDERYWLALNVKPNATDTLYNSLSQDANSEFNSSIFK
 KSVFESGRDPSSVKSTILPLMQLEVRLOKYYVKEYLPSLMSNITSNDRDLNINMENWAL
 AGQLLPYNDYRPFADRIILMAPLQVGLIYCILLTVLQISLYGKLHGEMARVLKPKHILY
 KLLISWATYFLLSIGPTVSAIFRIDFTPAFGGGFVVYWMSTWLVMMAVGCANENVLSL
 VLAYCPPYLSIWLMTWILLINISASFYFVVLNNEFYRYGYIMPIHNAVDIYKVIPLNLTKR
 KMGRNYGILVAVVALNTSLMPFCKMPAGKKMQKNAMQAAEAAVAATQRASRPANNTDK
 NNNPPGN

>YGR250C, 2846 bp, CDS: 501-2846 (SEQ ID NO 191)

TCTTGTGTACGTACGATGTTTCTCCCCGTGATCCGATTACTAGCCGAAGACGTAAAAATTG
 GCGCTTGATTCAATTTATGCCCTTCCCGGAATAGTTGACCAAAGGGCAAAAAAATTACAG
 TCGGAGATTCCCTATTGCGCGGAATTTAGTAGATCTCTTTCCGTGCATAACCCCTGCCCG
 TTAGTCGTTATTTACGTTAACATTTTCTTGCCCACTGCGCTATATAAATAAATACATAT
 ATATATGTCAAGCACATAAAGAAACTTCCCTTAAATATTGAATAAGTAAATAATAGTTG
 AAAAGTGGCTTTTGTTCGAAGGATTAGAGTGTCTTAATTTTAGTTCTGTTCAACGGTCTC
 AAAAAAGTGTGAACAAGTAAAGCATAGCACATCCCAAATTACAAGGCACCCCTGATTA
 AAAATCCAAAAATAAACCATTAATTTTATTTTACTAAAAACATTATACGTGAAAGACAAA
 CCGCATCAGAAGTTTCGAGGATGAATATTCCAGAAGAACCATCAGATGAAGTAATATCTA
 GTGGCCCCGAGGATACAGATATCTGCAGCCAGCAGACATCAGCGAGCGCAGAAGCTGGAG
 ACCAATCAATAAAAAATTGAAAGGAAAACCTCCACTGGTCTTCAACTGGAACAATTGGCCA
 ACACAAATTTATTAACCATTAAGATTAATATGGCAGTTACAAAGAAGAAGAAGATGATCACT
 GCAACTCTAGAATAACCGATCAATAATGGACACAATACAGCACTACAAAGGTATCTCCG
 TTACAACTCTGATACAGAAACATATGAATTTCTTCCGGATACAAGGAGGTTACAGGTTT
 TCCAAACAAAATAAAGACATCTATCTTTACGAGCATGGAAGTCAAGAGTATGAGAAATCTT
 ACAAGGATAACGAAGAGGAAGATGATTTGGAGATACGATACCGTTTTGCAACCACAAATTC
 AGTACCCCAAGTCATTAGAAAAATGCATGTAACAGATATCTCGGAATTACTCAAGAGCGAAC
 CTATTTGGTCAGCATATTGATAAATGGTCTATCGGTCTGMAACAAGCATGCCTAACCTATC
 CTGGAAATATTTTGTGCGCGGAATAGCAAAGACCCCTTTCTATTCCCTCAACTAAGTTTCT
 TATTTTCAAAATATGGACCAATTTTATCAATGAATTTGATATATGATAAAACGAAAGGCG
 AACCTAACGGATACGGGTTTATCTCTTACCCCTTGGGTTCTCAAGCTTCACTTTGCATCA
 AGGAACCTAATGGAAGGACCCGTAAATGGCTCCACACTATTTATCAACTATCAGTTGAGC
 GAAAGGAGAGAGAAAGAATCCATTTGGGACCATGTCAAAGAAACAAACATGATGATAAAT
 TCAGGTGTCTCTTTATAGGCAACTTGCCTTATCAAAATCCTGAAAAAGTAGAGACTTTGA
 TTACACCTAAAGCAAGTCTATCAAGTAATCAAGAAAGAGTTATCAAAAAAGTTTCCCGGAC
 TTGATATCATTTTATATTACTTTCCGAAGAGAGTAATCAAGAAAGCAGTACGTTACAGTAA
 GTTTCAATGAGGAGGGGTCAGTAGAATCAACAAATCTTCCAATAATACTAATGGAATG
 CCCAAGATGAAGATATCTTGAACGGTTATGGTTTCAATCAAGCTTATCAACCATGAACAAG
 CACTAGCAGCCATCGAGACCTCAATGGGTTTATGTGGCATGGAAACAGGCTCGTTGTTA

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ATAAGGCGGTTCAACATAAAGTTTACACAAACCACAATAGCCATGACAGGCACCCCTTCCA
 TCAGTAACCACAAATGATATGGAGCTTTTGGAAATTTGCAAAATAACCCAAATGTATGATTACA
 ATAATTATACATATGATAGATATTACTTCAACAATAATAAAAACGGGAACAGCAACCATA
 CCTCCAAATGTACGG/ATTTTGTATTCTGTAAAGATCAACCCCTGTGGCAGAGAAAATGGATC
 TGTTCATATCCTCAAAGGGGAATCTTTCAAGTGAAGGTCGTGCTCAACGCTGCCTAGATTCA
 TGGGCAACAAGTTTGACATGTACCAGTACCCATCAACTTCTTACAGCTTACCTATAACCAA
 TGAGTAATCAGCAAGAATCAAAUCTATA/GTCAAGCACATCCCTCTTCTTTCGACAGATG
 AAGATTTATATGATTTCTACAAATCTTTCCGGTGAAATAATCAGCGTTAAGGTCATTACTG
 TTGGGGGTAGTAAGAACAAGTATCGTCAACAAATCGAATGATAGCTCATCAGATAATGATC
 TGCCAGTGGGATCATCAAGAGGTTATGGTTTGTTCCTTTTGAAGCCCATTAAGATGCTG
 CTAAGCCAAATTTGAATACAGACGGGTATCAAGTGAGCAAGATCAAGTGTATCTGTTT
 CTTTCGCTCAGAAACGTTGGTAATTTATCTTCAAGTCATCATCATCAATCCCCAACTC
 ATAACTATCAAAAGTTCCAAAATTTTTCAGCCACATAATGATTATCATAAGGCTTATCCAA
 CAAAGTATAATAAGAAAATCTATCAATGCCCTTGATGACTTACGAACCAATCCCAACAGCAAG
 TCTCGAGGGGAAAATTAATTCATACCACATGCAAGTACCCCTAATACCAACACAAAGCCCGTGA
 ACAGTTACAACCTAATAAGTGCAACCAAAATAACGCTAACTGGATGATGCCAATGTTCC
 CATCATTTGGGTTTATTCCACAGGTGCCGCCAGTCCCTATATTAATACTCCGCAGAAATC
 CTGCAGCAAAATCATATTCCTATAATGGCAACCGTAGTAATGAAGAGGAAGAATTTTCTA
 GTGGTGATTAATTTATGGACACTAG

>YCR250C, 781 aa (SEQ ID NO 192)

MNIAEEPSDEVISSGPEDTDICSSQTSASAEACDQSIKIERKTSTCLQLEQLANTNLLTI
 RIKWQLQEREDDHCHNSRITDQIMDTIQHYKGISVANSDDTETYEFLLPDTRRLQVLEONKDI
 YLYEHC SQEYEKSYKDNNEEDDWRYDTVLQAQPKYPKSLENACTDISELLKSEPIGQHID
 KWSIGVNHALTYPGNIFVGGIAKSLSIGELSFLFSKYGPILLMKLIYDKTKGEPNGYGF
 ISYPLGSQASLCIKELNGRTVNGSTLFINYHVERKERERIHWDHVKENNDNDFRCLFIG
 NLPYHNPEKVETLITPKEVLEVIKKELSKKFPDFCLISYFFPKRSNTRSSSSVSFNEEGS
 VESNKSNNNTNGNAQDFDMLKGYGFTXILNHFQALAAIFTFNGFMWHGNRLVNVKAVQHX
 VYNNHNSHDRHPSISNHNDMEVLEFANNPXYDYNNYTYERYYPNNNKNNGNSNDTSNVRYF
 DSVRSTPVAEKMDLFYPQRESFSEGRGQKVRPRFMGNKFDMYQYPSTSYSLPIPMNQQES
 NLYVKHIPLSWTDEDLYDFYKSFGEILSVKVITVGGSKNKYRQSSNDSSSENDLPVGSRR
 GYGFSVSFESPLDAAKATLNTIGYQVSKDQVLSVSFAQKRGNLSSDDDDQSQTDNSSKFQ
 NFQPHNDYHKAYPTKYWKKFINALMTQNSQQQVSSENYFLEPLQYPNTNTKPVNSYNTLS
 ANONNNANMMMPNPFPSFGFIPQVPPVPYLIIPPQNPAANILPLMANGSNEEEEFSSGDYSMD
 Y

>YHR001W-A, 797 bp, exon1: 501-506, intron1: 507-569, exon2:
 570-797 (SEQ ID NO 195)

TTCTATTCGGCTTATAAAAAGCAAGGAATCCAAAAGAAATTAGGCTTCTCATTTCTATTTT
 AATTATACTAGTACGATTTCTCACTCTGTAAATTTAATATCAGTGTAAATATGCACCTAGTT
 ATCGGTAGTTTTTGCTAACCTTACGAGCCGCGAAACTGTCTCAATCTTCACCACTACCT
 CTAATGACTGAAGAATGCTATGCCGATATAACGCTGTCCGACTTGAATATATACCTTAAT
 TTACATAGTTTTTCAAGTGCGTATTACCTATTGCAAAGTAGTAATTTGTUACGTGATTTTGA
 TCCAATCAAACTAAATATGGTTCAACCCGTTGTTTCCGCATCAAAAAACCATACCATTT
 ATCAAGGGGACGGGATATATCACATAACAGTTTGAAATGCATAAATTTGTATAGATATKTT
 CTGGAATAATCTTCACAGCAAAAGCGCAAGTCGAATAATATATCGATAAATACAATCCAT
 AAGACTTAAACTAACCTCAATGGCGGTAAGTATCCTATCATATTTATGTGAGCTAGAACC
 GAATTAGTATACTAACATTTATAATACAGTACACTTCTCATCTGTCTTCAAAAACCTGGTC
 TACATTTCCGTAGACTTTCTTTAAGAAGTTTACAGCTTATGCTCCGAATTTAATGTTAT
 GGGGTGGTGCTAGCATGCTTGGGCTATTTGTATTCACAGAGGATGCCCTAACCTTTCAAC
 ATACGCTATACAAAAGATTCGGTTGTTAGGACCTACATTGGAAGATCATACTCCACCAG
 AAGATAAAACCTAATTGA

>YHR001W-A, 77 aa (SEQ ID NO 196)

MAYTSHLSSKTGLHFGRLSLRSLTAYAPNMLMWGGASMLGLFVFTGWFKEQDTLYKKIP
 LLGPTLEDHTPPEDKPY

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>YJL142C, 893 bp, CDS: 501-893 (SEQ ID NO 225)

EGCTGAATTAATTTTGGGTATACCGATCTTCCCAGGCGCTTCTGAATATAACCAATTAAC
AACAAATAATACACCGCTTGCATATCCTCCATCGTGGATGATAGATATGGGTAAAACTC
TGGAAAATTTATGAAGAAATGGGCACCAGAAGAAAGTTCTTCTTCTACACAAAAGCATCG
TATGAAAACATATTGAAGAGTTCTGCAGAGAATACAAATATAGTGGAAAAGCCCAGTAAACA
ATATTTTAAAGTCCAGAAACATTACCAGATATTTATTAGAACTACAGGTATCCTAAAAGCAT
ACAGAAGTCCCAAGAACTTATCGACCAAGAAATGCAGAATAGGGAGTGTTCATCCACTT
TTTAGGCGGTGTGCTAAATTTGAACCCGTTAGAAAAGATCGACACCACAACAAGCTATGCT
ACACCCCTTCAATAACAAAGCAGGAGTTTACAGGTGAGTGGTTTCTCCAGGATCGTCTTT
ACCGGGTCTCTCAGAAAACATGACGATGCAAAAGGCCAGCAAGTGAATATGGAAGTGC
GAACGACTCTAATAACAAATGACAGGACACAACTATGCTCTATAATCTTAGCTCTGCCACTGG
TGGTGTCTGATAGCGTCCGACATTTGGTGGTATCAGTAAAGGAAGGAGAATACATCTGGCGA
CATCTCCAATAAATTTTGGTGTCTTACTCATCTCTGTTCCAGAAAGGCCCAACAAGCCCGTTCAA
TAAACTTCACATTTGTCGAAGAAATAATCGTTATTTTGTCTGACTTTTCTTAAGTACCCAT
TTCATTTTATTACGGCTTGGTGGCATAATGATATACTAAATAAATATGAATTTTGGCTTT
CTTTAAATTTCTTTATACGTATAGTCAATACAAATTAATAAAGTAAACAATATATAA

>YJL142C, 130 aa (SEQ ID NO 226)

MTMQKASKVNMEVRTTLVTMQATTMSIILALPLVLIASTLVLSVKRRRIHLATSPIILL
LLILFKKQQARSINFLLSKNKSFLCLPLNYPHFITAWCHNDILNKYEFCLFLIFLIR
LVITINKVTL

>YJL144W, 815 bp, CDS: 501-815 (SEQ ID NO 227)

AGAAAGAAGTTCTGTGGTATTAACCGACGGCAGCAAGTTGGGTCAATACTTGAAAGCATTCG
CCATATGAAGGGTATGUGUGGGAAGATAAGAAGAACAATCTGAUCAAAGCAAAATGTCACA
AATGTCCATCCAACAGAAACACGGCCTTTACATTTTACAAAAACAAATCATCCAGGACCTT
GAGTCATTTGTTGGCATGATCTAATAATAGTCTCTTATATAAACCTTATAATAATTTCTT
ATTTTTCCCTTATATTACAGTAAATCACCATCTAACTGTATTATCTCTCAGGTACTCTTCA
CTTATATGGCTCAGAAAACACCGTACGAAACGAAGGGGCTGGGAAAATGTTTCTAGAAGG
TAATGGCAATAATACGGGATACAGATCCGATCAGATCCGCTTATATAAAGACAACGCACCG
AAGGTGAACAAGATCGCAGATAAAGGTATTTACAAGGGAAAAAAGTCAACAAAAACAAGA
GATAAGATAACAGAGAGAGATGTTAAGGAGGGAAACTTCAACAATATACAGGACACACA
AAAAAAGCAACAGTAGTATACTCAGGAGCCAGCGGGACCAGACTAGAGTGGATTCTCTGG
TAGAGGAGTCTCCCATGGCGATTTCGGGATCAATAACCAGCTTACACAGCTTCCCGTGA
TATACTACTTTGTAGAGCTGACTAATTTAGGCATACAGGAAACACAAGCAGTAATAATA
ACAACAACAATAATCATGGTGACGATGAAAACGGCAGTCCGATACGGCCACGGCAGCAGTC
TGGGTGCAGACCTTCACTCTCGCCCTTCTTCATGA

>YJL144W, 104 aa (SEQ ID NO 228)

MLRRETSTIYRTHKKSNSILRSQRDQTRVDSLVEESPMGLFGINNQPTQPGVIYYFVZL
TNLGIQENTSSNNNNNNNHGDDENGSRYGHSIAGGVHSHRCSS

>YJL166W, 785 bp, CDS: 501-785 (SEQ ID NO 231)

TGAACAGCTATACCACGAAATGAAGAGTCTATTTGCCAAGGATTTGAAGGCCAAAAATTC
TCAGGTCCATGAGTCTCGTGGCTTCAAAGCTGATGCTTAACTGCGTTCTTGAACAAAGT
TTACAAGAGAAGCAAAATGAACCTAACGCTAATCGATAAACAATTAGATTTCAAACTAGAT
AAGGACCATGTATAAGAAGTATATACCTCCAAATATAATATAGTATAAGCTTTAAGATAGT
ATCTCTCGATCTACCGTTCCACGTGACTAGTCCAAGGATTTTCTTTTAAAGCCAAATGAAAAT
GAAGAAAATGUGTATCGGAAATTAAGGGTAGTACGAGAAGGAAATTTGAGCCACCCCCCA
AATTTTATTATATAATAATAGGAAAAGCAACGACCTCATCTCTCGAACATTGTTTACTT
GAGCAAGTCCGATTAAAGAGTAACTTCTCGTACGTTAAATACAATAATCAACAAAACACT
ACACAAAAAATTTCTACGATAATGGGTCTCTCAAGCGGTAAACCTTACATGGGATGGTGGG
GTCACATGGGTGGTCCAAAGCAAAAAGGTATAACCTCATATGCTGTGCTCTCCATATGCTC
AAAAGCCATTACAAGCTATTTTCCATAACCGTGTATTCAATAGTTTATAGAAGATTAAAGT
CTCAATTTCTATATGATTAATACCTGCGGGAATTTATTGGTACCTGGTGAAGAACGGTA
ACGAGTATAATGAATTTCTGTACAGCAAGCTGGTAGAGAAGAGCTGGAAAGAGTTAATG

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TTTAA

>YJL166W, 94 aa (SEQ ID NO 232)

MGPPSGKTYMGWNGHMGSPKQKGI'ISYAVSPYAQKPLQGIFINAVTNSFRFRFSQFLYVL
IPAGIYWYWKNNGNEYNEFLYSKAGREBLERVNV

>YKL117W, 1151 bp, CDS: 501-1151 (SEQ ID NO 247)

TTATACAACCTGTTTTATGTTTTAAAAGAGCTTGTATAGTAATCTAAGTGGAAATACACT
AACAGTAAATAGGGCGTGTGGCGTAGTCGGTAGCGCGCTCCCTTAGCATGGGACAGGTCT
CCGGTTCGATTUCGGACTCGTCCAACTCTTTTATACU'ATTATTAATAAT'TTTT'P'CCCTGCCG
TTACTTGCCTTTTAAAATAACTGCCCTTTATGAATACAGAGTATAATTTTGTATATACAAA
EAGGTTGACTGTGATAATCAATACTTAATTTGTGGTTATTGTTACACATATACCTACAAA
AGTTACCAACAACCTGTTUGACTTTTAATGCTACCCGCCCTTCCGAGTGT'TTTTGAAGGGG
CCGACACCGAGCGGCAAGAATTAGCATGGAAAAAAGCATAAAAAGACCAAAATCGGTGGCAA
TGTA'TTAACTTGTTTCGAGAAACCTAGTGGACTCAATTCATTACAAACAAGTTCCCAAG
ATCATCGATTTCATAATAGTCATGTCCGATAAAGTTATTAACCCCTCAAGTGGCATGGGCTC
AAACCTCTACTACTACTGATCCAGAAAGAAATTATGTCTTAATAAAGTGTGTCAACTGCAG
ACTGTGATGCCCTGAGTCAACCAATTAAGCCATCATACATCGAATTAAGGCTCAATCAA
AGCCTCATGTTGCGGATGAAAATGTUATUAT'PAICAA'PACACAT'GATCTATACAAAGG
AAATTAACCTGAAAAAACAAATGCATAAGGTTCCTAATGGCCAGCACTACT'TTTTGAAAT'
TGTATAAAAAGGATTTAGAATCTGAATACTGCCACGTTTGACAAACGAAAACCTGAAGT
ACCCTTACATCAAAACTGATTTCGATAAATCGGTTGATCAACATCAACACACCAACTTC
AAGCTGAAGGTAATGATGCCGCTCAAGGAATGGATTTACGCCAAATGATGGGAGGTGCTG
GAGTTCCTGGAGGTGCTGGAGGCATGGACTTCAGCCAAATGATGCGAGGTGCTGGTGGCG
CTGGTTCTCCAGATATGGCTCAATTCAGCAAT'TATTTGGCTCAAAGCGGTGGTAATTTGG
ACATGGGAGATTTCAAAGAAAACGATGAAGAAGATGAAGAAGAGGAATAGAGCCCGAAG
TCAAACCTTAA

>YKL117W, 216 aa (SEQ ID NO 248)

MSDKVINPQVAWAQRSSSTTDPERNYVLLT'VSLADQDAPELTIKPSYIELKAQSKPHVGDE
NVLHYQLHIDLYKEIIPEKTMHKVANGQHYFLKLYKKOLESEYWPRLTKEKVKYPYIKTD
FDKVVDEDEQDEVEAEGNDAAQCMDFSQMMCCAGGAGGAGGMDFSQMMGGAGGAGSPDMA
QLQLLAQSGGNLDMGDFKENDEEDEEEIEPEVKA

>YKR075C, 1424 bp, CDS: 501-1424 (SEQ ID NO 257)

TTCAACAGAAATGCCGTAGCCGGAAAAACCGAAAGCGGGGGACAGTGAAGCGTGAGAGGG
GCCAGACAGUGGGAACCTTGAATGGGGTATTTTGTCTTTTGC'CGCATTTT'P'CCGCTGGTAC
CTCTATCTTTTAGGCGACCGGAAAAATTCATTTTCTCATCTTT'PP'TTTTTTTTCTGTTCCG
ACTCGATACTCTTTTCAAAGAAACCCCCGCGGGGAATGTTAGATTTGAGCTTTTCCGC
CAGGAAAAGAAAAACCTGGGGACATTAATCTTTGTTTTTCTTTCTCTTTTGTCTCTCC
TTGGATGACTGCAGAAAAAGTACAGTTACCGGCTCTTAGCAAAAACAAACATATATATAT
ATATATATGAAGCGTATGGTCAACACGGTTTTATAGGTTTTACTTTTGCATTCAAGTTC
AACTTTCCSCCTTTCTCTTATCGCATTCAGATACTACACACAACTGTTTCATACACACACA
AATAGATACATATACAGAAAATGACTAGTTTGGACGATACAATAATTTCGTACCAGAATA
TAATGTTACTGGATAACATGACCAACTACAACAAGCCTGCGATTGACTATTTCCATCATG
AATTTAATGATGCAAGCTTCCAAACATCGGCTTCATGGACACTACTATTCAGATGCCCA
AACATAAACTACTTCCGATTACCAAGTTGCTCTTCAGAGGACGTGCTAGATTACAACATGT
ACCTCGTTAGGCTACATCATTTGCTCTGGAGGCGTTGGTCCATAAATCACTATGGTTTAC
ACAACTCCAAATCCAAATCCACTGTCCATCAACTGGAACAAAGAAACCGATGTAACGGTGT
TGTACGGTCCAGATTTGACTAACATAGATAGTAATGAAAACGAATATCGCCGGTCCAGA
ACCAAAATTGACCAGAAACAAACAAAAAATCTAAAATCTGCTTTAAAGAAAAATACGGAAT
GCTGGGTAAACCGAGGAGGTGGATGAGATTAACGCTTCTATAGACAGCAATGACAACGCTT
TGGTGAATTAGAAGACATTTTATGCUCA'CGTCTGT'GT'GAT'P'P'UACACGTC'P'CCAT'P'
TUGACCAAGCATTTCTACATGCACTAAAATTTCCCTCCATAGATGAAGATTCTGAAGACCTT'A
TGAACGAAAAGAAGGAACAATTTCCCGAGGAAGTTGAAGTTTAAACCAAGCCGTGATGAAGA
GGAGATCGACTCAAAGGGGACTATCCGCGAATCCCTCATCAACATAAACGATATCCAAC

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ATTCGCGCCACCATCGCCGTCACCATCGTCGCCATCATCACCATCACCATCAAAATAGTT
CTCATTTCTGATGAAACAATAAAGGAAGCTCATTTATGAGTTGAGCAACTATACATTTGGCA
CTATCGAAGACACATTTTTTATAGGAACGAGGTTGTTTTTTAA

>YKR075C, 307 aa (SEQ ID NO 258)

MTSLDDTIISVQNIMLLDNKTNYNKFAIDYFHHFNDASLEISASWTLILLKMRKIILRL
PSCSSSDVLDYNYMYLVRLHHCLWRRWSINHYGLQNSKSNPLSINWNNKETDVTVLVYGPDLT
NIDSNENEISPVQNGIDQKQTKNLKSALKKNTFCWVTEEVDEINASIESNDNALVKLENY
SCPSSVDSHTSSIFDQHSCTCKISSIDESEDLNNEKKEQFPKRLKFNQAVMKREIDSKG
T4RESLININDIQHSRRHRRHHRRHHHHHQQSSHSDETIKEAHYEFSSNYTFTGTMEEDIF
YRNQVVF

>YLR216C, 1616 bp, CDS: 501-1616 (SEQ ID NO 279)

GAAGAATACAAAGAGGTCCAAGAAGACGAAGACUUGGATGTGTGGGACACGAGAATATCC
AAGACCGGATGCTACGTAGAGAACCTCGCATTACAGCTGTGCCATGCCGAAACAGGTGAC
TGGAGGCAGTGCTTCAACGAGATGGCGTTATTTAGGAAGTGTGGGAAAAGAATGGTAAT
AGAGAGCGCGTAAGCACAGTGGACGTCCATGGGACGACCAGTAAGGATTCCGAAAAGAAG
AAATGAAAATCTAAATCTCGTGATCTATAACTTGATATAATAGACAGCTGCAAGTGATCG
AAACACATTTGTTTCCCTTTATAGAACATAACTGTTACCGCTTTTGAACGGCATTTCATGA
GCTTCTAGAATATTTTTCCGCCCTAGCTGGAGAAAGTTCAGACAGAAAATTATTTAAATA
ACTCCAATATCAGAGGTGCTGATGCGCTCACATCACATAGAAAACCTGGTAAGACAATACT
CAGGCCATCAAGGACTAAATAATGACTAGACCTAAAACTTTTTTTGATATTTCTATTGGAG
GTAAACCCCCAAGGCCGTATAGTTTTTTGAGTTGTACAAATGACATAGTGCCATAAACCGCTG
AAAATTTTTTGAAGTTGTGTGAAGGAAATGCTGGPATGGCAAAGACTAAAACCTGATGTAC
CATTTGTGCTACAAGGGTCCATTTTCCACAGAGTGATCAAAGACTTCATGTGTCAATTTG
GTGATTTTACCAATTTTAATGGTACTGGCGGTGAGAGCATATACGATGAAAAATTCGAGG
ATGAAAAATTTACATGTTAAACATGATAAACCATTTCTTCTATCCATGGCCAAACCGCGGT
CAAAATACCAATGGATCTCAAGCTTTTCATAACCTGTGTTCCTACACCTCATTTGACCGGA
AGCACCTTGGCTTTGGTGAAGTGATTCAAGGTAAAAAGAATTTGTTCTGTTGATTGAAAAAC
AACAAATGTGACCAAGAAAACAACAAGCCATTGCGTGATGTAAGGATTGATGACTGTGCGC
TGTTAUCTGACGATTATCAAGTGCUAGAGAATGCCGAAGCTACACCAACACAGATGAGTACG
GCGATAATTTACGAAGATGCTTTAAAACAAGACGAAAAAGTTGACTTGAAGAATTTGACAC
CCGTCTTGAAAGCTATCGAAACGGTAAAGAACATTGTTACTGAAACAGTTCAAGAACAGA
ACTATTTCCGTGGCTTTAGAAAAATATGTCAATGTGATAAATTCTTGAAAGAGTATTTCC
CAGAAGATTTGGAGAAGGAACAAATGAAAAAATCAATCAATTGAAAGTGTCATTTCCAT
TGAATATTGCCATCTGTGCTCTTAAATTAAAGATTACAAGCAAGTATTAGTAGCCTCAT
CGGAGGTGTTATATGCCGAAGCGGCTGACGAAAAGGCCAAGGCCAAAGCTTTGTACCGTC
GTGGCCTGGCCTATTACCATGTTAATGACACAGATATGGCTCTCAATGACCAGAAAATGG
CCACTACTTTCCAGCCAAATGACGCTGCCATTTTGAAGCTATTCATAATACTAAATTA
AAGGAAGCAACAAAACGAAAAGCTAAAAGTCTCTTTGGAAGATGTTCTCTCTGA

>YLR216C, 371 aa (SEQ ID NO 280)

MTRPKTFDFDISIGGKPQGRIVFEIYNDIVPKTAENFLKLCEGNAGMAKTKPDVPLSYKGS
IFHRVIKDFMCQFGDFTNFNGTGGESIYDEKFEDENFTVKHDKPFLLSMANAGPNTNGSQ
AFITCVPTPHLDGKHVVFGEVIQGKRIVRLIENQQCDQENKPLRDVKIDDCGVLPDDYQ
VPENAEATPTDEYGDNYEDVLKQDEKVDLKNFDTVLKAIETVKNIGTEQFKQNYVALE
KYVKCDKFLKVFPEDEKFEQTEKINQLKVSIPLNIAICALKLDYKQVLVASSEVLYAE
AADEKAKAKALYRRGLAYYHVNDTDMALNDLEMATTFQPNDAAILKAIINDTKLKRKQQNE
KAKKSLSKMFS

>YLR346C, 806 bp, CDS: 501-806 (SEQ ID NO 289)

CTTATCTCAGGGTACCCATAATTTCAACCATCUTTAGCTTTCATTAATAACACAAATGAGT
TGCCCTTACTAGCCAAACCGGCTTATCTGTTAATCTTGCTTGCAACATCTTAGCTGAAAG
TGAAAAGGCACAGCGCACCTGCTGAATGCTCAACGTTTTGTAATAATCCGCCTATTTCCGC
GGAATCAATAGGGCTCCTAGCAGCGCCCATCAATTTTACGCTGCCCATTAATAATAT
ATTACCAAGATTTTCATTTCCCGGCTCATTCCTATCAATATTAAGTAATCAATCTTTTC

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CTCGTGATTCTTGTGATGCTCATTACAGAGGACTAATTAAGACATGTAGCACAATATA
 TTCATATAAAAGTTGGTGACAGTTAATGATTAATTGCAATTGTTTTCCTTGTTCCTTCTGT
 TATACCTGTGCAATTAAACATAAAGTGTATATGAATTTTAACCGGCACAAATAACAAAGG
 ATTATTTATCACCTTTAATAATGCAATCGATCAGTAATTTGCCATCCGCTTAGTTTCAA
 AAAACACAATCAATTGAGCTTCCACTATTGACAGAGTGGGTAGCATGTCCATGGAAATATA
 TCAACGTTGTTGGTTCAGGCAGATATGTCAGCAATAAACCTCATATAAATTACAGATATG
 ATTTACTCAAGGCTGCCAGGAAGCGGAAATGCAGGAGTTGCTTACAAGAAATGATATGA
 AAGGTAGACATAAACGTAATAAGAAAAGTAAGATAGCATTCGAGACTATACCCGAAGAAA
 ACTCTTCAACTCAAAGCCTTTTTTTAA

>YLR346C, 101 aa (SEQ ID NO 290)

MQSISNCPICLVSKNTINSASTIAEWVACPWKYINLVGSGRYVSNKPKDITRYDLLKAAQ
 EAEMQELLTRNDMKGRHKRNKSKIALETIAEENSSTESLF

>YML129C, 713 bp, CDS: 501-713 (SEQ ID NO 297)

TAATCAACTTGGCCAAGCAGAAATACGCAATGGTTGTTUGGCACTGTAAAGGAGCCTGCCTT
 ACAAGAGGTACCTACATAACGTTAAAAACTGGTCGAAAAGCATATTAGCGTTCAACPAAT
 GATTGGGGTGTCAACCTAATGTACTTTTCTCCCAATTTTCTTTTCATCCGTATATTTT
 ACCCTAAAAATCGACAAGCTAATAGCAAAACGAAAAACACCGTTGTCACTTCTATATAACT
 TTGCTTAAGTAAGTATTTTCTTTTAAATGTTACATACTGTGAATACACTCTTTAGAA
 AACACTATTTCTTCACTCTUGGAAGCAGATTTCGAAGTACTTCTTACTTCTGAGCTTTG
 CTTCTCTCTTCTTGGGATTAAATGTTACCGCTTATACGAAATCGGAGAGGATCAGAAATAA
 TGCATTGAAAGGAGCATAACTCTATACAGCGCTTTCGCAATGCTCAGAGCAACAGAACAA
 AAAATAGAACGCAGATAGTCATGTCCAAATACGCTTGGTATACCAGAGTTACAGATACAT
 TACATCGTCTAACGGTACTCACGTTGGTTGGTTGCTACGTTATAAATGTCGGGTGGCTTAG
 CTTACACTTTTATACATGAACGGTAAGAAGTACGPAACAACAAGTGACCCAAACAAAAGCCAC
 TTGAAGAAGACAATCAACAACCTGCAAAGTCCTACTGCACCTCCTACCGAGTAA

>YML129C, 70 aa (SEQ ID NO 298)

MSKYAWYTRVTDTLHRLTVLTLVGGTLYMSGGLAYTLYMNGKKYEQQVTQQKALEEDNQ
 LQSFTAPPTE

>YML132W, 1640 bp, CDS: 501-1640 (SEQ ID NO 299)

GTAACCTGGTTCTATCAATCTTCATGTACAGATAAGTAGGACAGACTCTTTCCCTGTGTAAA
 TATTITGIGACAGCTAAGTCTATTTTCTACTAGATGTTTACACAGTTTGTACACAGGAAAT
 CTACCGCTTAAATATGTATTTCAATCAAGCGGTAACCGCTGTACGAGCAGTGACATTGCT
 GGTGCGCACCCCTAAATGTGAACCAACGTCACGGCACACCGTGATGTACCCGCTTAAAGTTT
 TTGTAAATTCGTTATTACGATTATCGAGTTGGCTAGATAGAAAACCGGAAATGTAATGGA
 TGCCCTTTTTCGAATAGCTGAGTTTCTTTGCCTAAATAGCCCAATATTGTTGCCCTTTT
 CTATCACGAGGTTACTGAGCCATTGCATGAACCGCGCGCCCTCGCGCGCTTTTTTTTCT
 GCTGTGCTGTATAAAAGCGAAAAGCCAGAAGTTACTATCTCGAATAAAAAACCCCTCGAA
 CTGUCATCTCACTACCGAAAATGAAACGGAATGAACCTTAAAAATGGAAGAGTGTAGATG
 TATTATCCTTCAAACAGCTCGAATCCCAAAACATTGTTCTACCTCAAGATCTTTTCAGAA
 GCAGCTTTACCTGGTTTGTATGAAATTTACAAGTCTTTAGCGTTTTCGATCTGGAATGC
 TATTATGGCTACCACTTAGCGTCTGGTGGAAACTTTCCAACAATGTATTTACCCACTTA
 TAGTTTCACTCTGTGCTCTGTTTCTGGGACCAATATTTGTCTTGTATTGTTGGACTTT
 CTCGTAACCGTTTCTTATCGAACAACCTCMTTCAGTTTTCGAAGAGATTACTGAAAACA
 CACCAAGTTCTGATCCTCATGATTGGGAGTTGTTGCAGCAATCTAAATTCGTACTTAT
 ATGAAAATAACGTTTGGAACTACTAAGTACTTTTTTTTCAATGCCATGGTCTGTCAAGAAG
 CGTTACAGAACACCCCTTCTCGAACCATTTCCTTTGAAAAAAGATAAAGCTGCCAAGGTTA
 AGTCATTTAAGGATTCGGTCCCTTACATTGAAGAAGCATTCACACTTTATTTTACACACAC
 TTGAAAAACAATGGAAATTCCTTTAATACTGAAAAATCATGGAGCCCTGTTGGCCTGGAAG
 ATCCTAAACTTCCCAAGGAAGCTTACCGATTTAAGCTTACTTGGTTTTTAAAGAGGATTT
 CCAATATTTTTATGTTGATACCATTCCTTAAATTTTTCCTCTGCATATATGCTCACGGC
 GAATGTGCCTTCTATTACGCACTTGTATCTCGGTGGATTCTTTTCATGTTGGTACAAG
 GTTTCAAAAATATAACGGTTTTCATTATGAGCATGGAACACAAAGATGCAGTTCTTGTCGA

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CTATTATAAATCAGCAAGAAASTGGTGCGAATGGATGGGACGAAATTGCAAGGAAATGA
 ATAGGTACTTGTGAGAAAAAGCCTGCAAGAATGAAGAGTTTTCTTCGACGGGATTG
 ACTGTGAATGGTTTTTAACCACTTCTTCTACCGGTTCTATCTGCGAAGAAATCTATGT
 GGCCTTTACCATTGAATGTGCAACTATGCCCATACATTAAAGAAGCGCAA'TATCCGCA
 GTGAGGTGCTCT'TAG'CTAG

>YML132W, 379 aa (SEQ ID NO 300)

MKENELKNEKSVTVLSFKQLESQKIVLPQDLFRSSFTWFCYBIYKSLAFRIMLLWLPLS
 VVWKLNNCLYPLIVSLLVLEPLGLFVLVICGLSRKRLSKQLIQFCKEITENTPSSDPH
 DWEVVAANLNSYLYENMVWNTKYFF:NAMVCQEA'RTTLLLEP'PSLKKDKAAKVKSPKDSV
 PYTEALGVYFTEVEKQWKLFNTEKSWSPVGLRDAXL>KEAYRFKL'TWFLKRISNIPMLT
 PFLNFLCCLYVSRGMCLLLRTLYLQWILFMLVQGFQNI'RVLIMSMEIKMQFLSTIINEQE
 SGANGWDEIARKMNRYLFEKKAWKNEE'FPFDGIDCEWFFFNHFFYRVLSAKKSMMLPLNV
 ELWPHYKEAQLSRSEVLLV

>YMR009W, 1040 bp, CDS: 501-1040 (SEQ ID NO 301)

ACCGGTATTTTCATCTCTTCTAGATCAAGACTAACTGCTCGTTCACTACAAGTATTTTAC
 GATAGTCCATATTACTCTT'CAAT'PAAT'P'PTTTT'PTATATTCTGGCCCCGTTTTTGACA
 CAATTTTTTCCCTTCTCTTTTTCTCCCTATAAACTATGCAGAAGTAGCGATAATCACCATC
 'T'G'P'PAAT'GAT'TCACAT'G'GCGCAAGTCTGATTGCTCTCTCTAGATAGTGAGATGCCCTTCT
 AAATAACAGGAGAGAGGCCAAGACAGCATAACGGCGCAATGAAGGTAATTTCTGCCAGTTT
 TCT'T'GCAAT'GACGACT'GAAAGGGGCCCTTGTAAAGAGCCGCTCGACAGGGCGACGCCACAG
 TAGAGTCCGCTAACACCGAAATATGCATATTGAAAAACATCABAGTATAAAAGAACAAAGA
 GGGTGGCATCTGCAGATCAAAAAAACAATAAACCACCAACAAGACACTAAAAAAGGTCTG
 TAAAAAGGTCAAAAGTTAGAATGGTTAAGGTATATATTATGACAAACAAGGTTGACTCCG
 AT'FATCGCGCCAUCCCAATTTCTGGAAACAGAACT'PTCCCT'GGATGAATTAGCCAAAGTTAG
 GAGTGATTTATAAATACTCTGTCAAATGACCAACAACTGAATGAAATTCCTAGCCAAAGAG
 AATATAAAAAATAGAGATGTGGTCAACATCTCGCAAGCTTCCCTCAAAAAGTCAAGCAGAT
 TTAATGAAAAACTAGCAACATTTCTACCAAGAGCATTTACATGAAGACGAAGAAATAAGAT
 ACTGTCTCGAGGGTGTGGATACTTTGACGTCAGGGATGCTTCCACACCAGAGAACTGGA
 TTAGGTGTTTTGGTAGAGTCAGGTGATTTACTGATTCTTCCACCAGGCATCTATCATCGTT
 TCACCTTGACAACCTAGCAACCACATCAAGGCCCTTGAGACTGTTTAAGGACGAGGCCAAAT
 GGCAAGCTATCAACAGTFLCAAAT'CAAGGCTGAT'CA'FGCCCTTACGCAAGGACTACATTG
 CCC'GATCAAT'CACTACTAA

>YMR009W, 179 aa (SEQ ID NO 302)

MVKVYIHDNKVDSDYRAPHNSGTSLDELAKLGVLYKYCANEEEVNIELARQREYKNRDV
 VNICEGCSFKSEAEFNEKLATFYQEHLEDEEIRYCLEGAGYFDVRDASTPENWIRCLVES
 GDLLILPPGIYHRETLT'SNHEKALRLFKDEPKWQAINRSNQADSLPVRKDYIALNQY

>YMR011W, 2126 bp, CDS: 501-2126 (SEQ ID NO 303)

GCACCTTCACCTTTTAAAGTTTCTTTTTCTCCTCAGCGCGCAACCGCTTAAGCTAATC
 CTTATGAATCCGGAGAAAAGCGGGGTCTTTTTAACTCAATAAAATTTTCGAAATCCTTTT
 TCC'ACGCGT'PTTCTTCGGGAAGTAGATAGGTGGCTCTTCCACCTGTTTTTCCATCATTT
 TAG'TTTTTCCGAAGCCATGCGTGCCTTTTCTGT'TTTTGCGATCGCGAAGCAGGGCTGGAAA
 AAT'CAACGGTACGCGGCTAACGATAGTAATAGGCCACGCCAATGCGGTG'ACGACAAAC
 ATAAGTCGCGCA'PTT'PTAT'G'PTT'CAAAACCTAGCAACCCCCACCAAAC'PT'G'CATCGT
 TCCCGGATCACAAATGATATAAAAAAGCGATTACAATTCATATTCTAACCAGATTTGAG
 ACC'CCCTC'PTCTCAATTCTCTTTATACTAGATTATAAGCAACAACAAATTAATTTACAAA
 AAGACTTATAAAGCAACAT'AAATGTCTGAATTCGCTACTAGCCCGCT'GAAAGTGCCCT'CTC
 AACAAACTTCTATCCACTCTACTCCGATAGTGCAGAAATTAGAGACGGATGAATCTCCTA
 CTCAAACCAATCTCAATACACTAAGCGCTCAACTCCCAGCAAAGCCAAATCCCGCATATT
 GGACTGTTATCTGTTTATGTCTAATGATTGCATTTGGTGGGTTTGTCTTTGGTTGGGATA
 CCGGTACCATCTCTGGTTTGT'AAATCAAAACGATTTCAAAGAAGATTTGCTCAAATGA
 AACTCTGATGCTACCTATTATCTTTCCGACGTCGGCACTGCTTTGATCGTTGCTATCT'CA
 A'AT'GTTGTTGTGCCCTTTGGTGGGTTAACCTTAGGACGCTCTGGG'GATA'GTATGGACGTA

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GAATTGTTTTGATGTGGTCTGTTCTGGTATACATCGTTGGTATTGTGATTCAAATTGCTT
 CTAGTGACAAATGGTACCAATATTTTCATTGGTAGAATTATCTCTGCTATCGCTCTCGGTC
 GTATTGCTGTCTATCTCCAACCTTTGATTTCGGAACAGCACCAAAACACATTAGAGGTA
 CTTGTGTTTTCTTTCTATCAGTTAATGATCACTCTAGGTATTTCCTTAGGTTACTGTAACCA
 ACTATGGTACTAAAGACTACTCCAATTCAGTTCAATGGAGAGTGCCCTTTGGGTTTGAAC
 TTGCGCTCGCTATTTTCATGATCGCTGGTATGCTAATGGTTCAGAAATCTCCAAGATTCT
 TACTCGAAAAAGGCACATACGAAGACGCTAAACGTTCTTTGGUAAAATCTAACAAAGTCA
 CCATTGAAGATCCAAGTATTGTTGCTGAAATCGATACAATTATGGCCAAACGTTGAAACTG
 AAAGATTAGCCGGTAACGCTTCTTGGGGTGAGTTATTCTCCAACAAAGGTGCTATTTTTAC
 CTCGTGTGATTATGGGTATTATGATTCAATCCTTACAACAATTAACGTGTAACAATTACT
 TCTTCTATTATGGTACTACTATTTTCAACGCCGTCGGTATGAAAGATTCTTTCCAAACTT
 CCATCGTTTATAGGTATAGTCAACTTCGCATCCACTTTCGTGGCCCTATACACTGTTGATA
 AATTTGGTCTGTCGTAAGTGTCTATIGGGTGGTTCTGCTTCCATGGCCATTGTTTGTGTA
 TCTTCTCTACTGTCCGTGTACAAAGCTTATATCCAAATGGTAAAGATCAACCATCTTCCA
 AGGCTGCGGTAAAGTCAATGATTGCTTTTACCTGTTTATTCATTTCCTTCTCGCTATTA
 GTTGGGCCCAATTGCTACGTTATTGTTGCCGAATCCTATCCTTTGCGTGTCAAAAATC
 GTGCTATGGCTATTGCTGTTGGTGCCAACTCGATTGTTGGGCTTCTTCATTCGTTTCTTCA
 CTCCTTTCATTACAAGTGCAATTGGATTTCATACGGGTATGCTCTCATGCGCTGTTTGG
 TATTTTCACTTCTTCTACGTGTTTTCTTTGCTCTGTGAAAUCAAGGCTTAACATTAGAGG
 AAGTTAATGAATCTATGTTGAAGGTGTCAAACCATGGAAATCTGGTAGCTGGATCTCAA
 AAGAAAAAGAGTTTCCGAGGAATAA

>YMR011W, 541 aa (SEQ ID NO 304)

MSEFATSRVFSGSQQTSIHSTPIVQKLRTDRSPITQTKSEYTNAFI.PAKPTAAYVTVICLC
 LMIAPGGFVFGWDTGTISGFVNQTDFFKRRPFGQMKSDGTYXLSVVRTGLIVGIIFNIGCAFQ
 GLTLGRGLGDMYGRKIGLMCVVLVYIVGIVIQIASSDKWYQYFIGNIISGMGVGGIIVLSP
 TLISETAPKHIRCTCVSPYQLMITLGIPLCYCTNYCTKDYSNSVQWRVPLCLNFAPAFIM
 IAGMLMSPNPRFLVEKORYEDAKRSLAKSNKVTIEDPSIVAEMDTIMANVETERLAGNA
 SWGELEFSNKGAILPRVIMGIMIQLQSLQLTGNVYFFYYGTTIFNAVGMKDSFQTSIVLGIV
 NFASTFVALYTVDKFGRRKCLLGGSASMAICFVIFSTVGVTSLYPNGKDQPSKAAAGNV
 IVFTCLFIFFFAISWAPIAYVIVAESYPLRVKNFAMAIIVGANWINGFLIGFTPTPTSA
 IGFSYGYVFMGCLVPSFFYVFFVFCETKGLTLEEVNEMYVEGVKPKSGSWISKEKRVSE
 K

>YMR099C, 1394 bp, CDS: 501-1394 (SEQ ID NO 307)

AACAGTTACCTCGATCTACATATACTTCAATGCGAGAATGACTAATCTTTGCCATTGAC
 AAACAACCCCTTTTACTGCCAGCGCCCTTTCATAACCATGTAGTTTATATGCCCTAATTATA
 ATAAAGCATGACATATAATGCCAACCCCATATTTATATAGTTAACTTGAAACCGAGATTCT
 ATCTATTGCACCAGGAAAGTGCCCTTCTTCTTAAACATAAGTTACGTCCCGACCATTTCA
 TCTAAACGGCATCAATCATTGCAGCAGAAGAAATAGTGTGTAGATGTCCTCGTTCCGCTAG
 ACGCAGTCAATGATAACAAGGTCTTTCTTCAAGCTGTCTTTCCATAAAAAGGTATCGCAA
 ATGGGGTCACCAATGCGCCCTTTTATTTTTCACGCCGAAAGAAAACCTAGTAGGTCCCTAG
 AAATGAATAAAGAGGTGATTCTGAGGTTCAATTATAAGCCTTTGGTAAAACCTGAACCAAG
 AAAGATTAAAAACACAAAGCCATGCCTATCAAAGAACTGATAAAGAAGTTGTTTGGACTC
 ATCCAGCTCATGAGACCACCACCGTTTCATATTCTAAGTACCCTGCTACAGTTTATTCTT
 GGAAATTCAAACTCTGAAGAACCTTGTGGTTGTCTACTGCTCCTAAATCGGATCGTAGCA
 AACCTGTGAGAGGTGGTATACCTTTGGTCTTTCTTGTATTGGGAAAAAAGCACCGGATG
 AACATTTGAGTAAATTACCTCAACATGGTCTTGCAAGAAATTCTACTTGGGAGTTTTTGG
 GTCAAACTAAGGAAAACCCACCCACCTACAATTTGCCCTCAAAACAGAAATTGCTAACC
 CAGAATTGACCAAATGTGGCCAATGGATTATCTTTTGATTTTGACTGTGAATTAGGCTT
 CCGATTATTTGAAAACAGCCATAGAAATACAAAACACATCTACTTCCAACGAATTAAAGT
 TCAACTCGTTCTTCCATACTACTTCCCTATCGAAGATATTGAACGAACATGGTCTCTA
 ATTTAGCTGGCATGAAACTTTATGACCAACTGTTGAAGGAATCTTACGTCCACAAGCACC
 CAGTCTGTACCTTCAATCAAGAAACCGATGTAATTTATCAGAATGTCAGCCCGGAACGGG
 CCATTCAAAATAGTTGACAAGGGCGTTCAAAATTCACACTCTAAAAAGATACAACCTTCCCGG
 AACCTGTTGTTTTGGAATCCATGGATTGAGAAGTCTCAAGGATGGCCGATTTTCAACCAA

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AAACTGGTTACCAACAAATGATATGTATTGAACTGGTCATGTCATGATTTTATTTCCT
TGGCTCCTCGTAAAAAATGGAATGCTTATCAATTACTTTGCAAACAACAATCGAATATC
AAGCTATTCAATAA

>YMR099C, 297 aa (SEQ ID NO 308)

MPIKETDKEVVLTHPADETTSVHILKYGATVYSWKLKSEEQLWLSTAAKLDGSKPVRGGI
PLVFPVFGKNSTDEHLSKLPQHGLARNSTWEFLGQTKENPZTVQFGLKPELANFELTKLW
PMDYLLILTVELGSDYLKTAIEVENTSSSKELKFNWLPHTYFRIEDIECTMVSNLACMKL
YDQLLKESYVDIHPVVTFNQETDVIYQNVSAERAIQIVDKGVQIHTLKRYNLPDTPVWNF
WIEKSQGMADFEPKTYQQKICIEPGHVHDFISLAPGKKANAYQLLCKEELKYQAIQ

>YMR110C, 2099 bp, CDS: 501-2099 (SEQ ID NO 311)

AAGAGAGAGAAGCTAGATTATCATTACAGCAGCCACATAGTATACCAAATTCCAGTACAG
GCACACCAGAACATGATCAACACACTTAGAGGAAATGCCAACACGAATTTCCAGCCAAAA
ATTCCGAGTAGATTCAAGATGAAAGATTTTACATGCAATTTATATATAAATATATACCGT
CCTATATGGAATTTATGCCAACAGGGTATATAAATAGACAATTACCGGTGTACTGATATAT
CAACTATCCACTCCAGCCCTTTTATCTATCACTCAATTTTACATCAAGATCCCACTTTTA
GATAGGTTCCAAAAATCAATCTAATATTTAGTGTATTAATTAGATGGTGGATTGCTTACCC
TTTTTTTTGTCTGTTTGGAGGAGATTCTTCGGATTTTAGGGATAAACGGATACTCCATA
TATAAAAAACAAAACCTTCACCCATATGATTTATCTAAAAGGAATATTCTAAAACCATAGC
CATAGTAATTTATCACCACATGTCAAACGACGGCTCAAAAATATTGAATTATACCCAG
TGTCTAAAATAGATGAAATAGTTGAAATCTCAAGAAATTTCTTCTTTGAGAAACAATTGA
AATTGTCCACGAAAAATAACCCAAAGSAAAAAGATCTAGAAATTCAGGCAGTTGCAGTTGA
AAAACTCTATTATGCGCTCAAGACTCATGAGGAAGAACTGATCGATGCTATGTACAAGG
ACTTTCATCGGAACAAAATTGAATCGGTCTCGAATGAAACGACCAAACTTATGAACGATA
TACTTCACCTAATTGAGATTTTACCAAAATTGATCAAACTCGGAGAGTATCTGATTCTT
CTCCTCCATTTATCTTTGCTAAACAATCGTCCAGAAAATATCAAGGGCCACTCTCTTGA
TTATTGCTCTCTTCAATTTTCCCTTACTTTTACCAATTGCCCCATTGCGCAGCAGCTCTTG
CTGCAGGTAAACACCATTGTTCTGGAAGCCAAAGTGAACTAACACCACACACTGCTGTGTTA
TGGAAAAATTTGTTAACCCACAGCTGGTTTCCCTGATGAGATTGATTCAAGTAGTTTCAGGGAG
CTATAGATGAAACTACAAGACTACTAGATTGTCGAAAAATTTGACCTAATATTCTACACAG
GTTCTCCCCGTGTCGGATCAATAGTTGCTGAGAAACGAGCAAAAAGTCTAACACCTTGTG
TACTTGAACCTTGTGCTAAATCACCTACCTTTTATTACAGAAAAATTTCAAAGCAAGTAACA
TAAAAAATTGCTTTGAAAAGGATTTTTTTTGGTGCTTTCCGAAATTTCTGGCCAGATTGTG
TTTCACCAGATTATTTCTTACTACATAAATCTATCTATCCAAAAGTCATTAAAGACTGTG
AATCAGTACTAAATGAATTTTATCCAAAGCTTTGATGAACAAACAGATTTCACTCGTATGA
TTCATGAGCCTGCTTACAAAAAGGCCGTTGCAAGTATAAACTCAAGTAACGGCTCCAAAG
TTGTGCCTTCAAAAATTTCTATCAATTACAGATACTGAGGATCTATGCCTTGTACCACCAA
CCATAGTTTATAACATTTGGTTGGGATGATCCTTTGATGAAACAGGAAAATTTGCTCCTG
TATTGCCCATCATTGAGTACGAGGATCTTGATGAGACCATTAACAAGATAATAGAAGAAC
ATGACACTCCATTGGTGCATACATATTCTCTGATAGCCAACTGAAATAAATCGTATCT
TGACGCGCTTAAGATCTGGTGACTGTGTTGTCGGTGATACAGTGAATTCATGTAGGAATTA
CCGACGCTCCATTTGGAGGGATCGGTACTTTCAGGTTATGGTAACCTATGGTGGATATTATG
GATTCATAACCTTTAGTTCATGAAAGAACAAATTTTAAACCAACCATATTGGAAATGATTTTA
CCCTTTTTATGAGATACCTTCAAATAGCCGCACAAAACGAAAGCTCGTCCGTTTTTGCGA
TGGAAACAAAACCTTGCCTTTGACAGAAATGGCAATAACAAGTGGGGCTTACGCCAATATT
TTTCATTATCTGCCGCCGTTATTTTAATTAGTACCATTTACGCTCATTTGTTCTTCCCTGA

>YMR110C, 532 aa (SEQ ID NO 312)

MSNDGSKILNYTFVSKIDEIVEISRNFEEFKQLKLSHENNPRKIDLEFRQLQLKKLYYAV
KDHEEELIDAMYKDFHRNKIESVLNETTKLMNDILHLIEILPKLIKPRRVSDSSPPMFEC
KTIYEKTSRGSVLTAPFNPPIILAFAPLAATAAGNTIIVIKPSELTPHTAVVMENLLAT

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AGFPDGLQVVGGAIDETFRLLDCGKELLIPYTGSPRVGSIVAEGAASLTPTCVLELGOK
 SPTFITENFKASNIKALXPLIFFGANGNSGQICVSPDYLLVHKSIYPKVIKECESVLNEF
 YPSPDEQCTDFTRMIHEPAYKAVASINSTNGSKIIPSKIISINSDTEDLCLVPPTIVYNIG
 WDDPLMKQENFAPVLPFIEYEDLDETINKIIEHDTPLVQYIPSDSQTEINRILTLRSG
 DCVVCETVIHVGITDAPFGGIGTSGYGNYGYYGFNTFSHERTIHKQPYWNDFTLPMRYF
 PMSAQKEKLVRFAMERKPMFDRNGNNKWLGRQYFSLSAAVLLISTIYAHCSS

>YMR173W-A, 1685 bp, CDS: 501-1685 (SEQ ID NO 691)

AAAAAACCCACTCCGAAGGTTCCGACCATGACAAATCGCCCCCTAGCTGTGGCCATACAAGC
 TTGGCACCCGACGAAAAAGGGAAAAAGGAAAAGAAATGTCGTACAAGAACTCTTACAACCCAC
 GTTGAGATTTTCATTTAACAAGUCCCCCTTTTCATPATATAAGAAGGCATTAATTTTAT
 GTAATAAAAAAGAATTTCTCGAAATGTCTTACAATTAATTTTTCTTTCTAGAGTAG
 GGCTTTAATAGACTGATATATACGGTATTATAAGTGAACGAAAAAACAGCAATGGGT
 ATTTGATAAAGTGAAGCAATTTGCTAACAGCAATTAATAAUAUAATGATTCTGGCAATAA
 CAATCAAGGCGATTATGTTACCAACCTGACAATATGATCCCCAAGATAGAGTCAATCA
 ATTCAAAAGCAAAATCGGAGAGGACAGATTTGATAAGATGGAGTCCAAGGTTCTGTCACAA
 ATTTCTTAATACCTCTATAAATGACAACGACTCCAACAACAACGACTCATATGGTTCTAA
 TAACAACGATTCATATGGTTCTAACAACAATGATTCATATGGCTCTAACAACAATGATTC
 ATATGGCTCCAACAACAATGATTCATATGGCTCTAACAACGATGATTCCTACGGTTCTTC
 CAACAAGAAGAAGAGCTCTTATGGTTCTAACAATGACGATTCCTACGGCTCCAGCAACAA
 CAATGACTCTTTACGGTTCCAACAACAATGACTCTTACGGTTCCAACAACAATGACTCTTA
 CGGTTCACAACAATGACGACTCTTACGGTTCTGTCACAACAAGATAAGAGCTCTTACGGTTC
 CAACAATGACGATTCCTATGGCTCTAACAATGATGATTCATATGCTCTTCCAACAAGAA
 GAAGAGTTCTTATGGTTCCAGCAACAACGATTCGTATGGTTCTAACAACGATGATTCATA
 TGTCTTAACAACAATGATTCATATGCTCTAACAACCATGATTCCTACGGTTCTTCCAA
 CAAGAAGAAGAGCTCTTATGGTTCTAACAATGACGATTCCTACGGCTCCAGCAACAACAA
 TGACTCTTACGGTTCCAACAATGACGACTCTTACGGTTCTGTCACAACAAGATAAGAGCTC
 TTACGGTTCTTCTAGCAACGATGATTCCTTACGGATCTTCCAATAAGGACGACTCTTACGG
 TTCTTCCAACAAGAAGAAGAGTTCTTATGGTTCCAACAATGACGATTCCTATGGCTCTAA
 CAATGATGATTCATATGCTCTTCCAACAAGAAGAAGAGTTCTTATGGTTCCAGCAACAA
 CGATTCGTATGGTTCTAACAACGATGATTCCTACGGTTCTTCTAACAAGAAGAGTTCT
 TTATGGTTCCAACAACGATGATTCATACGGCTCCAGCAACAACAATGACTCTTACGGTTC
 CAACAATGACGACTCTTACGGTTCTCTAATAGAAACAAGAACCTCTATGGGTCTTCCAA
 CTACGGTTCTATCCAACAATGATGACTCTTATGGTTCTATCTAATAGAGGCGCTCGTAATCA
 ATACGGTGTGTGACGACGATTACTAAGTTTTTGGATGTCTTCGAACAAAAAATATATTAT
 TGTGTTTAGACTTAAGTATGAAATTTTATGTATGAGCTGTGGCTATGTATCCGCTGGCA
 AATAG

>YMR173W-A, 394 aa (SEQ ID NO 692)

MTTTPPTTTHMVLTTTHMVLTTMIHMALTTMIHMAPTMIHMALTTMIPTVLPTRRRAL
 MVLTMILTIRAPATTTMTLTVPPTMTLTVPPTMTLTVPPTMTLTVPPTMTLTVPPTMTLT
 APTMIHMHVLPTRRRVLMVPATTIRMVLTMIHMHVLTMIHMHVLTMTIPTVLPTRRRALM
 VLTMTILTIRAPATTTMTLTVPPTMTLTVPPTMTLTVPPTMTLTVPPTMTLTVPPTMTLT
 VLMVPTMTILMALTTMIHMHVLPTRRRVLMVPATTIRMVLTMTIPTVLLTKRRVLMVPTMT
 LHTAPATTTMTLTVPPTMTLTVPPTMTLTVPPTMTLTVPPTMTLTVPPTMTLTVPPTMTLT
 TKFLDVFDKKNILLCLDLSMKILCMSCGYVSAGK

>YNL031C, 911 bp, CDS: 501-911 (SEQ ID NO 325)

CAACAGUCCAGGCGCGAGTGAACAACATATTAATTAACGCCCTTCTTGTUAGTGTGTTTT
 GTTCTGGTCTGGTCTGCAATTCGCGCCCGAAAAAGCTTGAGACGCGAAGCTCCCGAAGC
 TCCTGCCATACAAATGCGAAACTCTCGGTCTAGTACCCTTTCCCGGTGCCAAACGACCA
 CAGTTGTCCGTTCGAGCAGCTCGCATTAAGCGCGTGAACCTATTCGACGCGCTTAAGGG
 GCTCCCTACGGATGGGAGTTGGTCAATTAGCGTTCATTATCGCCCAATGTGACGCAAAATC
 ACUGCTATGGCTCGGTGTCAAAACATAGCTTTGGGTGATAACAGCGTGTGTTGCTCTCTCG
 CGTTGCTCTTGTGACCGCAGTTGTATATAAATAATCTTTTCTTGTCTCTTTATATAGG
 ACCACTGTTTTGTGACTTCCACTTTGGCCCTTCCAACCTGTTCTTCCCTTTTACTAAGG

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ATCCAAGCAACACTCCACANTGGCCAGAACTAAACAAACAGCTAGAAAATCCACTGGTG
GTAAAGCCCCAAGAAAACAATTAGCCTCCAAGGCTGCCAGAAAATCCGCCCCATCTACCG
GTGGTGTTAAGAAGCCTCACAGATATAAGCCAGGTACTGTTGCCCTTGAGAGAAATTAGAA
GATTCCAAAAATCTACTGAACTGTTGATCAGAAAGTTACCTTTCCAAAGATTGGTCAGAG
AAATCGTCAAGATTTCAGACCGACCTGAGATTCAATCTTCTCCTATCGCTGCTTTGC
AAGAATCCGTCGAAGCATACTTAGTCTCTTTGTGTGAAGACACTAATCTGGCTGCTATTG
ACGCTAAGCGTGTACTATCCAAAAGAAGGATATCAAATTGCCACAGACTAAGAGGTG
AAGATCATGA

>YNL031C, 136 aa (SEQ ID NO 326)

MARTKQTARKSTGGKAPRKQLASKAARKSAPSTGGVKKPHRYKPGTVALREIRRFQKSTR
LLIRKLPFQRLVREIAQDFKTDLRFCSSAIGALQESVEAYLVSLFEDTNLAALIAKRVTI
QKKDIKLARRRURGRS

>YNL134C, 1631 bp, CDS: 501-1631 (SEQ ID NO 331)

AAACTCGGAAACTCTTTTCTATTCATCTTCCCTTCTCCTACGTGCCACGGAAGCAATA
AAAAGAACCGAAATAACCAACACCCCGTAACGTCAAAGCATTTCATGCTTAGAATGGAAACC
ATTTCTGCGAATGAAATGGCAATTGATCACAATTGATTGCTCGTTCCACTACCTGTGTCC
GCAATTTTTTAATGGTCATCAGAGCCCTGCTGACTAAAGTTCTCGGATCCGCTTACGG
TTGTGCGGUGTTTCCGCCCTGCGTACCTCTTACGATATCGGCTCCCTCCGTTG
GATTGGCATCGATTAGTAAGGACAGATGTTAAGGATTTAAGACCGTTTTTAAGGTATTTG
GGCAATGCTTCGATTAAAAAGGAGAGAGTTTTTTTTTGGCGTTTCTTCTCTCACTTC
TTGATTAGTACTGTAAATTCTAGTTGAAAAAAATCGTTAACTATACACAGCAAAAAGCAA
TATCATACTGCATATCAAGCATGTCCGCTCGATTCCAGAAAACCATGAAAGCCGTGTCA
TTGAAAATGGCAAGGCTGTAGTCAAACAGGACATTCCAATTCCTGAATTAGAAGAAGGAT
TTGTTCTAATTAAGACTGTCCCGTTGCCGGTAACCTTACCGATTGGAAACATATTGATT
TCAAGATTGGTCTTCAAGGTGCCCTCTTAGGCTGTGATGCAGCCCGCCAAATCCTAAAGT
TGGGCCCAAAATGTTGATGCTGCRCCGTTTCCCATTTGCTGATTACATTTATCGGCTTATTC
ACGATGCTTCAGTGAGGTTCCTCCCAAAACGGTCCCTTTGCTGAGTACTCTCCCAATTTCAT
CCGAGACTGCTTATAAACCAGCCAGAGAGTTTAGATTGTGCGGTAAAGACAAGCTACCCAG
AAGCCCCCGTAAATCTTTAGAAGCGCCAGTATCCCTCCCAGTCTCATTGACCACGGCTG
GTATCATCTTACACATAGTTTGGCTTGGACATGACATGGAAGCCCTCCAAAGCGCAAA
GAGATCAACCCATCTTATTTTGGGTGGTGGCACTGCCTGTGGCCAGATGCTTATTCAA
TGGCAAAAAAACTAAACGGTTTCAAGCAAGATCAATGCTGCTTCTCTGTAACATGAAA
AATTGTTGAAAGAGTACGGTGCAGATGAACCTTTTGACTACCAAGATGCTGACGTATCG
AACAGATAAAAAAGAAGTACAACACATTCTTACTTGGTGGACTGTGTCTCCAACACAG
AACTATTCAACAGGTGTACAAATGTGCCGCTGATGACTTAGACCGCTACGGTCGTTCAAT
TGACCGTTTTTAACCGAAAAAGATATCAAGGAGGAAGACAGGACCCAAAACGTCAGTATTC
AAGGAACCTTCTATATTTGATAGGAGGTAAAGACGCTCCCATTTGGCAGCTTACTTTGC
CAGCAGACCTTGAATACAAGGAAGCCGCCATAAAATTTATTAAAGTTCATCAATCCAAAA
TCAATCATGCTGAAATCCACCACATCCCAAGTGAAAGTTTACAAGAACGGGTAGATGATA
TCCACAGTTACTTGATGATATTAAGCACGCCAGCAATTCGCGSAAAACCTTGCTTCCCC
TCTTGAAACAA

>YNL134C, 376 aa (SEQ ID NO 332)

MSASIFETMKAVVIENGKAVVKQDIPITPELEEGFVLKTVAVAGNPTDWKHIDFKIGPQG
ALLGCDAAAGQIVKLGPVDAARFAIGDYIYGVVHGASVRFPSNGAFAYSAISSETAYKP
AREFRLCGKDKLPECPVKSLEGAVSLPVSLTTAGMILTHSFGLDMTWKPSSKAQRDQPILF
WGGATAVGOMLIQIAKKLNGFSKTIIVVASRKHKKLKEYGADELFDYHDADVIEQIKKY
NNIPYLVDCVSNTEITQQVYKCAADPLDATVVQLTVLTKKDIKEEERRQNVSLGFTLLYL
IGGNDVPFGTFTLPADPEYKHAATKFIKFINPKINDGEIHHPVKVYKNGLLDDIPQLLDD
IKHGRNSGEKLVAVLK

>YNR002C, 1349 bp, CDS: 501-1349 (SEQ ID NO 339)

ATGGACAATTTGAAGTTCTTGACTACCCCTATCTCACACIAGTACGTAATTCAATGTATC
ATTCGTATTGTTAAGTAGATAGAGACGCAATACAGGAAAGCTGACCTTCCTTCCAATCAAC

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ACGGCTGAAACGCTTTGTGACCAATTACGGACGCTTAAGAGCGGACGCGGCTGGAAACGG
 CTCCATCCCTAAATCGCGGAGGGAGAACTCCGATACCAGCCGACATGGCAATAATAGTGA
 CAGTAGATGCTACCAGCCCCCAATAATTTACAGTAGATCATCAACAGTCTCTCATTT
 CTGGAAATGATCAGCAACTTCGACGGATT(TA)CTCTCAAGCAGTACGCAC(TCG)GAGAAC
 AGCCGTGATCATCTTTGAACAAGCAAAATATATAAAGCAGGAGAACTGTCTTACCTAGAG
 CTACAATAGCCATAACTA)CTATGTAACATTCTACAGATCAATCABAAAACAATCTTCAAT
 CACAGAAAAAATAAAAGCCATGCTCTGACAGAGAAACAAAGCAGCGGCAACACCCGCTTTTG
 AGAACCCCTAAGGCACCTCGATTCTTCCGAGGG(TG)AGTTTCATCTCTGAAAAACAUGATCAGA
 GCGGCCACTCCCAACAGTCCATATGCCAAATATATACTGCGGGCAAAAAACAACGAGTATA
 TTTTACATCGGCCG(TCA)AAAAAT(TTT)TAAGGGATGATTTGTTTCGAGGCATTCGGTGGTACTC
 TGAATCCCGGTTTAGCCCCCGCGCCAGTCCATAAATTCGCAAACTCTGCTCCACTAGGAC
 TTTCCGGTTTTTGCCTTCACTACGTTTCTCTTATCCATCTTCAATGCCAAGAGCCCCAAGCCA
 TCACATATCCCTAATGTTGTTG(TG)TGGGTGTGCCATGTTTACGGTGGCCCTCGTTCAACTCA
 TTGCTGGTATTTGGGAAATCGCTTTACAGAACACTTTCGGTGGTACAGCCCTGTGTTTCTT
 TCGGCGGTTTTTGGTTAAGCTTCGGTGTATATACATCCCTTGGTTTTGGAAATTTACATG
 CCTATAAGGACAAGGAATCCGACCTTGGAAATGCGCTAGGGTTTTTACCTCCTAGGATGGG
 CACTCTTACCTTTCGGTCTTTTCGGTCTGCACCATCAAA(TCA)ACTATAATGTTTTTTCCT
 TATTCTTCTCTTAGCAGTGACCTTCTTACTTCTATCCATTGCCAACTTCACACGCCAAG
 TTGGCGCTCACTAGAGCTGGTGGGGTCTTGGTGTGATAGTAGCCTTCATTGCTTGGTACA
 ACGCTTACGCAGGIATTGCCACAAGACAAAACCTGTACATPATGGTCCATCCATTCGCAT
 TACCTAGCAATGATAAGGTGTTCTTCTAA

>YNR002C, 282 aa (SEQ ID NO 340)

MSDREQSSGNTAFENPKALDSSEGEFISENNDQSRHSQESLKIYTAKKNMAYIYIGRQK
 FLRDDLFEEAFGGTILNPLAPAPVHKFANPAPLC(L)SFCALTTPVLSMPNARAQGITIINVV
 VGCAMFYGGLVQLIAGIWEIALENTFGGTALCSFGGFWLSFGAIYIPWFGILDAYKDXES
 DLGNALGFYLLGNAL(TFG)LSVCTMKSTIMFFALFFLLAVTFLLLSIANFTGEVGVTRAG
 GVLGVIVAFIAWYNAYAGIATRQNSYIMVHPFALPSNDKVFF

>YOL139C, 1142 bp, CDS: 501-1142 (SEQ ID NO 347)

ACAAGTTTGGATACTGGTATTGTGACTCTTGTGAAGAAGAAGATA)CATCTTG(TG)TCTAT
 GTGAAGACCATTAAAGAACTGACCATGGTCATCTTCCCCCTGTGGACACGAAGGTCACT
 TCCAGTGCATACAAGAATGGTTTCTCGATCAGAAATCAACAAGAAATGTCCCCGGCGCTTGGC
 CCGGTGTTGCCAT(TCATCTAGG(TTCTCCACATAATGTATAGTTTAA)CATATCATCACCATT
 GTTTAGTTAAATCGTTTAGAGTAATATTACCCGTCAAAAAAGCTCGGCT(AAAA(TTT)ATTTA
 CCCTCTCCGAAAAGAAAAATTTTTTTCCTCGTCAATAGACTTTAATCCAAATACCTGATAAA
 GAGAGTTTTACATTCGAAGAGG)AGTGTAAATCTGGATTATATCTGTACATATGTGTTTT
 GTGTTAGTGTTCAGTACTTCCTAGGAGTTTACGAAAAATAAAAGCAATTTTTGTCTGAA
 AACTAGTGAAGGAAGAAAAATGTCCGTTGAAGAAGTTAGCAAGAGTTTGAAGAAACCG
 TTTCA)GTGATGATACCAACAGCTACTCCAAAGACTGTTTTAAGTGACAGTGTCTCACTTCG
 ATGTC)AAGCACCCATTGAACACCAATGGGACTTTATGGTACACAAAGCCAGCCGTCGATA
 AATCTGAGTCGTGGTCTGATCTAT(TACGTCCCG(TCAC(TTCA)TCCAAAC(TGTGAAGAAAT
 TTTGGGCTATCATTTCAAAATATTCCTGAGCCACACGAAC(TACCATTGAAATCAGATTA)CC
 ACGTCTTCCGTAATGACGTTAGACCTGAATGGGAAGATGAAGCCAATGCTAAAGGTGSTA
 AATCGTCTTTTCCAACCTTAGAGGAAAAGGTGCTGATATTGATGAATTAATGGC(AAAGAAC(TT
 TACTAGCAGTTATTGGTGAAACAATTGATGAAGACGACTCCCAATTAACGGTGTCTGTTT
 TAAGCATTAGAAAAGGTGGTAACAAGTTTGCTTTATGGACTAAATCTGAAGACAAAGAAC
 CACTATTGAGAATTTGGTGGTAAATTC)AAGCAAGTT(TTAAAA(TTAACCGATGACGGGCAAT
 TGGAATTCTTTCCACATTCAGTGCCAATGGTAGACACCCTCAACCATCAATCACCTTGT
 AA

>YOL139C, 213 aa (SEQ ID NO 348)

MSVEEVSKKFEENVSVDDT)ATPKTVLSDSAHFDVKHPLNTKWTLWYTKPAVDKSESWSD
 LLRPVTSFQTVSEFWAIIQNIPEPHELPLKSDYHVFRNDVRPEWEDEANAKGGKWSFQLR
 QKGADIDELWLRLLAVIGETIDEDDSQINGVLSIRKGCNKFALWTKSEDKPELLRIGG
 KFKQVLKLTDDGHLFFPHSSANGRHPQPSITL

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>YOR120W, 1439 bp, CDS: 501-1439 (SEQ ID NO 353)

TGTCTTACATATTGCAATGGATATGCTTGGGTGATCATACTTCTGGCTTTAGATATTTG
 AAACCTAACTCTTCTCAACAACTTCTATCGAGTGTATAACAATTGTAAAGTTATAACAC
 CCGCGAACAATCGGGGCAGACTATTCCGGGGAAGAACAGGAAGGGCGCTCTTTTCTCCC
 TCATTGTCAATAGCAAGGTCAATTTCCGCCCTCTCAGAAAGGGGTAGAATCAATCTAGCACGC
 AGATTGCAAAACACGGCTTAAATAATATGCCCTATCAGCCATTACCCCGTGTGACGAATCGCA
 CACCGCTGCTCTCCTTAATTCCTTAGAGTAGAAACCGAGCTTTCAGGAAAAGACTACGGC
 AGTAAAGAATTGCTTTACTGGGCGTATAAAACCCGGGAGAATCAAGACATTCTAATGACTT
 GATTACCCATGACAGCTTAATAGGTGCATCTTAGCAAGCTAAAATTTGGACAGCTCTCAT
 TACTAAATTAAGATAGAAAATTCCTCTCTACTTTAATGATTCTACCAAAAATCTCTTCTC
 TAAATACTGGAGCCCCAATUUCTCAAATAGGTTTAAAGTAUUTGGCAGTCGAAAGAGAACG
 ATGCTTATAAGGCTGTTTTAACCGCTTTGAAGATAGGCTACCGACACATTGATACTGCTG
 CTATTTACCGTAATGAAGACCAAGTCGGTCAAGCCATCAAGGATTCAGCTGTTCTCTCGCC
 AAGAAATCTTTGTTACTACAAAGTTATGGTGTACACACACCCAGAACCTGAAGTAGCGC
 TGGATCAATCACTAAAGAGGTTAGGATTGGACTACCTAGACTTATATTTGATGCATTGGC
 CTGCCAGATTAGATCCAGCCTACATCAAAAATGAAGACATCTTGAGTGTGCCAACAAAGA
 AGGATGGTTCTCGTGCAGTGGATATCACCAATTGGAATTTCAATCAAAAACCTGGCAATTAA
 TGCACGAACCTACCAAGACTGGTAAACTAAGGCCCGTTGGAGTCTCCAACTTTTCTATAA
 ATACCTGAAGATCTATTAGCATCTCAAGGTAATAAGCTTAAGCCAGCTGCTAACCAAG
 TCGAAATACATCCATTACTACCTCAAGACGAATTTGATTAAATTTTGTAAAAGTAAAGGCA
 TTGTGTTTGAAGCTTATTTCTCGTTTAAAGTAGTAACGATGCTTCACTATCGAAGCAACCGG
 TTATCCTTGAAATTGCGAAGAAAAATAACGTTCAACCCCGACACCTTGTATTAGCTGGC
 ACGTCCAAAGAGGTTATGTTGCTCTTGCCAAAATCTCTGAATCCCGATCGAATCAAAACCA
 ACAGGAAAATATTTACTTTGTCTACTGAGGACTTTGAAGCTATCAATAACATATCGAAGG
 AAAAGCGCCAAAAAAGGGTTGTACATCCAAATTGGTCTCTCTTTGGAAGTATTTCAAGTAA

>YOR120W, 312 aa (SEQ ID NO 354)

MPATLHDSTKILSLNTGAQIPQIGLGTWQSKENDAYKAVLTALKDGYRHIDTAIYRNE
 QVGGAIKDSGVRRRTFVETKLWCTQHHEPEVALDQSLKRLGLDYVDLYLMHWPARLDPA
 YIKNEILSVPTKKDGSRAVDITNWNPFIKTWELMQELPKTKTKAVGVSNFSEINHLKDLL
 ASQGNKLTFAANQVELIHLPLPQDELINFCKSKGIVVEAYSPLGSTDAPLLKEPVILEIAK
 IKNVQPGHVVISWHVQRGYVVLPKSVNPDRIKTNRKIFTLSTEDFEAINNISKEKGEKRV
 VHPNWSPFVFK

>YOR122C, 1090 bp, exon1 : 501-513, intron1: 514-722, exon2: 723-1090 (SEQ ID NO 357)

AGGAAGAGGAGGCTGCGTTTGACGACGAAGAGGATGATAATGAGCAAGAAGAAGAAGAAG
 AGGACCGCGATGAAGAGAACGCCCTCTCGTCTAAGAAATTTAAAAAGAGAAGGAGCAGCAA
 TGTACAGAGAAGAGGAAGAAGAAGAAAAAGATAGGAGCGAGACAAAAAGAAGAAGGCTTG
 CGGTCAATCGAGGACGACGAAGACGAGGATTACAGCAGACCTTACTTTGTTTATATATATT
 AGTATGTACAATCGCAAAGAAATGGAGTGTATGACATGTTGTAGTATTTAGTATGAGGTTA
 CTGTGTGGGAGGTTTTTACCATGATTTTTTCCCGCAACACCCCATCAAAATGCTCTTTGTACG
 AAACCTATTACCGCATTAATATTTTTTTCTTTTTTAAAGCTCAGTTGACCCCTTCTCAT
 TCTCTTTCTTAAAACAACTGCGTGATCCCTTGAGAAAAGATAAAATTACATACACAAUATAAA
 CCAACTACGATCGCAAATTATGTCCTGGCAAGGTATGTGAACGAGACAAATTATCAATTG
 ATTAAGAAAGAAATCAGTCGGAGGCTAGCTTGTGTGACAATGTTTGGCAATGCCCGATTT
 TTCTTGATGCGCCCTAATTTTCAAGATTAAACCACTCAGAGTAAATTACTAACTGGAAATATC
 AAAAAACATATGAAATTTCAAACATGAACCTCTTTTCGGTTTTTTTCTCTCTACTTTTAAAC
 AGCATACACTGATAACTTAATAGGAACCGGTAAAGTACAAAGCTGTUATCTACTCGAG
 ACCAGGTGACGCTGTTTGGGCTACTTCTGGTGGCTATCTTTGCAACCAACCGAAATTGG
 TGAATTTTCAAGGCTTCGACAATCCAGCTGGTTTGCAAAGCAATGGTTTGCATATTCA
 ACGCCAAAAGTTTATGTTTGTAGAGCTGACGATAGAAGTATCTACGGTAGACATGATGC
 TCAGGGTGTGTTTGTGTAAGAACTAAGCAAAACCGTTATTATTGCTCATTATCCACCAAC
 CETACAAAGUCGGTGAAGGCCACCAAGATTGTCCAGCAATTGGCTGACTACCTGATTTGGTGT
 TCAATACFAA

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>YOR122C, 126 aa (SEQ ID NO 358)

MSWQAYTDNLIGTKVDEKAVIYSRAGDAVWATSCGLSLQPNBICEIVQGFDNPAGLQSNGLHIQGGQKFMLLRADDRSIYGRHDAEGVVCVTRTKQTVIIAHYPPTVQAGEATKIVEQLADYDVGQY

>YOR261C, 1517 bp, CDS: 501-1517 (SEQ ID NO 361)

GTAAGGTAAGGCATCATTAGCAGGATCCATATTCACCTACCTGGGAATGTCTTCCCATGGCATTGAAGAAGCTGTGAGCAGCCGTTGCAATAGGTTGACTTCCCTGAACCTGGTGGACCAATABCATCTGAGCGAAGGGCATTATCTGACTCTCTAGTAGAAAAATCAAACTATTGACACAACAACATCAAAATGAAAAACAACCATTCTATTACGGTAAGTAGTGAAAGACTCACAAATGCAATCTTTCAATGAGCATCACTTACTTTAAGTAGCAATATTCTTAATCACTTATTACGAAATTTGATTTTACTAAAGTTCGGGGATACCTCAGTGGCAAAATCGTTACTCAAGCTTCCACGTAACTAGATACTACAAATGAAATAATTGTGAAGCCAACAGCTAAGCAATCTATAGTGTAAACGTTGGCTTTCTGTACAACGTGCTAGCTGAGCGCATTTTTCGAATTTAAAAAAGAAAAGAAAAGAAAGGAAAAATCAAAATTACAAATGTCTCTACAACACGAGAAAAGTTACCATTGCACCACTAGTTTGTCTATCTGCTTTGGATCATTATGAGCGTACGCAGACAAAAGAAAACAAAAGATGCGTTGGTGTCTATCTTAGGTGATGCTAACAGTTCCACTATCAGAGTCACTAATTCCTTTGCTTACCGTTTGAAGAAGATGAGAAAACTCTGACGTTGTGGTTTTTAGACCATAATATATTTGAAAAATGAATGAAAATGTTTAAAAAGATTTAATGCCAAGGAAAACTCATTGGATCGGTATCTATAGTGGTCTCTAAATTAAGGGCTTCTGACCTCAAGATTAATGAGCTGTTTAAAAAATATACTCAGAAATAATCCGCTATTATTAATTGTTGATGTCAAACAACAGGTGTTGGTTTACCAAACAGATGCATATGTCGGGATTGAGCAAGTTAAGGATCATGCTACCTCTACACAAAAAGACCTTTCTTCATTTGCCCTTGTACTATTGAGGCCGAAGAAGCTGAAGAAATTTGGTGTAGAACACTTATTGACACAGTACCTGATCAAGCAGCAGCTCGCTTATCTATCCGGTTGACCAACCAATTTAAATCTTTGAAAGGATTACAAAGCAAACATAAAAGACGTTTGTGAGTACTTAGACAAAAGTCATTAATAAGGAATTACCGATAAACCACTATATTGGGCAAGCTACAAGATGTTTTCAACCTTTTACCAAATCTGGGAACACCTGATGATGACGAAATAGATGTGGAGAATCATGACAQAATTAATATCTCAAAATAACTTACCAAAAGGCTTTAACTGTGAAAACATAATGATGAATTAATGGTTATATATATAAGCAATTTGGTTTAGGTCAAAATATCGCGTTTGTATGATTTTGAATGAAAACAAAATTTCAAAATAAAAAAATTCAAACAACAAAGAGTAAAGGACAAAACAAATCAAAAGTCTCTGATGACAGTGAGAGTGAGAGTGGTGACAAAGAAGCAACTGCGCCATTGATCCAACGAAAGACACAAGAAAAATTA

>YOR261C, 338 aa (SEQ ID NO 362)

MSLQHEKVTHAFLVLLSALDHYERTQTKENKRCVGVILGDANSSTIRVTNSFALPFEEDEKNSDVWFLDHNYTENMNEMCKKINAKKKTGWYHSGPKIRASDLKTNELFKKYTQNNIDLLIVDVXKQQGVGLPTDAYVALEQVKDDGTSTFKTFLHLPTTBAEEAEELGVEHLLRDVRDQAAGGLSIRELTNQLKSLKGLQSKLKDVVEYLDKVINKELPINHTILGKLQDVFNLLPNLGTDDDEIDVENHDRINISNNLQKALTVEKTNDLMVIYISNLVRSIIAFCDLIENKIQNKKIQBQRVKDKQSKVSDDESESGDKEATAPLIQRKNKK

>YPL271W, 689 bp, CDS: 501-689 (SEQ ID NO 391)

CAGCAGCCACAACCTCAGAGTGCTTACAAAAAAGAGTTGATCCCGCTAAAGAAAGCTCTGATTTACGTATTTATCCAGGTTCAAACGGATTGCCAAAAATAGTCGATAACCTCGGAGTAAGCAAAGCAACAATATACTTGTCTCTCGAAAAGGTAACCTCTTAACCTCTATAGAAGCATTTCTACTAGTTCTCTCGAAGAAAAAACTAAGAAAGCTATAGCTGTATCTTACCAAGCCATGAACTTGAGGAATTGGTAATCTCTTATTAGGAAATAAGCTAAACTAGGTAATAGCAGATGATTTACTAGCTTACTATCTCAUACTAAGTCTGGCAAGCGCTTATTTTTTAATACTTTTATACGAACCAATGAAATTTGATCCTCCCTTTTTCGTCTAGTTAAATGAAGAGATACAAGTAGGCCCTTTCTATTGAGTACTTAGCAAGATATGTATTTCTAAGAAACATCAACAGTTTCAAGCCACAACCGATTTCATAAAATGTTCTGCTGAGGAAAGCTGGTATATCATATGCTGCAATATTTGAATGTGGCGGCTCAGGCTATCCGTTCTTCATTGAAAACCTGAATTACAAACCGCTAGTGTCTCTTAACAGATCGCAACAGATGCTTTTATACCCCAATATAAAATCGCACTGCAGCTTCTGAACCCACTCCAAATACAAAATAG

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>YPL271W, 62 aa (SEQ ID NO 392)

MSAWRKAGLSYAAYLNVAAQAIRSSLKTEIQTA5VLNRSQTDAFYTQYKNCTMSEPTPI
TK

>YPR035W, 1613 bp, CDS: 501-1613 (SEQ ID NO 395)

TAGTGCCATTGTGTCATTATTATTATCCCCAAATATGCGAAAATAGTACACTATTTTTTGG
 CAGGAGACTAGGCTGATATGCCGCATTGATGTCTGTGTAGCGAAACACAAACAAAAAA
 GAAAAAGCTAGGATGAAAAAAGAAAAAGTAATATGAAAAAAGAGTCAAAAAATTAATTCATT
 TGTTAGTGTAAAGCGGTACGGTGTAAAGTAGTAGGCTTGATAATGAATTAAGATGACTCCG
 ACGCATATGTGTTCGCATGTATTATTTTAGTTFGTAGATTTCTTTTTTTTGTAAATATATA
 AGGGAGTGATTCCTATATATCGAATTCTCAGGCTTCCTTGGTTCCGTAGCTTGTTCTGTCTT
 TGTATTTCGTTAGGTAAGAACATCACACAAAGATAACTATAGAATCACATACATATTTGTG
 AGAAATTAACTTTCAATTTATATAGAAGAAGTTCAACCGAAACAAAAATTAACATAAT
 ATAATATAATATAATCAAAAAATGGCTGAAGCAAGCATCGAAAAGACTCAAAATTTTACAAA
 AATATCTAGAACCTGGACCAAGAGGTAGAAATAATTGCCGAATACGTTTGGATCGATGGTA
 CTGGTAACCTTACGTTCCAAAGGTAGAACTTTGAAGAAAGAGAATCACATCCATTCAGCAAT
 TGCCAGAATGGAACTTCGACGGTTCTTCTACCAACCAAGCCCCAGGCCACGACTCTCACA
 TCTATTTTGAACCCGTTGCTTACTACCCAGATCCCCTCAGGAGAGGTGACAACATTGTCTG
 TCTTGGCCGCATGTTACAACAATGACGGTACTCCAAACAAGTTCAACCCACAGACACGAAG
 CTGCCAAGCTATTTGCTTCCTCATTAACCATGAAGAAATCTGCTTTGGTCTAGAACAAGAACT
 ACACTCTATTTGACATGTATGACGATGTTTACGGATGGCCAAAGGGTGGGTACCCAGCTC
 CACAAGGTCCTTACTACTGTGTGGTGTGTGGTGGCGGTAAAGGTTTATGCCAGAGACATGATCG
 AAGCTCACTACAGAGCTTGTCTTGTATGCCGGATTAGAAATTTCTGTATTAACGCTGAAG
 TCATGCCATCTCAATGGGAATTCCTCAAGTCCGTCCATGTACCGGTATTTGACATGGGTAAC
 AATTATGGATGGCCAGATACCTTTTTCACACAGAGTGCCAGAAAGAGTTTGGTATCAAGATCT
 CATTCOCATUCAAAGUCATTGPAAGGTGACTGGAAACGGTGGCCGTTTGTACCGCTAACGTTT
 CCACCAAGCAAAATGAGACAACCAGCTCCTACGAAATACATCCAAACAAGCCATCCGAACT
 TATCCCAAGAGACACGCTGAACACATTAAGTTGTACGGTAGCGATAACGACATGACATTAA
 CTGGTAGACATGAAGACCGCTTCCATGACTGCCCTTTTCTTCTGGTGTGCCCAACAGAGGTA
 GCTCAATTAGAATCCCAAGATCCGTGCGCAAGGAAGGTTACGGTTACTTTGAAGACCGTA
 GACCAGCTTCCAAACATCGACCCATACTTGGTTACAGGTATCATGTGTGAAACTGTTTCCG
 GTGCTATTGACAATGCTGACATGACGAAGGAATTTGAAAGAGAACTCTTCATAA

>YPR035W, 370 aa (SEQ ID NO 396)

MAEASLEKTPQLLQKYLELDQREGRLAEYVWLDGTCNLRSGRTLKKRITSLEQLPEWNFD
 GSSTNQAPGHDSDIYLPVAYYPDPPFRGDNIVVLAACYNNDGTPNKENHRHEAAKLPAA
 HKDEEIWFGLEQEVYTLFDMYDDVYGWPKGCGYPAPQGPYYCGVAGAKVYARDMIEAHYRAC
 LYA5LEISGINAEVMP5QWLEFQVGPCTGLDMGDQLWMARYFLHRVAEEFGIKISFHPKPL
 KGDWNGAGCHAMV5TKEMRQPGGTXYIEQAIEXLSKRHAETHIKLYGSDNDMLTGRHETA
 SMTAFSSGVANRGSSIRIPRSVAKEGYGYFEDRRPASKIDPYLVTGIMCETVCGAIDNAD
 MTKFERESS

YBR133C, 2984 bp, CDS: 501-2984 (SEQ ID NO 53)

AACTTACGACAGAGTTGTAATGAATGCTACTGATGTCTGCTCTACTGCCA
 TCCGCTGTCCCTTCATGCGATAAAAGCTCCATTCTTTATTTATCTCATACC
 ACGAGAAAAAAATACCTGACATATTTTATTAACCCGCCCTTTTGAAGC
 CTAAAACAGATCTCAGGGCTCGAGTACTGTTTTATCTGAAAAATCTTCGA
 GCCCTCGTTTTCGACTGAGCTAAACCAAAAGAAAAATAAACAAATCAGAAA
 TGGAACCCGAAACAGCACGCTGCCGAGTGTTTTATATTTTCTTGAAACA
 AATGGCTTTATACAAATGTGTATGTCTGATAGAAAAATGCTATATTTCCA
 GTGACTTGTGATCCTATTCCCAAGCCCTATAGGAGCTATTTCAATTCGCC
 TGTGTGAAAGCGTGTTGTGTGTGTGTGTGTGTGGAATTGTCCGGACGTTCC
 TCTTCTTTTATACATATAATTTTTATATATACAAAGGGTTCAGTTTGCA
 ATGCATAGCAACGTATTTCTTGGTGTCAAAACAGGCTTTAATCMTAAACA
 GCACAGCAAAAAGTCAGTTTCCCTAGAAAATGTCTCTAGTCATTCCACCAG

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AACTGCCTAGTAACTATGATTACGTTTTCCTTCTATAACACGCCAAGA
 TATAAGGAAATAGTTGGGCAAGTTTTCAAAGATTTCCAAACACAATCCAT
 ACAGAACTGGAAACCGCTTCBAATTCCCTGAACCGCASTTGCAGCATATCT
 GTATACCCCGGTTCACGGTACAGAGCTAGACAAACAGCAACCGCTCT
 TACATAGGGCTGTATCCCTCTTGGCTGGAGCTGGAGCTCGCGATCCAAA
 TGTAAGAGATCTTGGCTTAAAGGTCCCTCTAAACGAATCTAACTACCCGA
 GGTTCGTGGGAATCAATAAGCTAATATTGGCGCTCCACGGACCTGTCC
 AACCTGCAATCTGTATGGACAGATGATTTACAGGCTCCTGCAAAATCGCAT
 CGTCTTTGCTGGCGCTGCGTTAACCATAATCCATTTCTCTGCTACTTTACG
 AAGACAGCGATCCATTTGGCCACTTGGGAACCTGTGGAATACCGTGGGAAA
 CAATGCGAATCATCTCCCTCTTTGACTATCTCTTTGGCTTTGCCAAGAAC
 CAGGACTCCCTCGTATGTGCTGAATAGATGGTTAGCCGAACCGCTCTCGT
 GTCTTTTGGTATCTTCATCCATCTTTGCCAGTAATCAGTACGATTAATCCC
 GTTTTACACAAGTTTAAACAGAAATTTGATTTTAAAGTTCCAAAAGCTTAA
 TGGAGATTCACAAAATTTGGGTAAATGAATTAATGCGTGATATTGCATGGGA
 TCGAGAAATACCCAATAATGTTAAGGGCGGAGAATCTGCCTATTTGGAA
 TATATAAATCTATTATTGAAAAAGGGCGACAAAGTATTAAATTCBAATAG
 TAATCACCAACTTTTGCTCCAAGAGGACTCTCGGATAATGCCGCTCTGA
 AACCTCATTCAGATAATTTAATTAATTCACATAATTTGACCTTTGAAAAA
 GATTTGGTGAAGTACGATCTTTACGAATCTGCCATATTAGAGGCGCTTCA
 AGATCTTGCTCCTCGAGCGAGTGCCTAAGAGACCGTTGCTGATCTACTAG
 CCGGTGCGGGAAGAGGACCTTTAGTGGATCGAATTTTAAAGATAATATCA
 ATGTTGTTTTATGGAATAGTAAGGTTTCTATAATTGCCATGAAAAAATCC
 ACAGGCATATCTGTACTTCCAAAAAGAAATTTTGACTCTTGGCATAATA
 GAGTGAATTAATCAAGGAGGATATGACCAATGGCAATCAACGAGCCG
 TCGGAAAAAGCGTATTCAGATAGATCTGTGCATAAGTGAATGCTGGGTTT
 GTTCGCTTGCAATGAATTATCACCAAGATGTCTCTGGTCTATTGAAAAAT
 ATCATTCACCAATGACACAAATTTTCATACCGAGGTCATACTCTTCATAC
 ATAGCAACCATTTCTACCAATTTAATTCACCAAAAAATCTCACAAACAAA
 TCGCTCTTTGGAGGCGCCCTGGATAGTCCATAGAGTGCCATCTGTATAT
 TATCTCAAGGGTAATGAAGTGTGGCGGTTGAGCATCCCATGCCCCAA
 AAACATACTCTCCAAGACGAAGATCATTTTACAGTTGAATTTCTCAAAAG
 TTCATTAAATGAGTTCAGATAAAGCAACCGCGGCAATCCATGGCTTTA
 TCGGATCTCTCTCGGCRAACTTATATAACAATATATCTTTGTCAACTTTG
 CCCAATCACAGCACAGTCCGTTTAAATTTAGCGAAGAAACGTTGATGAA
 TACCAGACGAGAAGAAATCTAATCAAGAAATGTGACCATAACCCAAATA
 TCACCTCGTGGTCTCCAATATCTTTCTTTGAAGCAACCAATATCTTTT
 ATAGATGACTCCGAACCTTTCTGTGCTGATGTCTCGGATACACTCCGATAC
 AGAACAAAAAGTTTGGTATGAATGCTCTTTCCAGACTTTTCATATACCTTA
 TGTGTGCAAAATTACACTTTCGGCGGTAACGTCTGCAAGCATGACTATCCG
 AGGTCTATAGTTACAGATCACACTAAAACPTTAGCCCNATATCGACATTA
 TTCAGCGACTACCAATCAAAAGCTAGATAATCAAAATTGATCTTGACCAAG
 ACATTTGAAAACGAAGAAGAACAGGGATTCTTATCCAATCTAGAAACTGGT
 TGGCAAAAGCGTACAAGATATTCACGGACTCAGCGAAACCGCCAAACCGGA
 CCATTTAGATTTCTATCAATAAGCCATATGTTTGATCTCAAATCTACTAAAG
 CCTTGAACCCCTCTAACGAATTGCCAAGCCACCAACCTCCAGGAAGAT
 GTTCCAGAAGTTTATGTGAGACTCAAGACTAGTGTTCACAGCTACATAA
 TGTCTGTGGCAGAGCCTTTTCCCTGUCTCTGTGA

YER133C, 827 aa (SEQ ID NO 54)

MHSNVFVGVKPGFNHKQHSKKSRLFNVSSSHPELPSNYDYVLLFITTFR
 YKRTVGGVFKDQQRQS(QNNKPLQIPEPQLQDICIPFNVKKI)NDQTPS
 YIGLLSSWLELRSRDENVRIHGLKVLINCKYARFVGINKLI)AFPHHS
 NLQLYGOMIYRLQNRILVFAAPALPISISLPLYEDSDPLATWELWNIVRK
 QCEYHPSLTISLALPRTRTPSYVLNRWLAEPVSCLLVSSSIFAENQYDYF
 VLHKFNQNLILKFKQKVGDSQILGNELCVILHGMEKYANNVKGESAYLE

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YINYLLKKGDKVLNSNSNHQFLLOEDSRIMFPLKPHSDNLLNSTYLTFEK
 ULVKYDLYESAILEALQDLAPRASAKRPLVILVAGAGRGPLVDRTFKIIS
 MGFMDSKVSIIAIEKNPQAYLYLQKRNFDCEWNRVKLIKEDMTKMQINBP
 SEKRIQIDLCISELLGSFGCNELSPECLEWSEIKYHSINDTIPTIRSYSSY
 IAPISSPLFYQKLSQTNRSLEAPWIVHRVFCILSSRVNEVWRFEHPMAQ
 KDTVQDEDDFTVEFSQSSSLNEFKIKHRGEIHGFCFFSANLYKNIFLSTL
 FNDSTVRLKFPSEETLMNTRREENLIKKCDHTPNMTSWSPLIIFPLKQFLSF
 IDDEELSVLMSRIHSDTEQKVWYEWLSLEFIYIMLSNYTSAVTAASMTIP
 RSTVTDCTFKTLAHRHYSAATTNQTLDNQIDLXQDTENEEFQGFLSNLETC
 WQSVODIHGLSETAKPDHLDSEINKPMFDLKSITKALEPSNELPRHEDLEBD
 VPEVHVVRKTSVSTLHNVCGRAFSLEPL

YBL085W, 3443 bp, CDS: 501-3443 (SEQ ID NO 31)
 AAAGGGGAAGTATGGCATGCCCTAGAAATCTTTTCTGGAAACTTGAAGCAT
 ATCATATAATTGTATGAACCTGTCCCTCAAAGATGTTACCAAATATTCA
 AGAGTATGTGAGCTTCTATCTTATTGACGCGTAAGAAAGGCTATCACGT
 GTGGGGGGGAGAGCTCAGCCACATTGCACTACTTTTGGAAACCGCTAGTC
 GGAAACGACATTTCCCGGTACCAAACAAACGAAAGGACGTGAAGGTAA
 ATGAATAACATGGCACTAAAAATTTGGCAGAAACGAAAAAAGGAA
 AAGGAAACTGAAACTATACGCTTCCCTTAGGATACCTTCGTATACAT
 CCGAAGAATTGGGTGCTCAATTAAACGCAATTCCTCCCTCTATCAAGCA
 GTTTTACTGCGTCTCTCTAAACAAACATTCCTTTACTCAATTTCAACAA
 AGTTCTAACTCGAGGTGACCGGAGGCCACTGTAATAATAAAAAATAGAAG
 ATGAGTCTTGAAGGAAATACCCCTAGGCAAGGGGCCAAATCTTTTCTCTCT
 GTATATTGCGGTAAATCAGTACTCTAAACGAATGGAGGACGAGCTCAATA
 TGAACACAGGTGATAAAATTAAGTCATTAAGTATGATGGGGASTACAAT
 GACCGCTGGTATTTATGGGCGCAATTTGAGAACCAAGAGGAAGSTTTATA
 GCCAGCGGTATTTACCAAAGAATAGCAATAGAAAAACCTAGAGAACCTGC
 ACAATACCAACCCCAAGAGAGTGGAAATTCCTGGCTGTAAATAAGGAAAT
 TTAATGATTCTGCGAGTAACATAGGTAAAGTCTCCTCGCATCAACAGGA
 GAACAGATATACATCATTGAAAAGTACAATGAGCGATATAGACAAAGCCT
 TGGAAAGAGCTAAGAAGTGGTTCAAGTGAACCAAGAGGTATCAAAATCGCCC
 ACACGCGTGGCCGAGTTAGCACTCCACAGTTGCAAGATGAACAGACTTT
 GATTCAAGAAAAACCAAGATGAGGAAAAACAGACACATGACTCGTTAT
 ITTCTAGCACAGCGGATTTAAACTTAAGTTCTGAATCTTTGAAGAATATA
 ACTAAGTCAAAATATATCAACAAAAACCTAGAACCGAGTTCCGGAATCAGT
 TCGTCAATTAGATTTGAAAATGGCTAAAAGTTGGAGCCACAGAAGAGGTTA
 CTGATTACTTTAGCTTGGTTGGATTGATCAATCCACTTGCAATAAATTC
 AAGAGCATCAAGTCTCCGGAAAAATACTACTCGAATTAGAACTCGAACA
 CCTAAAAGAATTGGAAATAAATTCCTTTGGTATAAGATTCAGATATTCA
 AAGAAATAAGGAACATCAAGTCTGCAATTGATTCCGTCTCAAAATAAACCTG
 GACGCCGACTACTCTACCTTTTGCTTTTGAAAACCAAGCTGCCCAACTAAT
 GCCTGACGCCACTGTAAATAGAGACGAATCCAAACAAATTTCCCTCCA
 AGTGTAACAAGTTGTCAAGTGAAGCTCTGATAGAAATCATCTTCGGTC
 ACCACAGAATTGCAAGACCAAGCTCGGTTGTTGTTAATCCCAATTTTAA
 ACTTCACGACCCAGCTGAGCAGATCCTAGATATGACAGAAGTTCCCTAATT
 TGTTTTGCTGATAAAGATATTTTCGAATCACCGGGGAGGGCTCCAAACCA
 UATCATATCCAAGTCCAGTTCAACCTCCACAATCCGCTCTTTTAATAAA
 CAGGTACACAAATAATAACGCAAGGTTTCCCTCCTCAACACACATATCCAC
 CTAAAAACAACAACCAACCGTTTATTCAAACTGGGCTAATTCCAAATTCT
 TCGACATCTTCCGATAAATCAACGGGCAAGTTCAAAATCCCTCGCATGAA
 TGGTCATGACTCGAATCTTAGGAAAAACAACACTGACATCTGCTACTATAC
 CTCTATTAAACACCGTTAAACACACATGAATCTCTACCCGCAATTTCAAAAT
 ATATCTTCAAAATGCTACATCTCATCATCCGAACAGAAATCCCGTTGTTTA
 CAATAACCATAAGAGGACCGAATCCCGAAGCTCATTGTTGATTGTTCA
 ACAGGATTTCAATCTATCCCGAGTCAAGTCAAGTTTCGACGAAGAAGAA

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ACGAAACAACCTTCAAAAGCTAGCAGAGCAGTCTTTTGACTCAGCAGCGCAG
 AAGTTCGTCTTACGGACATTTCAAGAGATGCCTCACTTTCTGAAATGAAAA
 AGCATAGGAGAACTCTTCTATATTATCTTTTTTTTTCTTCAAAAAGTCAG
 TCTAATCCAAACGTACCAACCAACAAACTTTCACTATCGATCCCGCAAA
 GATGACTTCCCATTCTCGTTCTCAGTCGAATTCCTATTGCGATGCAAGAT
 CACAATCTTACTCCCATAGTAGAAAACTCGTTAGTTACCAGCCCCCTTG
 AAACTTCTTTAAGUCCATATAAAATCCAAATCCAATATTGCTTTAGCGCA
 TAGCGAAACTCCTACTAGTAGTAATAATAAGGAGGCAGTATCACAAUCAA
 GTGAAGGGGAGCACAAGCACAAGCACAAGCACAAGCACAAGCACAAGCACA
 AAGAACAGTAGCTCCAAAGATGGCTCTTCCGAAGAAAAAACA AAAAGAA
 ATTATTTAGTAGCACCAAAGAATCATTTTGTAGGAAGCAAGGAATTCAAAA
 GATCTCCCAAGTGAACCTACCCAAAPATCTACCAATCGATACTTCCCAGG
 TCGAATGCTAAAAAGCAACAAACATCTGCTTTTACCGAAGGTATACGCTC
 TATCACAGCAAAGGAATCTATGCAAACTCCCGACTCTTCAGSCTGGATGA
 GCAAAAAGGTACCGGTGCTATGGGGACTTGGAAACAACGGTTTTCACA
 CTTCTAGCGTAACAAGGCTTTCTTATTTTACGAATACCAATGATGAGAAGGA
 GCTCGCGCTGATAGATATAACGGCACATAGGGTCTTACCTGCCAGTGATG
 ATGATAGGCTCATTTCTTTATACGCTGCGAGCTTAGGAAAAGGAATAAC
 TGTTTTCAAAATTGGTCCCTCCGCAACCGGGGTCCAAAAGGGGCTAACCTT
 TACAGAACCTCGCGTTCACTATTTTGCAGTTGAGAATAAATCTGAAATGA
 AGGCATGGCTGTCAGCCACAATAAAGGCCACTATTCATATTGATACAAGC
 GTCCCTGTCATTAGTTCAATGCCACACCAACGATACCTCTAAGCAAGGC
 ACAGACGCTATTGGAAGAAGCTAGGTTACAAACCCAGTTAAGAGATGCTG
 AAGAGGAACAGCCCAAGACATCAATTTCCATGGGATGACACCCAAAATAAA
 AGAAATTCTAATTATCCAATCGAACAAGATCAATTTGAGACCAACCATTA
 CCTGGAAAGTTCAAGCATTTGAATAAUCUUGGTGGCAGACTTTGA

YRIJ85W, 980 aa (SEQ ID NO 32)

MSLEGNTLKGAKSFPLYIAVNQYSKRMEDELNMKPGDKFKVITDOGEYN
 DGWVYGRNLRKKEGLYPVFTKRIAIEKPENLHKEPTQESGNSGVKYGN
 LNDASNIGKVSSHQENRYTSLKSTMSDIDKALBELRSGSVEQEVSKSP
 TRVPEVSTPQLQDEQTLIQEKTRNFENTTHDSIFSSTADLNLSSSLKNI
 SKSNISTKSLEPSSSVRQLDLKMAKSWSPPEVTDYFSLVGFQDQSTCNKF
 KEHQVSGKILLELEHLKELEINSFGIRFQIFKEIRNIKSADSSSNKL
 DADYSTFAFENQAQLMPAACTVNEDEIQQISSKUNKLSSESSDKKSSSV
 TTELQRPSSVVVNPNEKLHDPAEQLDMTEVPNLFADKDIFESPCRAPKP
 PSYPSPVQPPQSPSPNNRYTNNNARFPQITTPPKNKNPVTVYNGLI PNG
 STSSDNSTGKFKFPAMNGHDSNSRKCTLSATIPSTINTVNTDES LPAISN
 LSSNATSHHPNRNSVVVNNHKRTESGSSSFVDLFNRISMLSPVKSSFDEEF
 TKQPSKASRAVFDQARRKSSYGHISRDASLSEMCKHRNSSLFFSSKSO
 SNFTSPKQTFTIDPAKMTSHSRSSQNSYSHARSQSYSHSRKHS LVTSP
 KTSLSPIINSKSNIALNISTPTSSMNKEAVSQPSEGKHKHKHKSKHKH
 KNSSSKDSSSEKSKKKLFSSSTKESFVGSKEFKRSPSELTQKSTKSILPR
 SNAKKQQTSAFTEGIRSITAKESMQTAACSGWMSKKGTGAMGTWQRFFC
 LMGTRLSYFTNTNDEKERGLIDITAHRVLPASDDRLISLYAASLGKGY
 CFKLVPFPQPSKKGLTFTEPRVHYFAVENKSEMKAWLSAIIKATIDIDTS
 VPISSYATFTIPLSKAQTLLEEARLQTQLRDAEEEEECRQPCWEDTQNK
 RNSNYPIEQDQFETSDYLESSAFEYFGGRL

YDR545W, 5891 bp, CDS: 501-5891 (SEQ ID NO 137)

TTCTATTATATTGGTCTTTTCGAGAGCGGAAGAAGTTGTAGGCTAAGCGC
 AGGCTAAGCGCTAGGTCATATTTAACTATCCAAGACAATATCCACCAAG
 CGGCTGAGCAACGAACAGAATCCTGGTTCTCCTCGACTTACCAGATAGTT
 AAGATACTGTGCACCATGGAAATTGAAAACGAAAGTACGTACCGACTACT
 TTATTTTTTGCAGGCCCGAAATCAAGCGATGAATGAGACATCCTTCTGTTT
 TCTATGTTGGGACAGACAGTCGGCTTATCTTAGTGAGATTCTTATTAAC

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GAATTTTCTTGTGCTGCTGCTGGAGATTTGCACCTGCATAGCGCAGATTCT
GUTTCCTTCTCAATAGAGTAGCTTAATTTATTACATTCTTAGATGATGATAA
GACGCAAACTCGACAACTCTTTGCTTTATATTGATGGATTCTTGTCAAAA
AGCATAACAATCAACACATATTGTTAATTTGAAACTTACAAAAATAAA
ATGAAAGTTTCCGATAGGCGTAAGTTTGAAAAAGCAAACCTTTGACCGAGTT
TGAGTCGGCTCTAAATAACAAAAACGACTTGGTACATTGTCCCTCAATAA
CTTTATTCTGAACTCGAATCCCAACGGAAGTGGGTCAATTCTACGAAGACGAA
AAGTCTGGCCTAATCAAAGTGATAAAATTCAGAACCTGGTGCAATGGATAG
GAAAAGGTCTTTTGAAAAAATTGTCATTTCCGTCAATGGTGGGAAAAATG
TAAAAAGTTCTCTGACATTTGTTGAAGACGAAACAGATTTCAGGGCGGA
CCAATCCCTTCAAAGTATCTTATTCCCAAGAAAATCAACTTGATGGTCTA
CACGTGTCTTTCAAGTGCATACTTTGAAATTCATAGAAAGGATTACGATA
CCCTTTTCTTTTCTTACCTCAACAGAGGATACATATAATGAGTTGAGTTTTC
CGTGTCTCTGGAACGTTGTACCGAAATAGCGAGTCCCAAGCCGAAACGACAG
CTCTACGATGCGTACTTTCACTGACTTTGTCTTCTGGCGCACCTATTGTAA
GGAGTCTTCAGAAAAGCACCATAAGGAAATATGGGTACAAATTTGGCACCC
TACATGTTCTTGTTAATACACGTAGATGAGCTATGATTTTCTCTGATA
CCAAGCAAGTTTACCTGGCGAAAAGAAAGTCCGACAAAGAGCGGCTGAAGC
GTGATCTATGCCACGTAACCCATTGAGATAAAGTACTTTTCACAGATA
TGTAACGATATGATGAACAAAAAAGACCGATTTGGGTGATATTCTGCTAT
TATCTTCCGAGCATGTGCGCTCAATTTCCGGCGGGTCCCGGTGGTGGCG
CTGCTGACGAAGAGGATCGATCTATTACGAATGAAGAACCCCATTTATTTCC
TCTGTGGACGAGCATGGCTTCAAAATATGTAAGTTGGGTAGTCTTAAACAC
TCCACGAAGACTCAGAAAAACACTAGATGCCGTGAAAGCTTTATTGGTGT
CGCTTTGTGCTTGTACTGTCAAGGGATTAGATATATTTGATGACACCAAC
GGCGTTTGCAATGTGGAATGGATCAAAATTCGTACCACGAAGTAGCGCA
GGAAACUACGCTGAAGGACTCTTATAGAATAACTTTTGGTAACTTTCTTCTG
ATGGTATATCAGTATGTGGAACCTTTTAAATCCGAGTATGTCCGCGGC
TTTTTACTTTGCATGCAAGGCTCAGTTGATAACCTTTGGGGAGACTTGAA
CAACTGCTTTTATATGCCTACAGTGGTTGATATTGCCAGCCTCATTTTGC
GTAATGAGAGAAGTTTTGTTCCAGAGAGCCAAAGCGAGGAATTGACGAGTAT
CTGGAACAGATTCTTTTCTTCAAATGATACCTGTTAAATATCTGTAAAT
TGTCTCTGCCCAAGTTGAGAAGAGATACTAACAAATGACCGCGGCTCTTA
AAAATAAAGTCACTGTTCGAATTCACGAGCTTACGGTGCCACTTATGTGG
ATGGTCCATTTTGGCGTAGGATACCCCTTACCGTTATCCAGAGCTTCAGCT
ACTCGCTTTTGGCGGTCTCTCAGCGCAACGTATAAGTCCGATGATACAA
GACGCATCCAACTGTACACTGATTACAAACAGAACGGTTCATCGSAGCCT
CGACTTAAGACCGCTTGACGGACTCACTTCAGATACGTTGCTTTTATTTGT
CACTCTGCTATGCCAATGCCAATATGTCCGCTTGGTAACACTTATGACG
CTTTTAATCATGATCCTTCCATGGATGTGGTGGGATTTGAGGATCCAGAT
CAAGTAACAAATCGAGACATTTTCGAGGATAGTTTTGTATTCCCTACAACTT
TCTGAATACCCCGAAGGGCTGTCTGGTTGAATACGCAACTTTTCGGCAGT
ACATGAGGGAACTTCCCAAGAATGCACCTCAGAACTGAATTTTCGGCAG
ATGCGTCAGGGGTTGATTGCGCTAGGACGGCACTGCGTAGGTAGCAGATT
TGAAACAGATTTGTACGAGTGGGCGACGAGTGAATCATGGCCAATCAT
CCGTTCAAACAGGGCGAAATATTTACGGTGTGGATTCTTTTCGTTAACT
AGTGTCAAGTGGGACGACCGCCACTTTATTGCAGGAACGAGCTTCCGAGCG
CTGGATTCAATGGTTAGGCCCTGAAAGCGACTACCATTTGTTCAATCTCTA
GTACTCGGAATGCGGAAGACGTAGTGGCAGCTCAGCGGGCAGTTTCAGAT
CATGATCAAAAAATTTCAAGAGTAACGCGAAAAGGCCCCGAGAGCCCCA
GAGTACAAAAGATATCTTGGTGGCAGGCGAGAAATCTTTTGGCAGCTCCT
TTGAATTCAGGGACTTGATCAGTTGCGCTTATGTCATGAAATATACATG
GCGACACACCCCTCTGTGCCAGTACAGGCCCAACCCCTATGGTAAGAC
GGAATTTATTTCACTCCCCCTTGATAGCACTGGCGTCTAAGGGCGAGCTGA
AATATGTGTCTGTTTCTGTTTGTACCGTACACAGTGTGGCTTGTAAATTC
ATGATCAGGTTGACCCGATGCGGTTGCTTGAATGTGGCCCTGTAGAAA

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CTTTATTGAAGAAGGTTGCGATGGCGTTACTGATTTATACGTGGGGATCT
ACGATGATCTTGTAGCACTAATTTACAGACAGGATAGCTGCCGTGGGAG
AATATTCTTGAGTGCACCTTTAGGACCAACAACGTAAMTTGCTTACCT
CATTGTATATGAGTTTCACAACCTTTGAAACGGAGGTCTACCGGCAGTCCG
AATTTGGGGGCATACCTAACCCTTGATTTTGACGCTTTTGAGAAAACAAATC
TTTTTGAGCGGCACACCACCTGAGGCTCTACCTGATGCTGCCCTTCCAGCC
TATTGGGCTTACGGCACTGSCCAAGAACTCGATGGACATCAACGAGCTCA
AACGGTCGGAAGATCTCAGCAGAGGTCTATCCAGCTATCCAACACGGATG
TTTAATCTAATCAAGGAGAAATCCGAGGTGCCCTTAGGGCATGTTCATAA
AATTTGGAAGAAAGTGGAAATCACAGCCCCGAAGAAGCACATGAGGTTCCTTT
TAGCCCCCTTTGAAATTGAACCAGAGTCGAAGGCCATTGTAGTTGCAAGC
ACAACCAACCAACTCGAAGAATTGCCCTCCCTCTTCCAGAAAGTATTTAG
GGTAGGATAGCATAACGGGAAGCTGGGTGCTGCAGAAAAGGTGTCACGCA
CAAAGGAGTTTGTCACTGACGGTAGCATGCGAGTTCTCATCGGAACGAAA
TTAGTGACTGAAGGAATTGACATTAAGCAATTGATGATGGTGATCATGCT
TGATAATAGACTTAAATATTATGAGCTCATTCAAGGCGTAGGGAGACTAA
GAGATGGGGGCTCTGTATTCTATTATCTAGAAAAACAGTTGGGCGGCA
ACGAATCTAAGGGTGAATTACCACCGATTAGGAAGGCTGTATTAACCGA
ACAGGTACGCGAGTTCTATCGACTTGAATCAAAGAAAGCAAAAAAGGGCC
AGCATGTTGGATGCTGTGGCTCCAGGACAGACCTGCTGCTGACACAGTG
GAAGTGATAGAAAGAATTGGACAGATTGGCTGAAAAACAGGCCACAGCTTC
CATGTCCGATCATTGCCCTTACCCTCTAGCTTCCAGGACAGCAATAGCCACTG
ACAGGTGCAGAAAGTATTGACAGCAGTGATGAGGACAGCGACACGTGCATT
CATGGTAGTGCTAATGCCAGTACCAATGCCACTAUGCACTCCAGCACTAA
TGCTACTACCACTGCCAGCACCAACGTCAGGACTAGTGCTACTACCACTG
CCAGCATCAACGTCCAGGACTAGTGGGATTACCAGTGAAGTACCAACTCC
AGCATTAATGCTACTACCACTGCCAGCACCAACGTCAGGACTAGTGCTAC
TACCAGTCCAGCATCAACGTCAGGACTAGTGCGACTACCACTGAAAGTA
CCAAGTCCAAACACTACTGCTACTACCACCCAAAGTACCCACTCCAACACT
AGTGCTACTACCAACCGAAAGTACCGACTCCAACACTAGTGCTACTACCAC
TGCTAGCACCAACTCCAGCACTAATGCCACTACCACTGCTAGCACCAACT
CCAGCACTAATGCCACTACCACTGAAAGTACCAACGCTAGTGCCAAAGGAG
GACGCCAATAAAGATGGCAATGCTGAGGATAATAGATTCCATCCAGTCAC
CGACATTAACAAGAGTCCGTATAAGCGGAAGGGAGTCAAAATGCTTTTGC
TAGAGAGAAAGAACTGAAAGCACAAATTTCCCAATATTTCCGAGAAATATG
AATGCTCTTACACTTTCTTGGATTTCGGTCTACAGAAATTAAACATCTTTT
CCTCTATGGTATTGACGTATACTTCTGCCCCAGAGGGAGTATTACACAAAT
ACUGATTATGCAAGGGCTGTCAAAAGATGTTTCGAGCTCTGTGTCTGTTGG
GCTGGCCAGAAAGTATCGTATCGGAGGATGGCTTGGGAAGCACTAGCTGT
GGAGAGAATGCTGCCAAATGACGAGGAATACAAGAATACTTGGAGAGACA
TCGAGCCATATCATGGGGACCCCTGTAGGATATTTGAAATATTTTAGCGTA
AAAAGGGGAGAGATCTACTCTCAGATACAGAGAAATTATGCTTGGTACCT
GGCCATTACTAGAAGAAAGAGAAACAATTAGTGTATTGGATTGACACAGAC
GCAAGCAAGGGAGCCAAGTTTTCCGCATGTCTGGAAGGCAGATCAAAGAG
TTGTATTATAAAGTATCGAGCAACTTTCGTGAATCGAAGACAGAGGTGCT
GCAGTACTTTTTGAAGTGGGACGAGAAAAAGTGGCGGGAAGAATGGAGG
CAAAAGACCATACGGTCTTTGTGGAAGCGCTCGAGAAAGTTGGAGTTTTT
CAGCGTTTGGCTTCCATGACGAGCGCTGGACTGCAGGGTCCGACGTACGT
CAAGCTGCAGTTTAGCAGGCATCATCGACAGTTGACGAGCAGATATGAAT
TAAGTCTAGGAATCCACTTGCAGATCAGCTTGGCTCCGAGTTACCCCA
TCTAAAGTGCCGATTTGGACGGCATTCCTGTGATGCTCATAGGGCTGT
CTACAATAAAACATTTTGGCAGAAACTGGAATATCTTTTGGAGCAGATTT
CGSAGGTGTGGTGTGTACCACATTGGCTTGATTTGGCAAAAGCTTGAAGTT
CTCGCTGCAGATAACACGAGGGTACCGCTGTACATGCTGATGGTAGCGGT
TCAAAACAGCTGCATAGCGATGATGTTCCAGACGGTAGATTTGATATAA
TATTACTATCTAGAGATTGAGACAGAGAAGTTGAGACTGA

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YDR545W, 1796 aa (SEQ ID NO 138)
 MKVSDRRKFEXANFDEFESALNNKNDLVHCPSTLTFESIPTEVRSFYEDE
 KSGLIKVKVFRFTGAMDRKRSFEKIVISVMVGKNVQKFLTFVEDEPDFQGG
 PIPSKYLI PKKINLMVYTLFQVHTLKFNRKDYDTLSLFYLMRGYYNELSP
 RVLERCHEIASARPNDSSTKRTFTCFVSGAPIVRSLQKSTTRKYGYNDAP
 YMFLLHLHVDLSIFSAYQASLPGEKKVDTERLKRDLCPKRPTEIKYFSQI
 CNDMMNKKDLRGDILHLILHACALNFGAGPRGGAGDEEDRSITWEEPIIF
 SVDEHGKVKCKLRSPNTPPERLRKTLDAVKALLVSSCACTARDLDIFDDTN
 GVAMWKKWIKTLYHEVAQRRTTLKDSYRTTINPSSDNTSVCGKLFRRFYVRG
 PYPACKAQFDNLWGEI MNCFYKPTVVDIASLILRMREVLFRFPKRGID EY
 LENDSFLQMI PVKYREIVLFKLRRTNKMTAALKNKVTVAIDELTVPLMW
 MVHEAVGYPYRPELQLIAFAGPQRNVYVDDTTRRIQLYTDYNNKGSSEP
 RLKTLDBGLTSDYVFYFVTVL RQM QICALQNSYDAFNHDPWMDVVGFEDPD
 QVTNRDTSRI VLYSYMFLNTAKGCI VRYATFRQYMRSLPKNAPQKLNFRF
 NRQGLIALGRHCVGSRFBTDLYESATSELMANHSVOTGRNIYGVDSFSILT
 SVSGTTATLLQERASERWIKWLGLES DYHCSFSSSTRNAEDVVAGEAASSD
 HDQKISRVTKRPREPKSTNDILVAGQKLFSSSFEFRDLHQLRLCHEIYM
 ADTPSVAVQAPPGYGKTRIFHLPLJATASKGDVKYVSFLFVPTYTVLLANC
 MIRLSRCGCLNVAPVSRNPIEEGCGVTDLYVGJYDOLASTNFTORIAAWE
 NIVECTFRNTNNVKLGYLIVDEFHNFEFETEVYRQSQFGGITNLDFDAFEKAI
 FLSGTAPFAVADAALQRICLTCLAKKSMIDINELKRSEDLSRGLSSYPTRM
 FNLIKBEKSEVPLGFVHKIWKKVESQPEEALKLLLALPEIEPESKATVVAS
 TTFEVEBELACSWRKYFRVWVIEHGKLGAAEKVSRTKEFVTDGSMRVLIGTK
 LVTFEGIDIKQLMMVINLNDNRNLNIEELIQGVGRLRGGGLCYLLSRKNSWAA
 RNRKGEELPPIKRGCTTEQVREFYGLESKKKGKQHVGGCGSRTDLSADTV
 ELIERMDRLAEKQATASMSIALPSSFQESNSSDRCKYCSSDEDSDTCI
 HGSANASTNATNSSSTNAITTA STNVRI'SATTTASINVRTSAITTESTNS
 STINATTA STINVRT'SATTTASINVRTSAITTTSTNSNTSATTTRSTNSNT
 SATTTSTSTDSNTSATTTAS'N SSTNAIT'TASTNSSSTNAIT'TESTNASAKE
 DANKDGNADNRFHPVTDINKESYKIRKGSQMVLLERKKLKAQFPNT'SENH
 NVLQFLGFPSDEIKHFLPYGIDVYFCPEGVFTQYGLCKGCKMPFELCVCN
 AGQKVSYSREMAWEALAVRMLRND EYKEYLEDJEPYHGQPVGYLKYPVS
 KRGEIYSQIQRMNAYWIAITRRRFTTSVLDSTRGKQGSQVFRMSGRQIKE
 LYYKWSNLSRESKTLVQLQYFLNWDEKKCREPWEAKDDTVFVZALEKVGVF
 QRLRSMTSAGLQGPQYVKLQFSRHRQLRSRYELSLGMDHLRDQLALGVTP
 SKVPHWTFALSMLICFPYKKTFRQKLEYLLFQISEFWULLPHWLDLANVEY
 LAADNTRVPLYMLMVAWEKELDSELVDPDGRFDLILLCRDSSREVG E

YCR005C, 1883 bp, CDS: 501-1883 (SEQ ID NO 71)
 AGAGTTGTTGCCACAACATAAGCCGCTTTGAGTGTTGAACAAATCCGTC
 CTTGGGTCATTCAATCAATGCGCTTGGCGGTATCTCAAAAGACGGCAAACT
 AATAGCGCGCACATTGACGCAATTAATCCGCTGGTCATCGACTAGCGGCG
 AAGAGGTCACGACCTATTTTCTCTGCAGAAAAAACTCTGACCTTTTCC
 GTAGCTAGACGCTATTCAGGCGCTCAGCAATGCGAGGCACAGCGGAAAAA
 CAATAACAAATGGTAAGCGCAATTACCTTTTGAGCGTTACATTGATGAA
 ATTGGTGACGTTAATCTAAAGATAGTCATGCTCTCAAAAGGCGCCATTAT
 TCTCGACGCTTGAGCGTATAATAAGACTATTAAGAACTTGCTTCTTTAGATAT
 GGTGTTCTGTTCCATTAATTAAGTTTACAGGGAACAATATCAACACATATC
 ATAACAGGTTCTCAAAACTTTTTGTITTAATAATACTAGTAACAAGAAAA
 ATGACACCTTCTTATCTAAATTCAAAACAGAAATGTTGCATCATATTTACA
 ATCAAAATCAAGCCAAAGAAAAGACTCTAAAAAGAGAGATTTAGCGGAATCT
 ACCCCATCCATGCTCAAGATGTAAGGCAATTCGTTAAAGAGCATGCGAAA
 ACTAAAATTAGCGATGCTTCATTAAGAACAGGTATATGCGTGGTATAGAGG
 TATTTCCAGGGAGCGTATGGGAAGGTTCCGTTTGGACCCAGAAAGACGGTA
 TTCTGTTTCAGAGGTCTGATACCATCGCCGACATTCAAAAGGACCTGCCAAG
 CCATAACCAAGCTCACAAACCACTACCAGAAAGCTCTCTTTTGGCTTATTGCT

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AACTGGCGAGGTTCCAACTCAAGCGCAAGTTGAAAACCTTATCAOCTCATC
 TAATGTCAAGATCGGAACCTACCTAGTCATGTCGTTCAACCTTTGGATAAT
 TTACCAAAAGCACTTACAUCCCAATGGCTCAATTCTATTGCTGIAACTGC
 CTTCCAAAGCGAGTCAAAGTTTGCIAAGGCTTATGCTCAAGGAATTTCCA
 AGCAAGATTATTGGAGTTTATACCTTTTGAAGATTCACTAGACTTGCTGGGT
 AAATTGCCAGTTATTGCAGCTAAAAATTATCGTAATGTATTCAAAGATGG
 CAAAATGGGTGAAGTGGACCCAAATGCCGATTATGCTAAAAATCTGGTCA
 ACTTGATTGCTCTTAAGGATGAAGATTTCGTGGACTTGATGAGACTTTAT
 TTAACCATTCATTCCGGATCACGAAGGTGGTAATGTATCTGCACATACATC
 CCATCTTGTTGGGCTCAGCACTATCATCACCTTATCTCTCCCTTGCATCAC
 GTTTGAACGGGTCTGCTGGCCCTTCATGGGCGTGCTAATCAAGAAGTA
 CTAGAATGGTTATTTCGACTTAAAGAAGAGGTAAATGATGACTACTCTAA
 AGATACCATCCAAAAATATTTATCGGATACTCTAAACTCAGCAAGACTCA
 TTCCCGGTTATGGTCATGCTGTGCTAAGGAAAACGATCCTCGTTATATG
 GCTCAGCGTAAGTTTGCCATGGACCATTTTCCAGATTATGAATTAATCAA
 GTTAGTTTCAATCAATATACGAGGTAGCACCTGCCGTATTGACTGAACATC
 GTAAACATAAAATCCATGGCCAAATGTAGATGCTCACTCTGGTGTCTTA
 TTACAATATTATCGACTAAAAGAATCTTCTTTCTATACCGTTTTATTTGG
 CGTTTCAAGGGCATTTGCTATTCTTGCTCAATTGATCACTGATAGGGCCA
 TCGGTGCTTCCATTGAAAGGCCAAAGTCCTATTCTACTGAGAAATACAAG
 GAATTGGTCAAAAACATTGAAAGCAAACCTATAG

VCR005C, 460 aa (SEQ ID NO 72)

MTVPYLNSNRNVASYLQSNSSQEKTLKERFSEIYPIHAQDVRQFVKEHGK
 TKISDVLLLEQVYGGMRGIPGSVWEGSVLDPELGLRFRGRPIAJIQKDLPK
 AKCSSQPLPEALFWLLLTCEVPTQAQVENLSADLMSRSELP SHVVQLLDN
 LPKDLIIPMAQFSIAVTALESSEKFAKAYAQGISKQDYWSYTFEDSLDLLG
 KLPVIAAKIYRNVTKDGKNGEVDPKADYAKNLVNLIGSKDBDFVDLMRLY
 LTIHSDHEGGNVSAHTSHLVGSALS SPYLSLASEGLNGLAGPIHGRANQEV
 LEWLFALKEEVNDYSKDTIEKYLWDTLNSGRVIEPGYCHAVLRKTDPRYM
 AQRKFAMDHFDPDYELFKIVSSIYEVAPGVLTMEHGKTKNPWPNVDAHSGVL
 LQYYGLKESSFYTVLFCVSRAPGILAQLLTDRAIGASIERPKSYSTEKYK
 ELVKNIESKL

VOL126C, 1772 bp, CDS: 501-1772 (SEQ ID NO 345)

ATCCCCCTCATACTTTTCCGTTTGTATCTCCTACTTTCTTACTTCCTTTTTT
 TTCTTCTTTACTTTCCTTGGTTTACCATTGAACTCCATTTTACTACAGAC
 AATAGCTAGTCATTTCGCTATCTTCCGTTTGTCACTTTTTTTCAAATTTCT
 CATCTATATAGUGAAGTACGGAAAAGATGTCACCTTGGCCGCACTCCGGCC
 TTCCCCCGCCAAATGGACTCATCATCTAGGATACGGCCCCCTTAATCCGC
 AATTACTTTTCCCCATTCCGGCCGTAGCCGTTCTAAAGCCCCCGTGCCTTGC
 CCCCATACTCCCCAATGATCCGGGAAGTTCCGGTTTTTTTTCTTTGTT
 TAGTGGCAATTTGTGTGTTTGGCCAAAGTTGGGAAGGTCCGATTTGACTTTAA
 GGAACCTACCGAAGGTATCTAACGTTTCTAAAAACAATATACACCGCCGTG
 CGTAGATATATAAAGATAAAGATTTATCGATATGAGATAAAGATTGCTGC
 ATGATTCTCCCTCTGATTTCTTTTCCCTGTATATATTTTCTCCCCCTCTCG
 TATAAATCGTACAGTCAGAAGTAGTCCAGAATATAGTGCTGCAGACTATCT
 ACAAAAGTTCAATACAATATCATAAAGTTATACTAACATGCCCTCACTCA
 GTTACACCATCCATAGAACAAGATTCGTTAAAAATTGCCATTTTACGTCG
 TGCCGGTGGTATUGGGCAGTCTGTTATCGCTGCTTTTGAAGGCTCAGTTGC
 AATACCAGTTAAAGGAGAGCAACCGGAGCGTTACCCACATTCATCTGGCT
 CTTTACGATGTCAACCAAGAAGCCATCAACGGTGTACCGCCGACTTGTCT
 TCATATAGACACCCCCATTTCCGTGTGAGAGCCACTCTCTCTGCAGGTGSCA
 TTGAGAAGCTGTTTGCATAACGCTTCTATTGTTGTCTATCTCTGAGGTCTT
 CCAAGAAAACCTGGCATGACTCGTGATGACTTATTTAACGTGAATGCTGG
 TATCATTAGCCAGCTCGGTGATTTCTATTGCAGAAATGTTGTGATCTTTCCA

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AGGTCTTCGTTCTTGTTCATTTCCAAACCCGTGTTAATTCTTTAGTCCCAGTG
 ATGGTTCCTAACATTCCTAACAAACCATCTCAGTCTAGAAATTCGGCAT
 TGAAAGAGGATCATGGGTGTACCAAGCTCGACATTGTGAGAGCGTCCA
 CTCTTCTACGAGAGATAAACATTGAGTCAGGGCTAACTCCTCGTGTAAAC
 TCCATGCGCTGACGTCCCTGTAAATTGGCGGGCATTCTGGCGAGACTATTAT
 TCCGTTGTTTTCACAGTCAAACCTCCTATCGAGATTAAATGAGGATCAAT
 TGAATATTTATACATACAGTCCCAATACGGTGGTGATGAACTGGTCAAC
 GCCAAGAACGGTAAAGCTAGTGTACCTTATCGATGGCCCCATGCCGGTTA
 TAACTGTGTGTGCCAATTTCTTTCTTTTATTTCCTAACATTGAGCAGA
 TCCATGGAAACCTACTATGTGCCATTAAAAGATGCGAACAACCTCCCCATT
 GCTCCTGGGGCAGATCAATTATTGCCTCTGGTGGACGGTGCAGACTACTT
 TGCCATACCATTAACTATTACTACAAAGGGTCTTTCTATCTGCATTATC
 ACACTGTTAATAGGATGAACGACATGGAACGCAACCAAAATGTTGCCAATT
 TGGCTCTCCAGTTAAAGAAAAATATCGATAAGGGCTTGGAATTCTGTTGC
 ATCCGATCTTCATCATCTTAA

YOL126C, 423 aa (SEQ ID NO 346)

MILLILLFPFCIYFLPFCINRTVRSSPEYSAADYYKSSIQYHKSYSNMPHS
 VTPSIEQDSLKIALILGAAGGIQSLSLLLKAQLQYQLKESNRSVTHIILA
 LYDVNQEAINGVTADLSHIDTFISVSSHSPAGGIENCLHNASIVVIPAGV
 PRKPGMERDILFNVNAGLIISQLGDSIAECDDLKVFYLVISNPNVSLVPV
 MVSNIILXNHPQSRNSGIERRIMGVTKLDIVRASTFLREINTESGI/TPRVN
 SMPDVPVIGGHSGETIIPLESQSNFLSRINFDQLKYI/THRVQVGGDEVVK
 AKNGKGSATLSMAHAGYKCVVQPVSLLLGNLEQIHGTYYVPLKDANNFPI
 APGADQLPLPLVDGADYFAIPLTITTKGVSYVDYDIVNRNMDMERNQMLPI
 CVSQDKINIDKGLFVASRSASS

YBK019C, 2600 bp, CDS: 501-2600 (SEQ ID NO 39)

ATCGCTTCGCTGATTAAATTACCCAGAAATAAGGCTAAAAAACTAATCGC
 ATTATCATCTCATGCTTGTAAATTGTGATTCTTAATTGAAGGCTTGTGG
 GGCCAGGTTACTGCCAATTTCTCTTCATAACCATAAAAGCTAGTATT
 GTAGAATCTTTATGTTCCGAGCAGTSCGGCCCGAGGCACATCTCGGTTT
 CAGCAACCGGACCGGTGAAGACGAGGACGACCGGAGGACACTCTTCCGTC
 GGAGGCTGTTCGCCCGCTCGGCGGCTTCTAATCGTACTTCAATATAGCA
 ATGAGCAGTTAAGCGTATTACTGAAAAGTTCCAAAGAGAAGGTTTCTAG
 GCTAAGATAAATGGGGCTCTTTACATTTCCACCAACATATAACTAAGATTAC
 ATATCGATATGTATATGTTGGTAATGCCATGTAATATGATTATTAAGCT
 CTCTTCGCTCCATCCAAAAAAAAGTAAGAAATTTTGAAGATTCAAATATAA
 ATGACAGCTCAGTTACAAAGTGAAGGTACTTCTAAAATTGTTTTGGTTAC
 AGCTGCTCCTCGATACATTGCTTCACACACTGTGGTAGAGCTAATTGAGA
 ATCCATATGACTCTGTTGTTGCTGATAACCTGTGGAATTCAACTTATGAT
 TCTGTAGCCAGGTTAGAGGCTCTTGACCAAGCATCAATTCCTCTCTAAGA
 GGTGATTGTTGTGACCGAAAAGGTCTCGAAAAGGTTTTTCAAAGAAATATA
 AAATTGAATTCGGTAATTCACCTTTGCTGGTTTTAAAGGCTGTAGGTGAATCT
 ACACAAATCCCGCTGAGATACTATCACAATAACATTTTCCGAACGTGCTGT
 TTTATTAAGAGTTAATGCAACAATACAACGTTTCCAAATTTGTTTTTTCAT
 CTCTCTGCTACTGTCTATGGTGATGCTACGAGATTCCTCAATATGATTCTCT
 ATCCCAGAAGAATGTCTCTTAGGGCTACTAATCCGTATGGTCAATACGAA
 ATACGCCATTGAGAATATCTTGAATGATCTTTACAATAGCGACAAAAAAA
 GTTGGAAAGTTTGCATCTTTCGCTTATTTTAAACCAATTGGCCCAATCCC
 TCTGGATTAAATCGGAGAAGATCCGCTAGGTATACCAAACAATTTGTTGCC
 ATATATAGCTCAAGTAGCTGTGTTGGTAGGCGGAGAGAAGGTTTACATCTTCG
 CAGACGATTATGATTCCAGAGATGGTACCCCGATCAGGATTATATCCAC
 GTACTTGATCTAGCAAAAGGTCAATATTCAGGCCCTGCAATACCTAGAGGC
 CTACAATGAAAATGAAGGTTTTGTGTCTGAGTGGAACTTGGGTTCCGGTA
 AAGGTTCCTACAGTTTCTGAAGTTTATCATGCAATCTGCAAAACCTTCTGGT

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ATTGATCTTCCATACAAAGTTACGGGCAGAAGAGCAGGTGATGTTTTGAA
 CTTGACGGCTAAACCAGATAGGGCCAAACGCGAACTGAAATGGCAGACCG
 AGTTGCAGGTTGAAGACTCCTGCAAGGATTTATGGAAATGGACTACTGAG
 AATUCCTTTTGGTTACCACTTAAGGGGTGTCGAGGCCAGATTTTCCGCTGA
 AGTATSCCTTATCAGCCAAGATTTCTGACTATTGCTGCCGCCACCAGAT
 TTCAAGCCACGTTTGGCAATTGGGGCGCCAGCATGCTGACCTGAAAGTG
 AACGGACANTCAGTTGTTCTTGGCTATGAAATCAGGAAGCCTATTTGAA
 TCCTCATAGTGCTTATATAGGGCGCCACGATCGGCAGGTATGCTAATCGTA
 TTTTCGAAGGGTAAGTTTACTTTATGCAACAAAGACTATCAGTTAAACCGTT
 AATAACGGCGTTAAATGCGAATCATAGTAGTATTCGGTTCTTTCCACAGAAA
 ANGATTTTGGGACCCATCATTTCAAAATCCTTCAAAGGATGTTTTTACCG
 CCGAGTACATGCTGATAGATAATGAGAGGACACCGAATTTUAGGTGAT
 CTATTGGTAAACCATACAGTATACTGTGCAACGTTGCCCAAAAAAGTTTGGT
 AATGGTATATATAAAGGTAAATTGACTGCTGGTGAAGCGACGCCAATAAATT
 TAACAAATCATAGTTATTTTCAAATCTGAACAAGCUATATGGAGACACTATT
 GAGGTTACGGAGATTATGGTTCGCTTCAAAAAATCTGTTGATGTCGACAA
 AAACATGATTCTACGGGTAATATCGTCGATAGAGAAATTGCTACCTTTA
 ACTCTACAAAGCCAAACGGTCTTAGGGCCCCAAAAATCCCCAGTTTGATTGT
 TGTTTTGTGGTGGATGAAAATGCTAAGCCAAGTCAAATCAATACTCTAAA
 CAATGAATTGACGCTTATCTCAACCTTTTCATCCCGATTCTCAAATATTA
 CATTAGAAGTTTAAGTACAGAGCCAACCTTATCAATTTTATACCGGTGAT
 TTCTTGTCTGCTGGTTACGAAGCAAGACAAGGTTTTGCAATTGAGCCCTGG
 TAGATACATTGATGCTATCAATCAAGAGAACTGGAAAGATTGTGTAACTT
 TGAAAAACCGTGAAACTTACGGGTCCAAGATTGTCTACAGATTTCCTCGA

YBR019C, 699 aa (SEQ ID NO 40)

MTAQLQSESTSKIVLVTCACAYIGSHTWVELIENGYDCVVADNTSNSTYD
 SVARLEVLTKHHIPFYEVDLCDRKGLEKVFKEYKIDSVIHFAQLKAVGES
 TQIFLRVYHNNILGTIVLLELMQQVYKVSKEVFSSTATVYGDATRFPMNTF
 LPEECPLGPTNPFYGHTKYAIENILKDLVNSDKKSWKFAILRYFNPICGHP
 SGLIGEDPLGIPNNLLPYMAQVAVCRREKLYIFGDDYDSRDGTPIRDYIH
 VVDLAKGHIAALQYLEAYNENEGLCRENNLGGSGKSTVFVYHAFCKASC
 IDLPYKVTGRRAGDVNLTAKPDRAKREIKWLYPFIQVEDSCKDLWKWTE
 NPFQYOLRGVEARFSAEDMRYDARFVTIGAGTRFQATFANLSASIVDLKV
 NCQSVVLGYENEBGYLNPDSAYIGATIGRYANRISKGRFSLCNKYQLTV
 NNGVNAVNISSIGSFIRKRLTGPIIQKPSKDVFTAEYMLIDNEKDTFPGD
 LLVTIQYTVNVAQKSLEWVYEGKLTAGEATPINLTNHSYFNLNKPYGDTI
 EGNEIMVRSKKSVDDVDKNNIPTGNIVDREIATFMSTKFTVLGPKNDQFDC
 CFVVDENAKPSQINTLNEELTLIVKAFHPDGNITLIVLSTEPYQFYVGL
 FLSAGYEARGFAIEPGRYIDAINQENWKDCVTLKNGETYGSKIIVYRFS

YDR345C, 2204 bp, CDS: 501-2204 (SEQ ID NO 123)

TCTTAGCTATATTCTTCCAGCTTCGCCTGCTGCCCGGTGATCGTTCTGT
 CAGGTAGTTTTCGGGATTGCTCCGGCTCATATAATACCGCAATAAACAC
 GGAATATCTCGTTCCGGCGGATTCGGTTAAACTCTCGGTCCGGGATTATCA
 CAGACAAGCTTCGTGGAGAAATTTTCCAGATTTTCCGCTTTCCCCGATG
 TTGGTATTTCCGGAGGTCAATATATCTGAUCCGCCATTATAATGACTGTACA
 ACGACCTTCTGGAGAAAGAAACAACCTCAATAACGATGTGGGACATTGGGG
 GCCCACCTCAAAAAATCTGCCCACTATATCCCCAGAGAAATTTCTCCAGAAG
 AGAAGAAAAGTCAAAGTTTTTTTTCGCTTGGGGGTTCGATATAAATACAG
 CGCGTGTTTTATCTTCAGCATGAATATTCATATAATTTTACTTAATAGCTT
 TTCTATAAATAATAGAATCAAAACAAATTTACATCTGAGTTAAACAATC
 ATGAATTCAACTCCAGATTTAATATCTCCACAAAAGTCAAGTGAGAAATTC
 GAATGCTGACCTGCCCTTCGAATAGCTCTCAGGTAATGAACATGCTTGAAG
 AAAAAGGTGTTCAAGATGATTTCCAAAGCTGAGGCCGACCAAGTACTTACC
 AACCCAAATACAGGTAAAGGTGCATATGTCACATGTTGTTCTATCTGTGTGT

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TATGGTTGCCCTTCGGTGGTTCGTCTTCGGTTGGCACTGGTACCATT
 CTGGTTTCGTGCGCCCAACTGATTCTTCGAGAACATTGGGTATGAAGCAT
 AAAGATGGTAGTTATTATTTGTCTAAGGTTAGAACTGGTTTAATTGTCTC
 CACTTTCAACATTGGTTGTGCCATIGGTGGTATTATTTTGGCTAAATTGG
 CTGATATGTACCGTCCATAAAATGGGTTTCATTGTCGTTCTTCTTATCTAC
 ATCATCGGTATTTATTATTCAAATTGCATCCATCAACAAATGGTACCAATA
 TTTCATCCGTAGAAATTATTTCCGGTTTGGGTGTTGGTGGTATTGCCGTTT
 TACCTCCCTAIGTTGATTTCTGAAGTCGCTCCTAAGCAAAATGAGAGCTACT
 CTAGTCTCTGTACCAACTGATGATTACCTTGGGTATTTCTTGGGTTA
 CTGTACCAACTTCGGTACTAAGAACTACTCCAACCTCTGTGCAATGGAGAG
 TCCCATPACGTTTGTGTTTTCGCTGGGCTTTGTTTATCATCGGTGCTATC
 ACTTCGTTCAGAAATCCCCACGTTATTTGGTTGAAGCTGGTCAAATTGA
 CGAAGCAAGAGCATCTCTTTCCAAAGTTAACAAGGTTGCCCCAGACCATC
 CATTCAATTCACAAGACTTCCAAAGTTATTGAACCTAGTCTTGAAGAAGCT
 AGAGCTTGTGGTTTCAGCATCATGGGGTGACTTGTTCACTGGTAAGCCGGC
 CATGTTTAAGCGTACTATGATGGGTATCATGATCCAATCTCTACAACAAT
 TGACTGCTGATAACTATTTCTTCTACTATCGTACTACCGTTTTTAACGCT
 GTTGGTATGAGTGATCTTTCGAAACTTCTATTGTTTTCGGTGTGCTCAA
 CTTCTTCTCTACTTGTGTCTTTGTACACTGTGATCGTTTTTGGACGTC
 GTAACGTGTTTGTATATGGTGGCATTGGTATGGTCTGCTGTTATGTAGTT
 TACGCTTCTGTTGGTGTCCACCAGACTATGGCCAAATGGTGAAGGTAATGG
 TTCATCCAAGGGTGTCTGGTAACTGTATGATTGTCTTTGCCTGTTTCTATA
 TTTCGTGTTTTGCTPACCACTTGGGCTCCAATTGCTTATGTTGTTATTTCT
 GAAACTTTTCCATTGAGAGTCAAGTCTAAGGCTATGTCTATTGCTACAGC
 TGCTAATTGGTTGTGGGGTTCTTGATTGGTTTCTTCACTCCATTTATTA
 CTGGTGCTATTAACCTTCTACTACGGTTACGTTTTCATGGGCTGTATGGTT
 TTCCGCTACTTCTACCTTTTCTTCTTGTGCCAGAACTAAGCGTTTGAC
 TTTGCAAGAACTCAATGATATCTACGCTGAAGCTGTTCTACCATGCAAGT
 CTGCTTTCATGGGTTTCCAACATCTCAAGAGGCTGCTAACTACGATGCTGAT
 GCATTGATGCATGATGACCAGCCATCTACAAGAAAATGTTCCGGCAAGAA
 ATAA

YDR345C, 567 aa (SEQ ID NO 124)

MNSTPDLI SPQKSSSENSNADLPNSSQVMNMPEEKGVQDDFQAEADQVLT
 NPNTGKGA YVTVSICVMVAFGGFVFCWDIGTISCFVAQTDFLRRFGXKH
 KDGSYYLSKVRGTGLIVSIFNIGCAIGGII LAKLGDYGRXMG L I V V V I Y
 IIGIIIQIASINKWYQYFIGRIISGLGVGGI AVLSPMLISEVAPEKMRGT
 LVSCYQLMTLGLIFLGYCTNFGTKNYNSVQWRVPLGLCFAMALFMI GCM
 TEVPESPRYLVFAGQIDEARASLSKVNKVAPDHPFIQOELEVIEASVEEA
 RAAGSASNGELFTGKPFAMFKETMGINIQSLQQLTGDNYPFYGGTTVFNA
 VGMSDSPETSLVFGVVMFPSTCCSLYTVDRFGRKNULLYGAIGMVCCYVV
 YASVGVTRELWPNGEGNGSSKGAGNCMIVFACFYIFCTFATWAPIAYVVT
 ETEPLRVKSKAMS IATAANWLWGFLIGFPTTPTTGAINFYGYVFMGCMV
 FAYFYVFFVFPETKGLTLEBVNDMYAEGVLPWKSASWVPTSQRGANYDAD
 ALMHDDQPFYKMFGEK

YKR097W, 2150 bp, CDS: 501-2150 (SEQ ID NO 263)

ATAGGAAAAAACCGAGCTTCCTTTTCATCCGGCGCGGCTGTGTTCTACATA
 TCACTGAAGCTCCCGGTATTTTAACTTATACAAGCAAAACATGCCGGCTA
 GACTAGCAAGTTTTAGGCTGCTTAACATTATGGATAGCGGATAAAAGGCG
 CCAACAGGATTGTAAAGCTTAGACGCTTCTGCTTGGACAAATCCTACGTT
 TGTGTATTAAGTAAAGCTTGGCTGGGATAGCAACATTGGGCAGAGTATA
 GAAGACCAACAAAAAAGGTATATAAGGGCAGAGAASTUTTTGTAAATGTC
 TGTAACCTCTCTTCUATGNGTAATCAGTATTTCTACTTACTTCTTAAATA
 TACAGAASTAAGACAGATAACCAACAGCCTTTCCAGATATACATATATA
 TCTTTATTTTCAGCTTAAACAATAATTATATTTGTTTAACTCAAAAATAAAA

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AAAAAAAAA CCAAAC TCACGCAACTAATTATTCCATAATAAAATACAC
 ATGTCCTCCCTTCTAAATGAATGCTACAGTAGGATCTACTTCCGAGTTGA
 ACAAATAATCAGACAAGAATTGGCTCTTAGTGAAGAAGTCACCAACATCA
 GACCCAATTCCTCCAGCTCCCTTTTCTATGAAGATGGTCTAAAAGAAAT
 AAAACTCATTCATCAAGCGGTGCATTGATCGCTTATTCGGGTGTTAA
 AACCGGAAGATCTCCAAAGGACAAACGTATTGTTGAAGAACCTACCTCGA
 AACACGAAATTTGGTGGGCTCGGTCATAAACCATGTTCTGAAAGAACA
 TGGCTATTC AACCGTGAAAGAGCTGCAGATTACTTGAGAACAAGAGACCA
 CATTTATATTTGTCGATGCATTTGCAGGATGGGATCCAAATACAGAATCA
 AAGTCCGCGTTGTTTGTGCCAGGCTTACCACGCTTTATTCATGCAAAAT
 ATGCTTATTAGAATACAGAAGAAGAATTAGCCCATTTTGGAGAACCTGA
 TTTTACTGTCTGGAACGCTGGTCAGTTCCAGCCCAATTTACACACCCAGG
 ATATGTCCTTCAAAAGACTACTATAGAAATTAACCTTCADAGCAATGCAATC
 ATCATTTTAGGTACCGAATACGCCGGTGAATGAAGGATTTTTCAC
 AGTTATGTTTTACTTTGATGCTGTGCACCAATAACGTTTAACTTTGCAC
 CTTCGCCCAACCGGCTATTTCAAAACGGTGACCTTACTTTATTCTTTGCC
 CTAAGTGGTACCGGGAAAACCACTTTATCCGCAGACCCACATAGATTGTT
 GATTCGGCGATGATGAACAATTGTGGTCCGACCATGGTGTCTTCAATATCG
 AAGCTGGTCTTTACGCCAAGCTATTAATTTATCTGCCGAAAAGGAGCCT
 GAATTTTCGACGCTATCAAGTTTGGTTCTGTATTAGAAAACGTTATCTA
 TGACGAGAAGTCGCATGTAGTCGACTATGACGACTCTTCTATTACTGAAA
 ATACTAGATGTGCCTACCCAAATGACTACATTCCAAAGTGCCAAAGATTCCA
 TCTTTGCCGGACTCTCATCCAAAGAACATTATCCTGCTAACTTGTGATGC
 TTCGGGTGTTTTACCACCAGTATCTAAATTGACTCCTGAACAAGTCATGT
 ACCATTTTATCTCTGGTTACATTTCTAAATGGCTGGTACTGAGCAAGGT
 GTCACTGAACCTGAACCAACATTTTCATCTTCTTTCCGACCAACCTTCT
 AGCCTTGACCCCTATTAGATACGCAACCATGTTAAGCTACAAAGATGTCTC
 AACATAAGCTAATGCGTACTTAATCAACACCGGCTGGACTGGTTCTTCC
 TACGTATCTGGTGGTAAACGTTGCCCATTTGAAGTACACAAGGSCCATCT
 GGATTCTATTCTATGATGGTTCTGTTAGCCAAATGAAACGTACGAAACTTTAC
 CGATTTTCAATCTTCAAGTACCTACCAAGGTTAACGGTGTTCAGCTGAG
 CTTTATGAATTCCTGCTAAACACTGGTCTCAAGGTGAATCCAAATACAGAGG
 TGCAGTTACCAACTTGGCCAACTTGTGTTGTTCAAAATTTCAAGACTTATC
 AAGACACAGCCACACCAATCTATTACCCCTCGTCTCTCAANTCCAGTAA

YKR097W, 549 aa (SEQ ID NO 264)

MNP SKMNATV GSTSEVEQKIPQELALSDEVTTIRRNAPAAVLYEDGLKEN
 KTVI SSSGAL IAYSGVKTRSPKDKRIVEEPTSKDEIWWGFPV NKPCERT
 WSINREAA DYLRTRDHIYVDAFAGWDPKYRIKVRVVCARAYHALFMTN
 MLIRPTSEBLAHFGSPDFTVWNAQGFANLH TQDMSKSTIEINFKAMEM
 IILGTEYAGFMKKGTFTVVFYLM PVHHNVILHLSSANQGIQNGDVTLFRG
 LSGTGKTTLSADPHRLILGDEHCWSDHGVFNIEGFCYAKCINLSAEKBP
 EIPDAIKFGSVLENVIYDEKSHVVDYDSSITENFRCAYPIDYIPSAKIP
 CTADSHPKNIILTCDA SGVLPPVSKLTPEQVMYHFI SCYT SKMAGTFQC
 VTEPEPTFSSCFGQPFLLALHPIRYATMLACKMSQHKANAYLINTGWTGSS
 YVSGGRKRCPLKYTRAILDS LHDGSLANETYEPLPIENLQVPTKVNQVPAE
 LLNPAKNWSQGESXYRGAVTNLARLFVQNFKIYQDRATPDVLAAGPQFE

YMR173W, 1793 bp, CDS: 501-1793 (SEQ ID NO 313)

AAACAAGTGTAAACATAAATACATTCTGTAAATCTACAAAAATCGTTAGTG
 CTGTTTTCTTTTTGAGATTGAAAGTACGAATCATACACATCTCTTATTC
 TGAGAAGGGGTGCATATGACGTAAATCAATGCCGTACAAAGCGGTTTCGGGT
 GCTGGCCTGGCCCCACCACAGTTTTTGGCGTGGTTGATTTTTAAACCTTCG
 CGAAGGTGAAAAACCACTCCGAAGGTTGAGGATGACAAATCGCCCCCTT
 AGCTGTGGCCATACAAGCTTGGCACCGACGAAAAACGGAAAAAGGAAAAAG
 AATGTCGTACAGAACCTCTTACAAACCAGTTGAGATTTCATTTAACAACG

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CCCCCCTTCCATTATATAAGAAGGCATTAAATTTTTATGTAATAAAAAA
 GAATTTTCUGAAATGTCTTACAATTAAATTTTTCTTTTGTAGAGTAGGG
 CTTTAATAGACTGATATATACGGTATTATAAGTGAACGAAAAAACAGCA
 ATGGGTTTATTTGATAAAGTGAAGCAATTTGCTAACAGCAATAATAACAA
 CAATGATTCTGGCAATAACAATCAAGGCGATTATGTTACCAAAGCTGAGA
 ATATGATCGGCGAACATACACTCAATCAANTCMAAAGCAAAATCCGACAG
 GACAGATTTGATAAGATGGAGTCCAAGCTTCGTCAACAATTTTCTAATAC
 CTCTATAAATGACAACGACTCCAACAACAACGACTCATATGGTTCTAATA
 ACAACGATTTCATATGGTTCTAACAACAATGATTTCATATGGCTCTAACAAC
 AATGATTTCATATGGCTCCAACACAAATGATTTCATATGGCTCTAACAACGA
 TGATTCTTACGGTTCTTCCAACAAGAAGAAGAGCTCTTATGGTTCTAACA
 ATGACCAATCCCTACGGCTCCAGCAACAACAATGACTCTTACGGTTCCAAC
 AACATGACTCTTACGGTTCCAACAACAATGACTCTTACGGTTCCAACAA
 TGACGACTCTTACGGTTCTGTCAAACAAGAATAAGAGCTCTTACGGTTCCA
 ACAATGACGATTCTTATGGCTCTAACAATGATGATTTCATATGGTTCTTCC
 AACAAGAAGAAGAGTTCTTATGGTTCCAGCAACAACGATTCTGATGGTTC
 TAACAACGATGATTTCATATGGTTCTAACAACAATGATTTCATATGGCTCTA
 ACAACGATGATTCTTACGGTTCTTCCAACAAGAAGAAGAGCTCTTATGGT
 TCTAACAATGACGATTCTGACGGCTCCAGCAACAACAATGACTCTTACGG
 TTCCAACAATGACGACTCTTACGGTTCTGTCAAACAAGAATAAGAGCTCTT
 ACGGTTCTTCTAGCAACGATGATTCTTACGGATCTTCCAATAACGACGAC
 TCTTACGGTTCTTCCAACAACAACAAGTTCTTATGGTTCCAACAATGA
 CGATTCTTATGGCTCTAACAATGATGATTTCATATGGTTCTTCCAACAAGA
 AGAAGAGTTCTTATGGTTTUCAGCAACAACGATTCTGATGGTTC TAACAAC
 GATGATTCTTACGGTTCTTCTAACAACAAGAAGAGTTCTTATGGTTCCAA
 CAACGATGATTTCATACGGCTCCAGCAACAACAATGACTCTTACGGTTCCA
 ACAATGACGACTCTTACGGTTCTTCTAATAAGAAACAAGAACTCTTATGGG
 TCTTCCAACCTACGGTTCTATCCAACAATGATGACTCTTATGGTTCTATCTAA
 TAGAGCCCTCTCAATCAATACGGCTCTGACGACGATTACTAA

YMR173W, 430 aa (SEQ ID NO 314)

MGLFDKVKQFANSNNMNDSGNNNQGDYVTKAENMIGEDRVNQFKSKIGE
 DRPDKMESKVRQQPSNTSLNDNDSNNEDSYGSNNDSYGSNNDSYGSNN
 NDSYGSNNDSYGSNNDDSYGSSNNKKSSYGSNNDSYGSNNDSYGSNN
 NNDSYGSNNND SYGSNNDDSYGSSNNKKSSYGSNNDSYGSNNDDSYGSS
 NKKKSSYGSNNDSYGSNNDDSYGSNNDSYGSNNDDSYGSSNNKKKSSYG
 SNNDDSYGSNNND SYGSNNDDSYGSSNNKKSSYGSNNDDSYGSNNDD
 SYGSSNNKKKSSYGSNNDDSYGSNNDDSYGSSNNKKKSSYGSNNDSYGSNN
 DDSYGSNNKKKSSYGSNNDDSYGSNNNDSYGSNNDDSYGSNNRNNKNSYC
 SSNYGSSNNDDSYGSNNRGRNQYGGDDDY

YII057C, 995 bp, CDS: 501-995 (SEQ ID NO 217)

CCAACAGATTTCAASTCTGTGCGCTTAACCACTCGGCCATAGTGCCTAA
 AACAATGTAGGTTATTTAAGCAAGTATTGTAGATACITTTTCGTAATAAAC
 TACAATGCACCCACGACTCGCGGTGTAATGATGGCATGAATCATTTGAAC
 GAAGTTTTGCGGCTATACGGCTGAAGGACGAGACTAAAGGGACAGCAATT
 ATTAATGCGGGGTATAAATTTGAATAGTATTAAAGGGCACTGCGGTTTACG
 CATCAAAATGCTATTGTTGGGGTATTCTCTCTACITTTTTGTTCTTGGCTTG
 AACCTTTTTCGGCGGTTGGCAATCGTCCGTATATAAGCATCGGCTGTCCCA
 ATCCTCTATTGCGCTTTTCCCTTGCACCTCCTTCTCAATCTTCGTATCT
 TTCCGCTAAAGGTAGATCTTGATTACCTATCTGTGGAACACGATTAAAG
 TGCAAACGAAACAACGTACAGTATATAACAAAGTATTTTAAATAATAAGA
 ATGACGAAAAAGGATAACAAAGCAAAAGCGTCCTAAGATGTCCACCAACAC
 TACAAAAAGTGGTGAGTCTTTAAAGGTITTTGAGGATTTGCATGATTTTG
 AAACATATTTAAAGCGCTGACACGGAAACATCAAGAGTTCCACCATGTCCAT
 TGCCAACTCAAGTACTATCCACCTTTGTCTCTGCATGATGCGCATGATGA

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TCCCGAAAGATCAAAGAGACTGCCAATTCGCACTCTAAGAAAGTTTGTTC
GCCATTTACACCAGCATGTTGAGAAGCACCTGCTAAAGGACATCAAAACC
GCTATUACAAGCCAGAATTGAAATTCACGATAAGAAAAACAGGAATC
CTTTGACCGGATTGTTTGGAAATTATGGCGAAGAAACGGAGTTGAACGCCA
AGAAATTCAAGGTGTCTGTGGAAGTGTATATGTAACACCGATGGCGCAATC
GTAGATGTTGATTACAAGACAGAACCCTTGCAGCCACTCATCTAA

YIL057C, 164 aa (SEQ ID NO 218)

MTKKDKKAKGPKMSTITTKSGESLKVPEDLHDFETVYLRGETEDQEFDHVH
CQLKYYPFVLHDAHDDPEKIKETANSHSKKFVRHLHQHVEKHLKDIKT
AINKPELKFHDKKKQESFDRIWANYGBETELNAKKFKVSVEVVKHDGAM
VDVDYKTEPLQLI

YDR544C, 929 bp, CDS: 501-929 (SEQ ID NO 135)

TAAAGTAGTCGGTACGTACTTTTCGTTTTCGAATTTCCATGGTGCAAGTAT
CTTAACCTATCTGCTTAGTCGAGGAGAACCAGGATTCTGTTTCGTTGCTCAG
CCGCTTTCGTGGATATTCTCTTGGATACTTTAAATATGGACCTACGCTTAG
CCTGCTTTCGTAGCTTACAACCTTCTTCCGCTCTCGAAAAGACCAAATATAA
GAAAGTTATAAATTACATTTCCTTATTAGGTATACGACCTCGCGCTTCGA
AGTAGAGGAGCCCCCTTTTGGCGTACCTACATATGGCGCTCAGACAGACA
AACTTCCCCCAAAATGTATTACCCCGCCGAATAAGAAAACAGACCCATT
CACCCAGGACGTATCAAGTTACTTCCCTGGTGCATGTCCCACTATAAAA
AAATTTCCTTGACGCTAGATCGTTGGACTAAAATCTGCGTCACAATCGCT
AAACAGGAATATTGCCTATTTCGCTACAAGGTIACCTTCCTAGATGCTAT
ATGTCCCTACGGCCTTGTCTAACACCATCCAGCATGCAATACAGTGACAT
ATATATACACACCACACCACACCCACACACACCAACACACACCCACACA
CCACACACACACCCACACCCACACACACCCACACACCCACACACCCACA
CCAGAGAGAAGCCTAAGCCTAAGACTAAGACAAGCCAAAGCCTGACCAACC
TGTCTCTCAAAATACCCCTCCATTACCCCTACCTCCCCACTCGTTACCCCTGA
CTCATTCAACTATACACACCCCAACCACCATCCATCTCCCTGTGTACTACC
ACCAACCGACCGCTCCACCATAACCCCTTACCCTCCAATTACCCATATCCAA
CTCCACTACCCTTACCCTACCATCTCCCATCTACTACTCACCATACTAT
TGTTCTACCCACCCTATTGAAACACTAA

YDR544C, 142 aa (SEQ ID NO 136)

MSLRPCLTFSSMQYSDIYLIHTTFHPHTPHRTHHTETTFPTFPHPHTHTPT
PERSLSRLRLRQAKFDQFVSQETLHYPTSPLVTLTHSTIPFPQPPSISLCTT
TXRPSTITVTLQLPISNSTTYPTISHLLLTILLFYPPLLKR

YKK040C, 1004 bp, CDS: 501-1004 (SEQ ID NO 255)

CCCTTTTCCAGTCCCGCGGCCTCGAGATCCAGGCACCAGGAAGTAGGCA
CGCTGTCTATTCTAACACATTCAAGCGCCTAGGCCCCCTGACCTGGGTC
TAGTTTCCACTTTTTCATTACCTTTTCTCGGTCTTTTCTTGCTCCACAGG
CCGTTAATGGCCTGAAACAGTTTGTGACTTTGGACTTATGATAACGATG
TTTGTCCGGGTGCCACCGGATTCTACCGCGGCGAATCAAGTCTAGTCTGT
TTGCATCCATCAAGGCACTGCTCATTTGTGTAAAATTGTTCTACGCTTTTG
TCATCAATCATNTCTAAACTCACAGCCGCTAGGGTAGGTGTACCTGGCAG
TGGTAAGGTAGCCGGCTCGTCTTTGGTTCATGCGCCAACTACTGTGGAACGG
CCCGCGCTTAGCGTTCTTGGCTTCAACCTTAGAGCTGATACCTTTTGCC
TGGTCAAGGGCGAAAACGTCTACCTCGCTTTTCACTGCTGCTTTTGGCTTTC
ATGACTTCGTTTCAAGCGGTCTCTTTTGGCTCTCGCTTCTAACACACTTGT
AGCCTGCTATGCTTTTCACTTACTCGAAAAGCGTAGCTTCATGACTAGTT
GTACCAACGCCCTTTCTTTTCTTTTCTCTTTGACACTTCGGCGTATT
CATCGCCACTGGTACAAGCCGATGGTGCTTTTTTGCTCATTTTCTGTTTT
GACGTTGCGATGGTTTTCCCGGACCAATCGCATGGGTGCTGCTGGATGTTG
TCTTTGCTAGTTGCAACGTAGTCTTCTTCTCTCTTCTGCGCTTTCTGACGAA

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AAATGGCCTTACGATCTTTTTTTCGGCGTCTGTGTCATCGCTGTTCA
TATAATCGTCGTCACCTCATATCGGCGCTTTTACTGCATGCTGTCTTTTGA
AGAGAGTTTCATATGAAAAGTAGTGAAGAAAAAAMAAAAAAMAAAAA
AAAAAGGAAAAAGCTTACATACGGAAAGAGAAAMAAAAAAGAAATT
TTAA

YKR040C, 167 aa (SEQ ID NO 256)

MTSFQAVSFALGCNTLVACYAFTVLEKRLMTSCTNALSELFFLLTLRRI
HRHWYKFYGAFLLEFVLTLRWFRGPIDWVWVDVVFASCNVVF#SPALSDP
NWPYVSFFGVVVVIAVHIIIVVTHIGAPTACCLLKRVSIKSSSEKKKKKKK
KKKESLHTEBEKKKKKKF

YNL338W, 659 bp, CDS: 501-659 (SEQ ID NO 337)

TAAAGTAGTCCGTACGTACGTTTCGTTTCAATTTCCATGGTGACAGTAT
CTTAACIATCTGCTTAGTCGAGGACAACAGGATTCTGTTGTTGCTCAC
CCGCTTCCTGGATATTCCTCTGGAACTTTAAATAATGGACCTACGCTTAG
CCTGCGCTTAGCCTACAACCTCTCTCCGCTCTCGAAAAGACCAATATAATA
GAAAGTTIATLATTACATTTCCCTIATTAGGTATACGACCTCGCGCTTCGA
AGTAGAGGAGCCCTTTTTCGCGTACCTACATATCGCGCGTCAGACAGACA
AACTTTCCCCCPAAAATGTATTACCCCGCCGAATAAGAAAACAGACCCATP
CACCCACGACGTATCAAGTACTTCTTGSTGCAATGTCCCACTATAAAA
AAATTCCTTTGACGCTAGATCGTTGGACTAAAATCTGCCTCACAATCCCT
AAACAGGAAATATTGCCCTATTTTCGTACAAAGTTACTTCTTAGATGCTAT
ATGTCCCTACCGCCCTTGCTCTAACACCATCCAGCATGCAATACAGTGACAT
ATATATACCCACACCCACACCCACAUACCAUACUACACUACACCCAC
AUCCACACCCACACACCCACACCCACACCCATCACAACCCCTAACCCCTACC
CTATTCTTAA

YNL338W, 52 aa (SEQ ID NO 338)

MSLRPCLTPSSNQYSDIYIPTPTPTHHTPTPTPHPHHTHTHTMHNPNPT
LF

YJR115W, 1010 bp, CDS: 501-1010 (SEQ ID NO 235)

GCUAGTATUCCCTTTCTGAAATAAGCTAAACCTTTGCAACCAACAGGGGTG
CCGCCGTCTTAACCTTTCCAGCCTGGCAGCGCGTCGAGTCGCCGAATGTTG
CGGGCGCTGCCCCGCCCCGAACACCCGCGCCCGCCCTGCCTCAGCTTAACC
GAAACCCACACCGCTCTGCCATCTTCCATATACCCCTGCTCTCTTTTACA
ATGCCCGCTCTACAAAGCCAACTGCAAAAGAGCCCGCCCTTAGTCGGTTT
TCCCCACCTTTGAAATATAACUCCCCCCCCCCCCCCCCCGCATCAACTGGTAA
TTTAACCCCAACACCCAGGGGTCATAATTTAAAGCCGAAAAACCTTAAG
CGTTCTCGAAGAAATCTTCTCTGTAGATGATGTCTGTAGCAAACTTATCTTT
TAGAGTGTTTGTGCTTACTGCATTGTCTAGATCAAAATTTACGTAGCCGCC
CTTTTCAACCCCTGTGGAAGAGTAGCATACAGCAGCGTAGTCAACGTGC
ATGTTTCACAAATACACCTACAAATATTAATATACAAATAGTAAGGTGATGAA
CACACACACACACACACACACACACACACACACATATATATATATA
CAGGAGATCAAGTTAGTGTGAGGGGACGACTAATGAGTTTGAAGTCTTT
AAAGTGTTAAAGTTATTTTCCCTCTCTCCACCTCGTTGCCAACCTCTCA
CCCACCGCTTAGCAGCATGTCTCCGTACATGACCATACCTCAGCAATACT
TATACATAAGCAAGATACCTTTTCAAGCTGTCTCAGTGCGGCCCTTACTCGA
CACCAACACAGAGAACTTGATCTACGAAAAATGGTGGGCCACGCCAATAT
GCTGGACAGGATCTTCSACGAAATAGACCAATCCACAGCGAGGTAGTAC
TGCTGACGCTGCCGATGGTTCTTCTACTGCGAAGCTCATTCGGCTTCC
CCAGCATCCAGCGACTCTCTCTCTCTCACTAATAACATCCGGCCCATTAG
CAATTATGTGA

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YJR115W, 169 aa (SEQ ID NO 236)

MPNTNRTILIYNSKVMNTHTHTHTHTHTHIYIYTGQVSVRGRLLSLKFF
KVLKLPFPSPCLSLATSHPLSLSPYMTIPQQYLYISKIRSKLSQCALTR
HHRELDLRKMGVGHANMLDRILDEIDEIDSEVVLCDADCSSTAEHSA9
PASSDSSPLTNIRPISIM

YBL072C, 1103 bp, CDS: 501-1103 (SEQ ID NO 27)

CTCCTACACACCAGCATCGCTGGGAAAGCTTGAGGGCTTTCTCTTACGCAGTGTTCATGGTGTACGGG
ATGGAACGTGTTTCAATATACGTTATTTACAGGCCATCTTAAGTTATAGGAAATTACACTTGCCATTTG
CTTTTTGGTACTCACAAGAAGACGTTATAAACACACCAGGACAAAACTATCTGCTATCGTCAATAGAG
TAATCGAATACATATTATTTTGAATGCTACAGGACCTCTCTTTGAATGGAATAGATAGTGGAAAAAGT
AAACTTAACATAAAAGCGATGATATAAATTTGTGACAGGAGCAGTGCCTAACTGAATCCTTTCTCTTACC
CCAAAAATCAACCCCTCTTATCAAAACGCCCACTTTTTCACAAGAAGAGATGAAAAGAAAACCAAGCATAT
TTCAAGATAAGAAAAAATTTCCGCAACTTTTGTACGTTCTTTATTTTACTAACAGCGTCAATPAAATTT
TCTATTACAGTTACAAAAATGGGTATTTCTCGTGAATCTCGTCAAAAAGATCCGCTACCGGTGCCAAGC
GTGCTCAATTCAGAAAGAAGAGAAAGTTTCAATTAGGCCGTCACCCAGCCACCAAGATTCGGTGTGCTA
AGAGAATTCACCTCTGTTAGAATAGAGGTGGTAAACAAGAAATACAGAGCTCTAAGAATTCGAAACCGGT
ACTTTTCTTCGGCTTTCTGAAGGATCTCCAAGAAGACCAAGATTGCTGGTGTGTTTACCATCCATCCA
ACAATGAATTTGGTTAGAATTAACACTTTGACCAAGGCTGCCATTGTCCAAATTGATGCTACTCCATTC
GACAATCGTTCCAGGCTCACTACGGTCAAACCTTGGGTAGAAGAAGAACGTCAGGGAAGAAAGAAATTC
TTGCCAAGAGCAAGAAGGCTCAAAGAAAGTGGGCTGCTAGAGCTGCTTCTGCCAAGATCGAATCTTCCG
TTGAATCTCAATTCAGCGCCGGTAGAATATACGCTTGTATCTCTCCAGACCAAGGTCATCCGGTAGAT
GTGATGGTTACATCTTGGAAAGGTGAACAATTACCTTTCTACCTAACAAGATTGACTGCTAAGAAATAG

YBL072C, 200 aa (SEQ ID NO 28)

MGISRDSRHKRSATGAKRAQFRKKKKFELGRQPANTKIGAKRIHSVTRTGGNKKYRALRIETGNFSAW
EGISKTRIACVWYHPSNNELVRTNLTAKAIVQIDATPFRQWFEAHYQTLGKKKNFKZEETVAKSKN
AERKWAARAASAKIESSVESQFSAGRLYACISSRPQGSGRCQGYILEGEELAFYLRRLTAKK

YBL092W, 893 bp, CDS: 501-893 (SEQ ID NO 33)

TACTGGAGAAGAGTGTCTTGATTCCAGCAGAAGGTAATACGCACCTTTCTCATCTATTTTCAGAAATCGTT
TTATCAAAATACCTTTTAAAGAAATTTAGATTTTGAATAATTAGTTTATTTCTTTTACAAAGATAATCAAC
AAACAGGGACAATAACATGAAGATAAAAGTATGTGACATATAGAATGCTAGAAATGAATAGCCTAGACT
GCATTTCTTATGAGAGCAACGTTTGATATTTGTGGCGATTGGACAAACATAGTACATGCCAAAAATGAGA
TGAAATGTCCAATTTEAACCTGAATTAACATACACGCGCAAGCTGTATTTGTTTACTGCTACACCTAGAG
TTAGCCGATCAAAGAGACAGTGGCAGATATATGGGAAAATTTTCTCCGGAAGATTCCATCCGAGAGTCT
CATAAACAGTCAATTTCCCAACATACAAATCTCTCGGAGCTGTATATCTAACAAACTTTTAAATTTTCAATTT
TTTTTTTTTTTGATTAGATGGCTCTCTTACCCTCACCCAAAGATTTCTCAAGAACCAACCAAGAAAGTTCA
AGCGTCATCACTCTGACCGTTACCACAGAGTTGCTGAAAACCTGGAGAAAGCAAAAGGGTATTGACCTGT
TTGTTAGAAGAAGATTCAGAGGTAACTCTCTCAACCAAGATCGGTTACGGTTCTAACCAAGAAAGACCA
AGTTTCTGTCAACATCTGGTCCACAAGACTTTCTTAGTCGCTAACGTTAAGGATTTGGAAACCTTCACCA
TGCAACCAAGACTTACGCGGCTGAAATTTGCTCACACATCTCCGCTAAGAACAGAGTTGTCATTTTGG
CTAGAGCTAAGGCTTIGGGTATCAAGGTCACCAACCCAAAGGCTCGTTTGGCTTTGGAAGCTTAA

YBL092W, 130 aa (SEQ ID NO 34)

MASLEHFKIVKKHTKKFKRHHSRYHRVAENWRKQKIDSVVRRRFRGNISQPKIGYGSNKKTKFLSPS
GHKTFILVANKDIERITMHTKTYAAETAHNTSAKNRVVTIARAKALGIKVTNPKGRLALEA

YBR009C, 812 bp, CDS: 501-812 (SEQ ID NO 37)

GAAAAATCCCCCGGGCATTTCTTTATCTTCCACGCTAAAAGTCAAGGAGAGATATTACGCCAGGATCC
CAAAGTGCAGAGCAAGGAATGTGAGAAATTTGTGAGAACATCAATGTATGGGACAATGCCAAAAATGTG
AGAACGAGAGCAAAAAATCTTTTGTATCTCCCCCGCGAATTTGGAACCCCGTTCCTGAAAACCTCGCA
TCTTCACATAGTAAAATGTTCCGAGCGCTTCTCCCATTAATGTTAGTGGTAAAAACCGAAGTTCTTT

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ACTTTAGCAAATGCCCGGAATACGGTGGTAAATTGCCACCCCCCTTCCCGAATTCATTGGGTAAAGAC
CAATTTGATGGATPAATTGGTTGTGGAAAAGGTCTAATTCTTTTCCTATAAAATACCGAGATATTTCTT
CTATATGATGGTTTCCCTCCCATTTATTCTACTCTATAGTACTAAAGCAACAAACAAAAACAAGCAACAA
ATATAATATAGTAAAATATGTCCGCTAGAGCTAAAGGTGGTAAAGGTCTAGGTAAAGGTGGTCCCAAGC
GTCACAGAAAGATTCTAAGAGATAACATCCAGGTAATTAAUTAAAGCCAGCTATCAGAGAGATTAGCTAGAA
GAGGTGGTGTCAAGCGTATTTCTGGTTTGATCTACGAAGAAGTCAGAGCTGTCTTGAAATCCCTCTGGG
AATCCGCTCATCAGAGACTCTGTACCTACCCGAACACGCCAAGAGAAAGACTGTTACTTTCTTTGGATG
TTGTTTATGCTTTCAAGAGACAAGGTAGAACCCTATACGGTTTCGGTGGTTAA

YBR009C, 193 aa (SEQ ID NO 38)

MSGRGKQCKGLGKGGAKRHRKILRUMIQGITKPAIRRLARRGGVKRISGLIYEEVRAVVKSFLESVIRD
SVTYTEHAKRKTVTSLDVVYALKRQGRITLYGFGG

YBR189W, 1501 bp, exon1: 501-507, intron1: 508-920, exon2: 921-1501
(SEQ ID NO 59)

TGGCTTCTTCTTTGCCCTGTTTTGCCAGCTGGTTCGATACGGGCACGTAACCTGATTTAATTCTTGGTCCC
TTTCTAGTGATAAATCTTCGAGAGAGGGCATACTEGTTGTAAAAAGTAGTCGCAACAGTAAGTCGTAA
AAAAGTAGATGTAATGGAAGGCTTTGAAGGAACGCTAGCCAGCTTTTCTGTATCATTCCTAGCCTAAAT
TGACAGCATCTTGACCTTCTAGTATGGAACTTTCAATTTCCAGAAAGCGGTCTTCCCCCTTCGCAUGAT
TTAATCCGTACATTTACACATCTGTACATTTTTCATTAATTCGCAAAACAAAGSTTACTTGAAAAATCAT
AAAGTTGGCGGCTTCAGGTGCAACGGCTTCACCTCATGTAGUTTAACATTCAATCCCATTAACCATTTATG
CATAAATTTCTGAAGCTTTACTTAAATAAAATGTTTCATTTGCATAGACAAGAAAGAAAGCAACAAGACA
ACTAAGACTAACAACAATCCCAACTACGTATTAGACTATATCGAAGAGGAGGGAATTCCTTCACTCTG
ACTCGTTGATTTTGAAGAGGTTCCGGTCCCTCATAAATATTTGAGAATATGAANTCCMTAATAGTATA
CCTTTCATTTAGTAGCAACGACAACAGCCTCAATTACTATCCATATTTATGAATATCTTTATTTACACTGAA
CTCCCGACACTTCAGTTAAACAGGGATACATTAGAATCAAGGTGATCTAATAGGGAACATCTCTCTCG
TAACAATGGGACAGTATTTTATTTTCCAAAGGCGGATACCTAATPATGCGTTTCTTAATCATATCTCTACA
ATATTTATGAGCACCTACCTGGGCGCTTGCAGACTTTTGTTCGCGAANAACCTTTTGACTAACCAAGAAATC
CAATTTTACTTTTTTTTTTTTAGGAGCTCCCAAGAACTTACTCTAAGACTTACTCTACACCAAGAGACC
TTACGAATCTTCTCCTTTCCAGCCAGAAATTGAAGTTTGGCCGGTGAATTCGGTTTGAGAAACAAGAGAGA
AATTTACAGAATTTCTTTCCAATTGTCTAAATTCGTCGTCTGCTGCCAGAGACTTGTGTTAACTAGAGACCA
AAAGCACCCAAAGAGATTGTTGGAAGGTAATGCCCTGATCAGAAGCTTCCTTAGAGTTGGTGTCTTGTCTC
CGAAGACAAGAAGAAGTTGGATTATGTTTTGGCTTTCAAGCTTGAAGATTTCTTTGGAAGAGAGATTGCA
AACTCAATCTCTACAAGTTGGGTTTGGCCAAAGTCTGTCCACCACGCCAGAGTTTAAATCACTCAAGACA
CATTGCTGTGGTAAGCAAAATCGTCAACATCCCATCTTTCAATGTTAGATTTGGAUTUTGAAAAGCACAT
TGACTTGCCTCCAACCTCTCCATTCCGTGGTGTCTAGACCAGCTAGACTTGCTAGAGAAACCGCTGCTAG
AAAGCCTCAAGCTTCCGGTGAAGCTGCTGAAGAAGCCGAAGACGAAGAATAA

YBR189W, 195 aa (SEQ ID NO 60)

MPRAFTYSTYSTPKRPYESSRLDAELKLAGEFGLKNKRETYRISFQLSKIRRAARDLLTRUQKDPKR
LPENAIIRRLVRVGVLSDEKKKLDYVLAALKVEDFLERRLQTQVYKLGAKSVHHARVLTQKSHIAYGK
QIVNIIPFMVRLDSEKHIDFAPTEPFGARFCRVABRNAARKAEASGEAAEEAEDEE

YBR191W, 1371 bp, exon1: 501-511, intron1: 512-899, exon2: 900-1371
(SEQ ID NO 61)

AATCCTTATTTGTCAGAAATCGAAGCCGTTAATATTTAAAGCCTAATTCCTCCATGCCATCTTGCAITCAC
TTTGGTATATATCTCTTGACCTCAATATATCTCGTAAATATAAATCGCAATATTATACCTGTTAGTCTG
ACAGTTTTTACACCTGTACATCTTCCACATCACCACACCCCTTTTCTTACTGAGGCAAGCATGAGTTTCAA
JATCGCCCTTTTTCUAGUGUTAGAACATGCTUAGAACCGAGGAAAAGCAACCGCTGCCAAACCTCCTTT
GATGTGTTGGCCCAACCGCTACTAGTGGCGGTGCTGGAAAGCCAGCCAGCGGTGGCGGCCACATACGAG
AGCTGGAAACCTAAACCGCTCTCTCGCCCTCTGTGAATTTTATCACC AATGGAGTGTCAATGTCTGCTAA
AGATAATATAGAAAGTAGTGTGCAATTTACAGGCATTACCGATTGAACTTTGGAATTAAGAGAACCAAGAC
AAAAATAACTAGCAACAATGGGTAAATCGTAATGTCATTTAATCTTATGAACTTACAGCCACGAACGAATC
ATGGTATCTCAAAACGAACATAATCGTACAGAAATAAAAGATTTAAAGACGTGTCTAGTGTGTAATTA
GCAAACATATCAATAGAGUAAAATATTGGGCAGATAAGATGATGCTACACTGATTCTGAGAAAATACG
TGACATGATAGGCTTTTAAACGGGCTGTAAGTCATTTACTTTACAGTCTGTGCTTTGAAATTTAGTTCAC

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A/PTAGAAGTGTAGTAATTACAAGCCCTTTTTCAAAACATTCCGTTATGTGCTGGGACGUATCTCAGAAA
 CTCGCCAAAACAAATACAACTACTAACATGATTTCTTATAAACTCTTAATTTTGATTTATTTCCCTTATAATAC
 AGACACGGTTACAGATCTCGTACTCGTTACATGTTTCCAACGTGACTTCAGAAAGCATGGTGCCGTCCAT
 CTTTC/TACTTACTTGAAGGCTCACAAGCTTCCTGACATTGTCGACATCAAAAGCCAAATGGTTCTATCCAA
 AAGGGTATGCCACACAAGTTTACCAAAGTAAGACCCGCTCTGTCTACAACGTTACTAAGTCTTCTGTT
 GGTGTTATCATCAACAAGATGGTCCGTAACAGATATCTAGAAAAAAGATTAAACTTAAGAGTTGAACAC
 ATCAAGCACTCCAAGTGTAGACAAGAATTTTTGGAAAGAGTTAAGGCCAATGCTGCTAAGCGTGTGAA
 CCTAAGGCTCAAGGTGTTGCTGTTCAATTGAACAGACAACCCAGCTCAACCAAGAGAATCCCGTATCGTT
 TCTACTGAAGCTAACGTTCCCTCAACCTTGGCCCCAGTTCCATACGAACTTTTCATCTAA

YBR191W, 160 aa (SEQ ID NO 62)

MGKSHGYRSRTRVMFQDFRKHGAVHLSTYLKVKVKGDIVDIXANGSIQKGNPHKIFYQKKTGVVYNVTK
 SSVGVIIKMKVGNRYLEKRLNLRVEHIKHSKCRQEFLEVRVKANAAPAAAKAQGVAVQLKRQPAQPRES
 RIVSTEGNVQTLATVPYETFT

YCL035C, 833 bp, CDS: 501-833 (SEQ ID NO 65)

CCGAAAGAAACCCCATGTTCTTGTTTTCCTGCTCCCTCCAATGCTTTATCACTCTCTCACACTGTCACAAT
 CGTGTTTGCTTCATCCTTAGAAAGGATACCACATTGATAAACAACATATATAAAGTTTAACTATTACCT
 TGATCACTTTACACGTCAAGGTCAAAAACAGTTTCATAGTTACCACTTGAAGTATGGCTCCATCATCTA
 TAAAAATGAAGTTTCATGCACAAGTGAGCTGTCTACAGATAACGAGCAGCCGCAACGGCGTTTCCAGAT
 TGCGATGCTTGTCTTCTTCTTCTACTACTGCTTACTACCCCCCTTGGCCCTCCTGATTCAAGTGATGT
 GCGAATTTTGTCTTGAAAGGAGTAAATATATAAAATAAATCAAAAAGTTTATATATATATAAAAAGGGACT
 TTAGCATATAAAATAAAGAACCTTCGTGCACTACTTATACGAGCATTTCGATAATTTATACAAATAGACAAAA
 CCTCAGAACGCAAAAAAATCCTATCTCAAGAAACTATCAAGCACGTCAACACCTTATTCAGAAAAACG
 AGATCTTCGTGCTATCCAAAACGTACTGTCCATACTGCCATGCAAGCCCTAAACACGCTTTTGTGAAAAGT
 TAAAGGTTCCCAAGTTCAAAAGTTCTGCTTTTTCGAATTTGAATGACATGAAGGAAGGUGCAGACATTTCAGG
 CTGCGTTATATGAGATTAATGGCCAAAGAACCGTGCCAAACATCTATATTAATGGTAAACATATTGGAG
 GCAACGACCACTTGCAGGAATTGAGGGAGACTCGTGAATTGGAGGAATTGTTAGAACCATTCTTGGCAA
 ATTAAT

YCL035C, 110 aa (SEQ ID NO 66)

MVSQETIKHVKDLIAENELFVASKTYCPYCHAALNTLFKCLKVPRSKVLVLQLNDMKEGADIQAALYBI
 NGQRTVPMIYINGKHIIGGNDDLOELRETGELEELLEPILAN

YDL004W, 983 bp, CDS: 501-983 (SEQ ID NO 81)

ATSAACATAGATATAATAGTTTITAAAATGGTCAACGTATGCGATGCACAACCTAAAAGGTACCAATTTC
 ATTAAAATATATATAATATTACTTCTTACTATTACACGAAAGACAAGTGTGAAATGCCTAGGAGATTGAT
 GATTGACAAGCTCTGGCTTTCGAATAAAAATACTTATACACAACCTTCAAATAATATAGAAAAGAAAGAA
 GACTATAAGCTAAAAATGTAGACAACCTTCATTTAAATATTATTCTTAGGACTTTGGTAATAATAGCTAAT
 TTTGTATATTATTCACCTTCGGTCAACCGCTCTGTAATTCACCTTTTAAAGAAAATAGATTCUCCAGCCAAATCAAA
 GCGCATTTATGGAGTCTGTTAGGAAGGGGCGCTCCCATCATTTGTAAAAGTTTCATGTTAAATTAGATGGAG
 GATAACAATAAACCTATCCTACACACACTGCTAAAAGAGGCTCAATCAATTTGTGAAGGTATAACTGTA
 GCCGTGAGGATAGGAAAATGTTACGTTCAATTATTGGAAAGAGTGCATCAAGATCATTGAATTTCTGTCTG
 CTAAGCGTTTCATATGCAGAAGCTGTTGCUCCATCATCAGGTTTGAAGTTACAATTTGCTCTACCCACCG
 AAACTTTATATAGTGGCTCCGAAGTTACTCAAGTGAACCTGCCTGCTAAGTCAGGACCTACTGGTGTAT
 TGGCCAAACCATGTTCCCAACGTTGAACAACTACTACCAGGTGTGTTGAAGTTATGGGAAGGCTCTAACT
 CTAATAAAATTTCTTTATATCAGGTGGATTTTGAACAGTTCAACCCAGACTCGCAGTTATGTGTAACTGCAA
 TTGAAGCTTTTCCATTGGAATCCTTTTTCACAAGAAAATATAAAAAATTTGTTGGCAGAAGCTAAGAAAG
 ACGTTAGTTTCATCTGATGCCAGGGAAAGCCGCAGAAGCTGCAATTCAACTAGAACTTTTAGAAAACCTAC
 AATCCCTATTGAATAG

YDL004W, 160 aa (SEQ ID NO 82)

MLRSIIIGKSASRLNFVAKRSYAEAAAASGLKLQFALPHETLYSGSEVTQVNLPAKSGRIGVLANHVP
 TVSQLLPGVVEVMRGSNSKKFFTSGGHAIIVQPSQICVPAIRAPLESFSQNNIKNLAAEAKKNVSSSD
 AREAAEPAIQEVLENLQSVLK

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YDL075W, 1263 bp, exon1: 501-557, intron1: 558-978, exon2: 979-1263
(SEQ ID NO 85)

ACTATATTTTCTTTTCCCGAACCCTCTCCCTTTCTGGGCCCTTTTTCATTATTACACAATATTTTTCATAC
CTTTACCTCCGTACACCAATCTTTATTTTACCCCCATACCTTTGTATTCTGAAATTGAGAAATGATTT
GTGGTGCTTTTITTTTGGACAACTGCTCTCGTGGACAGTTTGAACGGCTAGGCGACAGTTTTGCCAA
CCGAAGCAACTGGGACAGCCAGAAAGCTTTCTCTCGATGGTGGATCATTCCTTGGCAGGCGGAGGAT
GGGAAAGCTCCGTTCAAGTTTGGCGCTTTCTTTCTGGCATTTCCTTCTCCCAACTGGCGAGGCAGAC
ATACCTTGACTTTACCTCATGCTCGCATTAGGCCGGTTGAATCTCATAGCTTGAAAGATAGTATTGAATT
ATATTGAAGATTTTATAACTAGTGATAATTTTCATTCAAGTTTTAAAGAAAGAATTAATAAGCAAAACAG
ACTCAATCAAAAGCAAAAATGGCCCGTTTAAANAAGTTGTCACTCGTGAATACACCATTAACCTTGCACA
AAACATTTATGTAAGAAATAAAAAATATAATGCCCAAGGCTTTGTCTCTGAATGGTTAATTAAGAAGAT
ATTTCTATAGTCAAGGAATACAATATCAAGAATTTGTACCACAGAAACCTATCAACAAGATCATTTGAT
CAAGATATATTTTATATACCGGAATTTGAAGACCATAATCAATATTATAACATCCAAGAGGGGAAAGAT
ACACTTCGGCTGGACCTTAAAGAGCGATGAAGACAGAAATAGTTATCTTAAATAGTGGAAATCCTACATTT
TAAGTCGACAAATATCCATATCCCAAGTTTGACTAAATATCAATCAGAACAAATTCGCTCTCCAATATA
CAAAACCATTCATCAAGATTACACTAATATTAAATGAACAATCGTTACTAACAACAAATTTACCAATTT
TATTTTAAATAGTTGCACGGTGTCTCTCTCAAGGAAGAGAGCTCCAACAGCTGTCAAGGAAATTAAGAAG
TTCCGCCAAGTTACACATGGGTACTGATGATGTCCGTCTAGCTCCAGAATTGAACCAAGCTATCTGGAG
AGAGGTGTCAAGGCTGTTGAATACAGATTAAGATTGAGAATTTCCAGAAAGAGAAACGAAGAGAGAC
GCCAAGAACCCATTGTTCTCTTACGTTGAACCTGTCTTAGTTGCTTCTGCCAAGGCTCTACAACTGTT
GTTCCTCGAAGAAGATGCTTAA

YDL075W, 113 aa (SEQ ID NO 86)

MAGIKDVVTFREYTNLHKRLHGVSEFKRAPRAVKEIKKFAKLHMGTDDVRLAPRLNQAIWKRCVKOVEY
RLRLRISKRNEEDAKNPLFSYVEPVLVASAKGLQTVVVEEDA

YDR064W, 1495 bp, exon1: 501-521, intron1: 522-1060, exon2: 1061-1495
(SEQ ID NO 89)

TGACGGTCTGTTTACAGGAATGGAAGATGCTTTATGCCCGCGCATTAGAAATGATCAGAGAGCGAGTCCG
GTACTTTTAAATTGATAGAGCTTTCTTCAAGCTTTGGACGGATGACTCAGACGTTGAAGAAATTGAGCGAGC
AATTAGAAATTTGTTAGTATAGTCTATCTTAAACACTAAACTACCTCCTATAATCATGTAGTGTACTTT
AAACATTTTITATCTTCATAGCAATAATATAAGCCTTTTACCACCCATAAAACCTAAAGTAGACCCAA
ACATTTTAAAAAATTTTACGTTATAATTTTTCTTTGTCTCTTTCTGAGCGCGCAAAAGTAGCGGT
GAAATTTTGATACGAATGAGATTTCCACTTCTGTACAGATGGAAATTTATGTTGGCCGACATATATCAC
AGTCGTGATTTGAATTAACAATTTCTTTCTCATTAATATTTATTTCAAACGGTTAAUCCACTAAATCATC
AACAACAATCAGTCAAAATGGGTGATGACAGTGGCGTATGTTTATTAACACCATAGCGGAGATATTA
ATGCAAAACTTTGCATTTGAATAGTTTCGCTAAATCAGATGACACTCTAATGTGGAAATCAAAAAGTGGATTT
CTAATATATTTGTCTCTGTCCGATCACAATTTCTATTACAAGTTCCCGTCTGTACACAGGTACAGTTTA
TACTGGAGAGTAGTTTCTACTTCGCTGTACATTAGCTTGGGTGATTCCAAATTTCTTTTACAAATATGTTGC
ATTAGTTTAAACAGGTTATACTATCTGCCCTTTCTTCACTATAATTTACGCCGGAAAAATTACTGATGCTTA
GCCGCCCTTTATGAATTAGTTTTCACAAAGCTCATAAATACACGCTTAACCTATCGGAGGAGAACCAG
ATTGAAGATTCACCCGGAATAGCTTACTTTAATGGAATTGTATGGTCTGAACGAGGAAATATGTCTATG
ATACACTTTTCTTCAAGCCATATCAATCTTCATGTTACTAACAATCGGATAAATTTTGGAAATATCCAA
TTCCACTAAATATTACTTTAAACAGGGTAAAGGTATTTCTTCTTCTGCTATTTCCATACCTTAGAAATGC
TCCAGCTTTGGTTCAAGTTGTCTCTGAAATCTGTCAATTGAACAAATTTGTCAAGTACCGGAGAAAGGTTT
GACTCCATCTCAAAATTCGTGTCTGTGTGAGAGATGCTCACCGGTGTTACCCAAGCTCCTGTTATCACTGG
TAACAAGATCATGAGAACTTTGAAGTCCAAATCGTTTCGCTCCAGAAATCCCAAGAAGATTTGTACTACTT
GATTAAGAAGGCTGTCTCTGTTAGAAAGTCACTTGGAAAGAAACAGAAAGGACAAAGACGCTAAGTTTCA
ATTTGATTTTGAATCGAAATTTAGAAATTCACAGATTTGGCCAGATACTACAGAACTGCTGCTGTCTTACCAC
AAACTGGGAAGTACGAATCCGCCACTGCCCTCGGCTTTGGTCAACTAC

YDR064W, 151 aa (SEQ ID NO 90)

MGRMHSAGKGISSSAIPYSRNAPAWFKLSSESVIRQTVKYARKGLTPSQIGVLLRDNHGVTQARVITGN
K(MRLKSNGLAPEIPEDLYVL)KKAVSVRKHIHNNRKDKDKFRLILIESRIHRLARYRNVAVIPEX
WKYESATASALVN

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YDR099W, 1322 bp, CDS: 501-1322 (SEQ ID NO 93)

TTGTTACGACCAATCCGTAATTCAGCGGTGGGTATTCATATGACCAGAGATAATAATACAGCGAATACT
 ATTGAAATCGTCCCTTTTGTGTTAGGAAGAACGGACAAATCGGTGCTCTGCTCGAAATGATTAGTAGT
 GTGTACCCCGGATCAGCAAAATGACACACACGAATACGAGCAAAAAGTCGGTCGAAAGGGGCAATGT
 TATTATAAGTCCCTCCAGTAGTCTTTTTTTTTTCAAATATTCATCATCAAAGGTTACGAAATCTTTTGA
 CCTATCTTAACATTCGTTCTTTTTTATCAAAATTCATTAACCTAATTTATTTTTTCAAAAAAATTGCCCT
 CTCCCGGTTTTTAATCATTATTTTTTTTCGATTTGATTAAGCGGGAAAAGCAAACAACCGAAGAACTTCGA
 CAGAAGGTAAATACTCTTACAAATTCAAAACGAAGTAAAAAGAAAAATTATCAAATCAACAAAAAGTAC
 CCGTTACAACAAAAAATGTCCCAAACTCGTGAAGATTCCTGTTTACCCTAGCTAAATTAGCTGAACAAG
 CCGAACGTTATGAAGAAATGCTCCAAAACATGAAGGCCGTTGCTTCATCAGGTCAGAGTTATCTGTCTG
 AAGAACCGGAATCTATTTCTGGTTGCTTACAAGAACGTCATCGGTGCTCGCCGTGCTTCATGGAGAAATAG
 TTTCTCTCGATCGAACAAAAAGAAAGAAATCAAAAGGAGAAATCTGAACATCAAGTTGAATTAATCCGTTCTT
 ACCGTTCTAAAAATTGAAACTGAATTGACCAAAATCTCTGACGACATTTTATCTCTCTTAGATTCTCATTT
 TAATCCCTTCTGCTACTACTGGTGAGTCTAAAGTATTTTACTATAAGATGAAGCGTGACTACCACCGTT
 ATTTAGCTGAATTTTCCAGCGGAGATGCAAGAGAAAAGGCAACCAACTCCTCTTTGGAGGCTTATAAAA
 CCGCTTCCGAAATCGGCACAACTGAATTCCTCTCCAACCTCACCCAATTTCGTTTAGGCTTAGCTTTGAATT
 TCTCGTCTCTCTATTTAGGAAATTCAAAACCTCTCTGATAAGGCTTGCCACTTGGCCAAACAAGCCTTTG
 ATGATGCTATTGCTGAGTAGACTTTATCTGAAGAATCATACAAGGATAGCACTTTGATCATGCAAT
 TATTAAAGGGCAACTTGACCTTATGGACCTCTGATATTTCTGAATCTGGTCAAGAAGATCAACAACAC
 AACAAACACAGCAACACCAACAGCAACAAACAGCAACAACAAGCTCCAGCTGAACAAACTCAAGGTGAAC
 CAACCAATAA

YDR099W, 273 aa (SEQ ID NO 94)

MSQTREDSVYLAKLAEQAEERYEEMVENMKAVASSGQELSV EERNLLSVAYKNVIGARRAEWRIVSSIEQ
 KEESKEKSEHQVELIRSYRSKIETELTKISDDILSVLDSHLIPSAITGESKVFYFKMGDYHRYLA EFS
 SGDAREKATNSSLEAYKTASRIATTTTLPPTHPIRLGLALNFSVFYIEIQNSPDKACHLAKQAFDDAIAE
 LDTLSEESYKDSLIMQLLRNLTLWTSDISESGQEDQQQQQQQQQQQQQQQQQAPAEQTQGEPTK

YDR134C, 701 bp, CDS: 501-701 (SEQ ID NO 97)

GGAGTTTTCCTATTTTCGAATTCATCCCTGGGTTTGAGCTGCAGGACACGCTGCAGTGGGGGAAGCCCTTT
 TAAATCCCGGAGTCCGGTCCGTGCTCCTTTTAGACCGCTCTTCCATCCCGCTTCGGATGGITTCCTACT
 GAGAAAAGGGGCTACGGCTATGGTCTGTTAGTCCCTTTTCAGGGACCAAGTGACAGGGGTGAATCAACGGCC
 CCTTCACAGAAACCGCGCAGGAATTTTCTGCTGTTTGTATTTTTTTTTTTCTTGTACTTATCTCACTT
 TTCTTTTCTTAACCTATTTTTTTTTCAATTTTCTGCTACACTTCCACAACATATAGGATGGTTTAET
 CATCTCTCGAAGTATATAAACCGTTGCTGGATCGTGGTTGTTCTTCATCGACTTCTCTCTGCTAGACTC
 TCTTTTTTTAAATTTTTTTCATAGAATAAAAAACCAAGGATAACAAACATCTTCTTTGTTTGGCTTCAAA
 ATAACTACAAATTAATAATGCAATTCCTTACCGCTGCTCTATCGCTGCTACTTGGCGCTGTTGCCTCCG
 CCGCTTCTAACATTACCACTGCTACTGTCACAGAAGAATCTACCACTTTGGTCACTATCACTTCTTGTG
 AGGACCACGTTTGTCTGAACAGTTTCCCCAGCTTTGGTTTCCACTGCTACCGTCAACGTAATGACG
 TTATCACTTAA

YDR134C, 66 aa (SEQ ID NO 98)

MQFSTVASIAAIAAVASASNITPATVTEESTTLVTTTSCUDHVCESETVSPALVSTATVTVNDVIT

YDR171W, 1628bp, CDS: 501-1628 (SEQ ID NO 103)

CTGGGGTTGCTTAACAAGTGACCAAGGGAAAAAGTGAACATTTTAAGAAGAACAAATAAAAAGCAAGAG
 ATGGAAATGGTAATGCTTGGCTCTCGAGAAGAGTACGATAAACGAGACTTCTTTAAACACCATATGAC
 ATACTTCAATTCAGCTTTTCCCTATCAGCCGCTCGAGCAGTTATATAGGTGTGTTTCCCCAGTAATTTGG
 CCGACGCCCAACACTGGCTAGGCGGCAACGCCCTGGAAACCGCGCTTAAAAAGTTCTGGAAGGTTCCGGAAT
 TGAGAACTGCTCAGGGGCGAATAACAGGGGCGGCTTTCGGGCAAGGCGCACGCCCTCTGTGAAGTTACTT
 ATATAAGACTTGTCTGTCATCGTTTCTTGAATCCCGGACAGGAATATCTTTTATTCTCATACATACGGTC
 AACAACTATAATTATACATAACATAGGGACACGTTTCAGGCAATTGTCCATATCCACACAAATTAAGAT
 CATACCAAGCCGAAGCAATGAGTTTTTATCAACCTCCCTATCTCTTTATGACGTTTGAACGCATTAT
 CCAACCAAACTGGCCAGAGAGGGGACGAAGGATATCTTCCCAACCAACAAAGGCCACAGACATACCATC
 CCCATTATGGACAAGTGACGTTTGGCGGGCAATCACTCTCGTTCATCATCCATTGTATAGCAGATACAAATG

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GTGTTCCCTAATACCTATTACTACCAGTTCCCTCGGACAAAGCCATTACTATAGTCCTGAATACGGTATATG
 ATGACGAGGATGGTGAAGAAGAGGACCAAGACGAAGATATGGTGGGTGACAGCGGCACTACAAAGACAGG
 AAGATGGTGGCGAGGACAGCAACTCGAGAAGATATCCATCATATTACCATTCTAATACTGCCAGGAATA
 ATAGGACCAACCAACAGGCPAACAGTTTAAACGACTTATTAACCCCGTTAATAGGTGTTCCACCATATG
 AAGGCACCTGAACACAGAAATTGAAGCAAAATACCGAACAGGAGGGCGAAAAGGCAGAAGAAAAGGATAAGA
 AGGATAAGTCTTGAAGCAUCCAAAGAGGAAGCTGGCGAATCCAACAAAGAAAAACCTTTTGAATCAGCTGG
 AGGAATCCTCGAGACCACCATTAGCCAAAAAATCTTCATCGTTCCGCTCACCTACAAGCGCCTTCCCCAA
 TACCTGACCCGCTACAAGTATCCAAGCCTGAAACGAGAATCGACTTACCATTTTCAACAGAAAGTGAATG
 TCTATGATACCGAGGACACTTACGTAGTTGTTCTTTCGCTTACCAGGTGCTAACCTCTAGGGCTTTCCACA
 TTGATTAACCATCUATCTTCTCATGAGATGCTTCATCAACGCTAAAGATTGGAAGACAGAGTGGGCATTGAGG
 AAAAATTCTTGAAGATCACGGAACTAAAATATGGTTCGGTTTGAAGAGAACCGTTAAATTTCCCCGTGCTGC
 CACGCATTAAAGGACGAAGAAATTAAAGCTACTTACAAACAACGGTCTACTACAAATTAAGGTCCCTAAAA
 TTGTCAATGACACTCAAAACCCGAAGCCAAAAAAGAGGATCGCCATTGAGGAAATACCCGACGAAGAAT
 TGGAGTTTGAAGAAATCCCAACCCCTACGGTAGAAAAATGA

YDR171W, 375 aa (SEQ ID NO 104)

MSFYQPSLSLYDVLNALSNTGQRGQQGYRQRPQRPRYRHPHYGOVHVHVGHHPRHPLYSRYNGVPTNTY
 YYQFPQGAYYYSPEYGYDDEDEGEEEDQEDDMVGDSDGTTTQREDGGEDNSRRYPSYHCTARNMRPWQQ
 ANSLNDLLLTALIGVPPYEGTEPELEANTEQEKEKGEKDKDKKSEAPKEZAGEINRKRKFLNQLBESSRP
 PLAKKSSSFALHQAQSPJPPLQVSKPETRMDLPFSPEVNVYDTEDTYVVLALPGANSRAFHIDYHPS
 SHEMLIKGKIEDRVGIDEKFLKITELKYGAFFERTVKFPVLPRLKDEEIKATYANGLLQIKVPKIVNDETR
 KPKPKKRIAIEEIPDEEELFEENPNPTVEN

YDR399W, 1166 bp, CDS: 501-1166 (SEQ ID NO 129)

TGGTTATCCCTTTTGAACIGCATCTGGCATCGTTAACAGTAAGGUCATCTGGMACATCAAGCAAGCAC
 TCCACTTTTACGTACACAACCATAGTTGGTTAACTAAGAAAAGACAGTACATATTTCCCTCCCGAGTCAC
 TTATTTTCTTTCTTCTCTGAAAAATTAATTAGATTAATTTCAATTAATATCAATTTCCGCTTATCTGAC
 TTCTTTTCAATTTTCTCTATATTTTCGCGTTTACTAGGAAGAAAAAGGAAAAAAATTTTCCCTCTC
 CATCTGTCCCAAATCGGGTAGCGATGAGCTGCTTATAGAAATTTCTATTTAAACATGTTTGATAAGCCCA
 ATTTCCGCTTAGATTTTGTTCCTCTTCGCTAGTTTGGTTTGGCTTAACCTTTTCTTACTTTAGTCTCCATCT
 AGCTGGAGTAATACGATGTAGTGCCTTGTAAATCTTCTTATTTTATATTACCGTTCGCTTCATTATA
 TCCATTAACGTTCCCATATGTCCGCCAAACGATAAACAATACATCTCTGTACACAAACGTACATCAACTAT
 GTCAAGTATCCGCTGAGAGAAATTAAGAAATTTCAAGCCGGACTTAATCATTCGCCATTGGTGGTGGTT
 TCATTCCCTGCTAGGATCCCTACGTACGTTCTTAAAGAGCCCGGCTGCTCAACCATCAGAATTTTTCCTA
 TTATTTTGTCTTTGTACGAAGATTTGAACAGTGTAGGCTCAGAAAGTTGAGGAAGTTGGTGTAAAGGTTA
 GCAGAACACAATGGATTGATTACGAGCAATGTAAATTAGATCTAGTCCGCCAACCAACCTTTATCGTTG
 ACCAAGTCGATGACACCCGTACCACTTCAATTACCTTTTGAAGTGAATTTGAAAAGGATCGCAGCTGAAC
 AGGCCAAAGCCTAAAGGTATCGATACTGAAAAGTCTCCAGAGATGAAAACAAACTTCCGGGATTTTTGTCTC
 TACACGATAAGCAAAAACCAAGAAAGCAAGATTTTCCCTGCCGAAATGTTGAATGACAAGAACCCCTTATT
 TTGCAGCTAAAACTGTTCCAGACAAGTGGTATGCATATCCATGGGAATCTACTGACATGTTTTTCCATA
 CTAGAATGGCTATTGAACACGCCAATGACATCTTTATTTCTGAGCAGGAACACAAGCAATGA

YDR399W, 221 aa (SEQ ID NO 130)

MSANDKQYLSYNNVHQLCQVSAERIKNPKPD(LIA:GGGGFIFARILRTFLKEPGVPTLR)PAFILSLY
 EDLNSVGSEVEEVGVKVSRTQWIDYEQCKLDLVGQNVLLIVDEVDDTRITLHYALSELEKDAAEQAKAG
 IDTEKSPENKTNFGIFVLHDKQKPIKADLPALMLNCKMRYFAAKTVFDKWAYYPWESTDLVHTRMALIE
 QGNDLFLPEQEHKQ

YDR418W, 998 bp, CDS: 501-998 (SEQ ID NO 131)

TGCACCTGTGGATGTTTGGGTTGTGTATTTTGCTTTTCAACATACAGATATTTTGTTTAAGCAAGTGAA
 ATATACCAATATCATAAAACAGGTACTTCATAGACCATAAACCNTAACCCAGATTATCCTCTTAGATAGC
 AATCCTAATGTAAACAGAGATCCGTTTGGGTGACTTTATACTAATAAGATATGTCTACTTCCCTTTCTG
 CTCGAGCAGCCTGGCAGTCCCTCTTACGCCCTTTTTCCTTTTCCGAAGGTTTTCCTCCCTAAGCCCCCTG
 GCTCTAGGCCGAGAAAATGTTAATGCTCCTTCTACAGAAAATGCTTGTGCTCACACACAGGACAGGTCG
 CCGACGACCGCTTCCGCTAATCTTCTCAATGTTGTAATCTTCTTTGGCGGTACATTACTAGTATGAAAT
 GGAATAAAAACAGTACCTAATTAATTTTACTTACTTCCCGTTTAAAGCAACCCCAAGTGCCCAATAGAAGG

[illegible]

YDR513W, 932 bp, CDS: 501-932 (SEQ ID NO 133)
TCTCCCTCTCCTGCCATATAACUUAAGTGGTATTTTCCAAATGCCCTTATCTGGTGGAAACCTGATCTTTAT
ACCATTCCTGCACTTTTCACAGGGTCAATTCGCCGTGGATATATACAAAACCTTGAATTTGGACACCTGCTTGT
CACATGATGTAAAATCTCCATATCTGTATATAGCTTCTAAATTGCCCTCCAAATGGAATAGCAACTCGTCA
GTTCATCAAATGCCCTCTCGGCAACTCATCGTTCGCGGATATTTTGTACTCATCTCTTTCCTGTTTCTTCC
TCAAGCTGCTCTCTTTTACCTTAATAGAACCATCGCTCCCTCTTCAATTTATCTTAATACCAATCCAA
TAGCAGAACTATTACTAAGATCCGATATTTTCGGCCCCCTTCGCAAGGGGCTCCGCGCACATTTCTTCAT
GAATTTTTCATATAAAAAGTCCAGGACGCCAAGAAAAGGTGCCCTCTTGATTAACGGACACTTCAAACCTA
CTGTTATATATTGTTTCATGGAGACCAATTTTTCCTTCGACTCGAATTTAAATGTTATTATCATTAATCA
CGTTGTTTTCGCCACAAGAATTATTCGCTAAAGATTTTTTATCTACTCCAAAAATGGTATCCGAGGAAACAG
TTCTTCACGTAAACGATCTGATTCGCCAAAAGGAAGTCTTTGTTTCAGCAAGACATATCTGCCCTTACT
GTAAAGCTACTTTTCTTACCTCTTTTCAAAGAATTGAACGTTCCCAAATCCAAAGGCCCTTGTGTGGAAAT
TAGATGAATAGCAATGGCTCAGAGATTCAGAGCGCTTTAGAAAGAAATCTCCGGCCAAAAAAGCTGTAC
CTAACGTATATACATCANTGGCCAGACACATTCGTGCTAACAGCGATTTGGAAACTTTGAAAGAAAAATGGCA
AGTTAGCTGAATATTGAAGCCGGTATTTCAATAG

YEL009C, 1346 bp, CDS: 501-1346 (SEQ ID NO 139)

AGTTTCACTAGCGAATTATACAACCTCACCGCCACACAGCTCACTCATCTACTTCGCAATCAAAACAAA
ATAATTTTATTTTATAGTTTCAAGTTTATTTATCAGTATCGTATTAAATAAATTAAGATCATTGAAA
AATGGCTTGTCTAAACCGATTATATTTTGTCTTTTAAAGTAGATTATTATTAGAAAATTAATATAGAGAAATT
ATGTGTAAATTTATTGAAAGAGAAAATTTATTTTCCCTTATTAAATTAAGTCCCTTTACTTTTCTTGA
AACTGTCAGTTTTTTTGAAGAGTTATTGTGTTTGTGTACCAATTGCTATCATGTACCCGTACAAATTTTATT
CAAGATGTTTCCGTAACGGTTACCTTTCTGTCAAAATTATCCAGGTTTACTCGCCAAATAAAAAATTTCCCT
ATACTATCATTAATTAATTCATTATTATTACTAAAGTTTGTGTTTACCAATTTGTCTGCTCAAGAAAATA
AATTAATAACAAATAAAATTTCCGAATATUAGCCAGTTTATTTGCTTTTAAATCCCAATGCGTTTCTCAC
CAATGGATGGTTCTAAATCAACCAACGAAATGTATCTGCTTCCCACTTTCTACTGCCAAACCAATGTTTGT
GCCAATTCATTTTTGATAAATTCATCAAGACTGAAGAGGAATCCCAATTATCAAAACAGGATACCCCTTUGA
ACCTTGATTTTGTATTTTGTCTTTTCCACAAACGGCAACTGCACTTGATGCCAAGACCGTTTGTGCCAATTC
CGGAGCTAGATGAAGCTGTAGTGGAAATCTTTCTTTTGTCTCAAGCACGTGATTCAACTCCCAATGTTTGA
ATGAAAACCTAGAAAGACAACCTTAAGAATTCGACATCCTTGTGTTGACAAATGACATTCAGTTTACCACTG
ACGATGTTTCTATTCCTTGATAAGGCAATTGAATCCACTGAAGAACTTTCTCTGTGTAUUAATCCATCTGTG
AAGTCTCGACAACCTTCATTCCTTACCCACTCTGTTCTGAGAAGATGCTTAACTGACTCAAAACAGAAAGG
TTAAGAAACCAAAATTCAGTCCGTTAAGAAGTCACATCTGTTTGGAAAGGATGACGAATCGAGACTGGAGC
ATCTAGGTGTGTTGTTCTTACAACCGCAACAGCGTTGATTCCTTCTCCCAATTTGTGCGGAAATCCA
GTGATCTGTGCTCTTAAACG(GC)TAGAAACACCTGAAGCCGCGCAGGCGTTCTGTGCGGAGAAAGTTGC
AAGATGTGAACAACCTTGAAGACAAGTTGAAGATTTGCTTTTCAAAAAATTAATCACTTGGAAAATCAGG
TTGCCAGATTAAGAAATATTAGTTGTGCGAACGCTGA

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YELC09C, 281 aa (SEQ ID NO 140)

MSPEYQPSLPALNPMGFSPLDGSKSTNENVSASTCAKPMVGLIFDKFIKFERCPFIKQCTPSNLDPDF
 ALPQTATAPCAKTVLPPLPLDDAVVE3FPSSSTDSCTPMFEYENLEDNSKEWTSLFDNDIFVTTDDVSLA
 DKAIBSTFEVSVLPVPSNLKVSSTTSPLETPVLEDAKLTQTRKVKKFN3VVKKSHHVGLKDDERLDHLGVVA
 YNRKQRSIPLSPIVPESSDPAALKRARNTTEAARRSRARKLQRMKQLEDKNVEELISKNYHLENEVARLKK
 LVGER

YGL123W, 1264 bp, CDS: 501-1265 (SEQ ID NO 163)

TGCGCTATTCACTAAGGATTCTTAAGSTTTTUTTAATAGTTTTCTACGTCCGCCATGCGATTGPTTGGT
 TAGAAGACTGCTTTCTAAATATGCTTCCGCTGTATTTAAGCTAGACCCATACACCCGCTCTATGGGATTA
 TTTACTTTGTTGAATTTTAAAGATTTGTGATAATGGAACCTGGACGCAACATTTGATGGAAAACGCATGT
 CATCATTAAC3AGCTAAGCTTAGGTATCTGTCTTGCCTTAGTATTGCACGCAGCTTCCCAGGACGCCTAG
 CTATTTTTCATCTATTCCCCCTCTGTAGTAACGTAAGAGTTTTCAAGTTTTTAATTCACACTTTCTCTT
 CCTTGTGTTTCCAAFTTCCCTTCTTACTGCTTGATACCTTTTCAATCCCAAAGAAACCGTGTCTTTATA
 TATTGTCGATTGAAAGTTACCTACATCAACTTTCCGCTGTTCCATTCCGACTATAACAAACAACCAATAA
 GCTCAACTAATTAAGTAATGTCTGCTCCAGAAGCTCAACAACAAAGAGAGGTGGTTTTCCGTTGCGCGTA
 ACAGAGGCCCTCCAAACAGAAAGAGCAACCAAGAAACACTGAAGAAAGGGATGGGTTCCAGTTACCAAAC
 TAGGTAGATTAGTCAAGGCTGCTAAGATTACCAACCATTTGAAGAAATCTTCTTGCACTCTTTGCCAGTCA
 AGGAATTTCCAAATCATTCACACTTTGTTGCCAGGTTTGCAAGACGAAGTCATGAACATCAAGCCAGTTC
 AAAAGCAAACCCAGAGCCCGTCAAAAGAACAGATTTAAGGCTGTGTGCTGTTGTTGGTGACTCTAACGGTC
 ACGTTGGTTTTCCGCTATCAAGACCGCTTAAGGAAGTTTGTGCTGCTGCAATCAGAGCTGGTATCATTAATGCCA
 AGTTGTCGCTTATCCCAATCAGAAAGGCTTACTGGGGTACCAACCTTGGGTCAACCACATTTCTTTGGCCA
 CCAAGACCACTGGTAAGTGTGGTTCCGTCAGTGTAGATTGATCCCAGCCCCAAGAGCTTCTGCTATCG
 TCGCTTCTCCAGCTGTCAAAAAGTTGTTGCAATTGGCTGCTGTGTAAGATGTCTACACCCAATCTAACG
 GTAAGACTAGAACTTTGGAAACACCTTGAAGGCTGCTTTGCTTGTATTGGTAACACATACGGTTTCT
 TGACTCCAAACTTTGTGGGCGGAACAACCATTTGCCAGTTTCTCCATTGGACATCTACTCCGATGAAGCTT
 CTGCTCAAAAGAAAGAGATTCCTAA

YGT123W, 254 aa (SEQ ID NO 164)

MSAPEAQQQKRGGFGGHNRGRPNRRCPRNTEEEKGWVPVTKTGRIVKAGKCTTYI3ETFLHSL2VKFFQTI
 DTLPLGLQDEVMMNIKPVOKQTRAGQRTFRKAVVVVGDSNGHVGLGIKTAKEVAGAIRAGIIIAKLSVIP
 IRRGYWGTNLGQPHSLATKTTGKCGSVTVRLIPAPRGSGIVASPAVKKLLQLAGVEDVYTQSMGKT3TL
 ENTLKBAFVAIGNTYGFITPNTWARQPLPV3PLDIYSDEASAQKKRF

YGR209C, 815 bp, CDS: 501-815 (SEQ ID NO 187)

ATCATCCAGACTTTTACGGGTGGCAACGGAAACCAACGTATTTAGAGATTGTTTTTTGGTCAAGCGAGGA
 ACCCCCTGTTGGCAAAGTTGCCAGGTATATCATGGGTGCGGAGGTCAACATTCCAAAGCATTCAAACCCCTT
 GGCGGCGTGAGAGTCAGTGAAGAAAGTCTTTGTTGAGCCCGGTAAGAATGACATACTCGGCTTCAAGATC
 GCTCCAAGATCAGCATAACTTGAGTGCCAGTGCAATATTAACTAATCATCAAAGTATATGCTGAATTCCTT
 CATACTCTTAGTAAAGGAATGCTCCCTACAGCTGCTCTCTTTTCTTACTAAAGCGCGTTCAGTTTCCAACC
 AGCCGAAAGAGGGATATCAATATATAAGAAAGCCATTCGGGGGATGAAAAGCTGACAAAGAGAATAACGA
 GGACCAGTTTTTATTTGTTGCTCAGCAAGAATTATACAGGCACACATACACGAGAGTCTACGATATCTT
 TAAATAACACATCAATAATGGTCACCTCAATTAATAATCCGCTTCTGAATACGACAGTGCTTTAGCATCTG
 GCGACAAGTTTACTCGTCTTCACTTTTTTGGCCACATSGTGTGGGCCATGTAAATGATTGCACCAATGA
 TTGAAAAGTTTGCAAGAAATATTTGACGCTGCTTTTTTAAGAGTTGGAATGTTGAATGAAGTCTCAGATG
 TTGCTCAAAAAGCTCAAGTTTCTTCCATGCTTACCTTAATCTTCTACAAGGCGGTAAGGAGGTTAUCCA
 GAGTCGTCGGTGCCAAACCGAGCTGCTATCAAGCAAGCTATTGCTTCCAACGTATAG

YGR209C, 104 aa (SEQ ID NO 188)

KVTQLK5ASEYDSALASGDKLVVVDFEATWCGPCXMTAPMTK3FABQVSDAAPYKLDVDFVSDVAQKAF
 VSSMPTLIFYKGGKEVTRVVGANPAATKQAIASNV

YHR039C B, 1007 bp, exon1: 501-563, intron1: 564-666, exon2: 666-1007 (SEQ ID NO 197)

GTACATGCACCACTCGCTTCAACTGCGTCAGATAGTTGTAGTCCCTCTGGACATAAGCATTTTCGTTGCT
 GCTTGTGCTGCTCGCTCCGCTGTTTTCAACGCCCTCACTCGATATATACTCCTTAGGATCATGTGTTTGACCTG

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AGCAATTGTCCCTTGTCTTGTGCTTCTTGGGAACACTCCAAAAGCAAGTTTGCACUCAAACATCTTGGAC
 ACTTGTATTTGAACTCTTTTATTCCGCATACACCACACAACACCGCCATACTTGCATAATTGCCACACCC
 TTTCCCTATTAAGTGGACTCCTATTCCAGCTCATCTCATCGAATATGAACTTTGACATCCACTATTATTA
 CCGCGAATTTTTTTTTTTTTTCAATTTGCTTACCCCTGCCCTGGGSTATCAAAAATTCATCTCTAAAAAGGGA
 GCGTGATAGATAAAGCAATCACACCTTAAACAAATACATTTTCTTTTCTGCAATCTCCAAAGTGTGC
 AAGGTATACAAAGCAGAAATGGTATGTGCCATTACATTACGTGTCAACACTTCTGTCTCTAACAAAGCGTT
 CTTACTAACATGAAAACTTTTTTAAABCTGTGCTCTCTTGTGTGGACTGGTACCTCGTGACAAAGGTAT
 TGCTTTTTTTCATTTGTTGCTCAGAACTATGTAATATTCTCTTTAGTCCCAAAAAAACGGAAATTGCCACCC
 TACTACAAGCTGAAAAGGAACCCACGAAATAGTATCAAAAGCCTAGAAAAGTACAGACAAGATAAGTTTGA
 AGCAAGCCAAAGACTGATGTCAGCCAAAGGAAATCGACTCATACAAAATTCAAAAAGACAAGGAATTTGAAGG
 AGTTTGAACAAAGAAATUUCGGTGGTGTGCTGTAATTGSAAGAAAGCAGAGGCTGGTGTCCAAAGGTG
 AATTAGCTGAGATTAAGAAATTCGACAGAGAAGAAAAGGATCACGTTGTCAAAATTTTGATCGAGACTTG
 TCATCAAGCCCTTCTGCTGAAGTCCATATCAATGCCTTGTA

YHR039C-B, 114 aa (SEQ ID NO 198)

MSQKNGIATLLQAEKEAHEIVSKARKYRQDKLKQAKTDAAKEIDSYKIQDKELKEFEQKNAGGVGRLE
 KKARAGVQGELEAIKKIAEKKDDVVKILIEYVIKPSAEVHINAL

YHR053C, 686 bp, CDS: 501-686 (SEQ ID NO 199)

AACTTCAACGATTTCTATGATGCATTTTATAATTAGTAAGCCGATCCCATTACCGACATTTGGCGCGCTA
 TACGTGCATATGTTCAATGTATGTATCTGTATTTAAACACTTTTGTATTATTTTTTCCCTCATATATGCGC
 ATAGGTTTTATACCGATCATTTAATTATTACTTCCACCACCTTTATTTACGGCTGATATCTTAGCCTTGT
 TACTAGTTTACAAAAGACATTTTTTCCCTGTCACTGTCAGAGATTCCTTTTGTGCTGGCATTTCTTCTA
 GAAGCAAAAAGAGCGATCCGTCTTTTTCCGCTGAACCGTTCCAGCAAAAAGAGACTACCAACCCAAATAGG
 ATTTGTGAGAAATCATATAAAGAGAGAGCAATAACTCCTTGTCTTTTATCAATTTGCATTATTAACATCTTC
 TTGTTAGTGCATATCATATAGAAGTCATCGAAATAGATATTAAGAAAAACAACTGTACAAATCAATCA
 ATCAATCATCATATAAATGTTTACGGCAATTAATTAACCTCCAAAATGAAGGTGATGAGTGCCATATGCC
 AATGTGGTAGCTTGCAAAAATAATGAACAATGCCMAAATCATGTAGCTGCCCAACCGGGGTGTAAACAGCG
 ACGACAAATGCCCTTCCGGTAACAAGTCTGAAGTAACCAAGAACTCATGTGCTCTCGGGAAATGA

YHR053C, 61 aa (SEQ ID NO 200)

MFSELINFQNEGHECQCQCSCSKNNEQCQKSCSCPTCCNSDDKCPGKNSSEETKKSCCSGK

YHR055C, 686 bp, CDS: 501-686 (SEQ ID NO 201)

AACTTCAACGATTTCTATGATGCATTTTATAATTAGTAAGCCGATCCCATTACCGACATTTGGCGCGCTA
 TACGTGCATATGTTCAATGTATGTATCTGTATTTAAACACTTTTGTATTATTTTTTCCCTCATATATGCGC
 ATAGGTTTTATACCGATCATTTAATTATTACTTCCACCACCTTTATTTACGGCTGATATCTTAGCCTTGT
 TACTAGTTTACAAAAGACATTTTTTCCCTGTCACTGTCAGAGATTCCTTTTGTGCTGGCATTTCTTCTA
 GAAGCAAAAAGAGCGATCCGTCTTTTTCCGCTGAACCGTTCCAGCAAAAAGAGACTACCAACCCAAATAGG
 ATTTGTGAGAAATCATATAAAGAGAGAGCAATAACTCCTTGTCTTTTATCAATTTGCATTATTAACATCTTC
 TTGTTAGTGCATATCATATAGAAGTCATCGAAATAGATATTAAGAAAAACAACTGTACAAATCAATCA
 ATCAATCATCATATAAATGTTTACCGCAATTAATTAACCTCCAAAATGAAGGTGATGAGTGCCATATGCC
 AATGTGGTAGCTTGCAAAAATAATGAACAATGCCMAAATCATGTAGCTGCCCAACCGGGGTGTAAACAGCG
 ACGACAAATGCCCTTCCGGTAACAAGTCTGAAGTAACCAAGAACTCATGTGCTCTCGGGAAATGA

YHR055C, 61 aa (SEQ ID NO 202)

MFSELINFQNEGHECQCQCSCSKNNRQCQKSCSCPTCCNSDDKCPGKNSSEETKKSCCSGK

YHR056C, 2999 bp, CDS: 501-2999 (SEQ ID NO 203)

ATGCTNTAGTTAAAGGTAAATTAACATAGAGAACGTGGGAACACTTCCGCACTGTGACCACCGGAACGTAU
 CTCTGGTTAGCCCAACCATTAGTCCCACTTACATCCGATCAAAATGCAACAGCAAGTATTAATTGGCGA
 AATCATATCATTTTTGAATATAACCTTGGCGTCCCTACTAAGGATCGTTATACATCCCTAGCTCGGTAGTGT
 TGATTTTTTGCAGGAATGATGCAAGGAGAGGAAGAACAGAGAGCACTTGTGTCTTTTAAATGTATCTTA
 GCAATTTATGAGACGAGCATTTTGTGTCTGTCTGTGACTAGTGGTAGCTTTTGGCGTCTGTCTTTTAAAT
 CATGATGGACATGCAAGTGAGAAAAGTGAGGAAGCCGCTTCTTGCACCCCAATGCAGGAAGAGAAAAGAT
 CGGCTGCCACAGGGCCAAAACCGATATGTCCCAATTCGGTCAAGTATTAACAAGCCGGACTGTTTTTATC

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CAGATGGACCTGGTAAGATCGTGGCTGTCGCCCTCTGCGTCTCCGGATGTCCACGACCGGCAATGCCCAAG
 GTTCCAAACCATTTTAGTCAGGGGAAACGGTGTAAATCAGAAAAACGTAATGATTCAAACCGCAGTATCCGA
 TTATGCAAACGTCGATAGAGGCATTCAACCTCTCGTTCAACCCCTCTGTGGATACTGCGATGCAATGGGA
 CCAAGGCCGCTAGCTACCGAGAATAATAACCAATAATAACTGCTCCTCGTCAGAATAGTAGTACCG
 TTAGTAGTAATGTTCATGGAAACACTATTGTGAGAGCGGATAGTCCAGATGTGCCCTCCATGGATCAGA
 TTAGAGAATATAACACACGAATTACAACCTGGTTTAAACGCTCAAAGTTTGTACTATACAGATAAACCACTACT
 CTTTTAAATGTTGGTATCAATCAAGACTCGGCCGTTTTCGATCTAATGACTTCTCCGTTTACTCAAGAGG
 AAGTATTAATCAAGGAGATAGACTTTTTTAAAAACAATTTGCTTGATTACAAAGCTTGCAACTGAAAA
 GTTTGAAAGAAAAATUGAATTTAAATGCCGACAATACCAACGCAAAACAAAATTAACAAAACAGGTGAGA
 ATTTCTAAGAAAGGCAACGTTGACGGTAAAGAGCCGGATTGATCATCAGACTTCGAGGACTTCTCAGT
 CCTCAGAAAAATACTTTACAGCGCTCACAATAACAGATGTGCAAGTTTAGTCCAAAGTGAAACCGGTTGA
 AGGATAUUUUCAAUTAACTTTTCACTAAAAACCTCACTCAATTTTAGAGATCATTAATCTTTCAAGTTCT
 ATAATATTTTGCACGATATCTGCCATATTAATCAGTTCAAATTAAGTCTCTCTAACCAATAAAAAATCACC
 AACAATATATGGAAGTTTGCAAAGTTAACTTCCCAACCAAAACCAATAATTAATTGAGACACTAAACTCTG
 AATCCCTTAACAATCTAATATTGAAGAATTTTGGCAATCTTTGACAAAACCTCTTACTAGAATTTG
 TTCATAACTCTTTTCCAAATGCTCATACCTCTCTCTCAATCTCAACGGTGGATCTTCTCTTATCTCAAC
 TGACCAAACTAGGCGAATTAACCTGTGCTTCTACTGTTGTTAAACGATTCAATGACCTTCAATCAATAAGC
 AGGCTATTAAATAACCACTTTTCGGCATTAATGAATAATTTGAGGTGATTTCGAAGCCAAATCACATCTGA
 TAAACCTGGATATTATAGACCAAGAGACAATCAAAATTAATGCCATACAAAAATTTATGAATCTCTCT
 ACATGCATGATGATCAATAATCAAGTTTAGACGAAGATTGAGCTGTCTGTTAAGCTTCCAGATAAAAC
 ATTTCAAGTTATTTCACTTTTGAAAAAAATGTTATTAATCAAGACATTCGCTCTTAGGTGAGCTTCTCAT
 TCAATGATACCGCTGCTGAAAAACCTATCTCGGATACCTGCTCTCTATTTGATAAGAACGACATTTCTTTAA
 TTGCTAACGATTTAAAACTACTGGAACCGCAAGCAAAATTGATAAATATTCTGCAAGGTGTTCTCTCT
 ACTTGGCAGTAAATTTAACCAAAATTGAAAGTCTGTTAGAAACCTTGACTATGGGCGTAGTAATACAG
 TAGACTTATATTTTCATGACAACGAAGTCAGAAAAGAAATGGAAAGACACTTTAAATTTTATCAATACCA
 TTGTTTATACAAATTTTTCTCTTTTGTTCAAAAAGAACTCTCTTTGTCTCATGGCAGTTCAACATCTCT
 CTAAACAATAAGACCTCGAACTCTGAAAGATGTGCAAAGGATCTGATGAAAAATTATTTCTAATATGC
 ACATTTTCTACTCAATAACATTTAATTTTATCTTCCCATAAAGTCGATAAAGTCATTTTCAAGCGGCA
 ATAATCGCTTTTCATTTCTAATGGTAAAGAACTTTTATTTCCGCAAACTCACTTTTATTTGAAATCTTACAGAATT
 TTATAGCAATCACATTTGCTATTTTCCAAACCTGTGAAGTAATAATATATGACGAATTTTACAAAAATC
 TTTCAAAATGAGGACATTAAATGTTCAATTTCTTATTCATTCATGACAAGATTTTCAAAATTTTAAAAAAA
 TAGAAATTATCGTATCTCTTTTACGAGATGAATGAATAGCAACGGAAGTTTCAAACTCATTAAGGCTT
 TCAACAAGGTTTTGAATCTGATTAATATATGCTGAGATTTAGCAAGAAAAACAAAAATTTTGGGAGAA
 ACTCTGAATAACATAATGTTTACAGATTATAGTCAGTCGGCGAAGAAACAAAAATGTTCTCTTCAAAATTC
 CCGTTAGTGAACGAAACAGAACTTATTTAAATTTAAGGAGATTTAGATTTTTTAAATGGAAGAGAAAG
 TTGTCAAAGGAGTATAATTATTGACAAGGATTTGGAATCTGATAAATTTGGGTATTACTACGGCAAACT
 TCAACGATTTCTATGATGCATTTCTAATATTAG

YHR355C, 832 aa (SEQ ID NO 204)

MVAVPSAAGMSTHGNGQGSNHPSQGNQVWQKNVMIQTQYPIMQTSIEAPNFSNPSPVDTAHQWIKAAASY
 QNNNTNNNTAARQNSSSTVSSNVHGNITIVRSCSPDVPMSDQIREYNTRILQLVNAQSPDYTDNTPYSFNVGI
 NQDSAVFDLMTS
 FFTQEEVLIKEIDFLKNKLLDLQSLQLKSLKEKSNLNADNNTANKINKTGENSESKKGKVJGKRAGFDHQ
 SRTSQSSQKYFTALTITDVQSLVQVKPLKDTPNYLFTRNFIIIPRDHYLPKFYNILHDIICHINQFKVSP
 NNKNHQQYMEVCKVNPFPKAIITETLNSESLNNLNIEEFLPIFDKTLLEFVINSPNGDTCPSPSTVD
 LPLSQLTKLGELTVLLLLLNDSTLFLNKQAINNEVVSALMNNLRILRSQITLINLEYVDQETLKFIAITK
 FYESLYMHDDHKSSLDEDLSCLLSFQIKDFKLPHFLKKMYYSRHSLLCQSSFMVPAENLSPIPASIDT
 NDIPLIANDLKLLETQAKLINILQGVFPYLPVNLTKIESLLETITMGVSNSTVDLYPHDNEVRKEWKDTL
 NFINTIVYTNZFFLVQNESSLSMAVQHSNNKTSNSERCADLMKIIISNMILFYSTTFNFIPPIKSIK
 SFSYGNRRFHSNGKEFLFANHPIEILQNFIAITFAIPQRCEVILYDEFYKNLSNEEINVQLLIHDKITL
 RILKKITETIVSFRDEMNSNGSPKSTKGFNKVLNLIKYMIRFSKKKQNFARNSNNNVTDYSQSAKNN
 VLLKFPVSELNRIYLKFKETSDFLMEREVVR311TEKDLESNLCITTAENFNOFYDAFYN

YJ1138C, 1688 bp, CDS: 501-1688 (SEQ ID NO 223)

CTGTTGAATCATGGTAAAAGAGAAAATCAAAGCACGTTGACCTGGATATAACCTCAGTAGATCGAAAT
 GCTTCCAGAAACAGTACTGCAGAGAAACATGATATTGAGAAACCGACATCTAAGCCCAATCTGCTTTT

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AAATTTGATTGGGAGTCTACGGATTATTTAGACCCGGTCCAAAGAGCATTCCCAAAGCCTGATACCTGA
 TGCCATCCCCTCTACCTCTTAGCTATCAATCAATCAALTAAACTACTACATAGTATACATTAGCTGTACA
 GTCCCTCACATCAGACGAAATACAAAAGGCCGGGTGAAAGCGTGGATTTTGGCTACCTTTTTCTTTTTTTC
 GAAATTTTTTTTATTTTTTTTTCAGCATCATATATAPAAAGAAATCTCATCTCAACCAGAAAGGAAACAGCA
 GATCCCAATACACATAGTAGGAAAAAAGGTTGCTAAACAAAGGACTGGTGTGTACAAGAAACTAA
 TAAATAGTAATTGCAATATCTCTGAAGGTATTACTGATATGGAAGATCCCAAATTCAAACCAACTATG
 ACAAGGTGGTCTACAAGTCCGATGATATGGAATTGGACGAAAACCTGGTAAAGAGGTGTTTCCGGTTACG
 GTTTTCGAAGAACCATCTGCCATTCAACAACGTGCCATCATGCCATTATTATGAAGGTCACGATGTCTTGG
 CTCAAGCTCAATCTGGTACTGGTAAGACCGGTACTTCTCCATTGCTGCTTTGCAAGAATTGACACCT
 CTGTCAAGGCTCCTCAAGCTTTGATCTTGGCTCCAACTAGACAAATTCGCTTTGCAAAATCCAAAAGGTTG
 TCATGCCCTTTGGCTTTCCACATGGACATCAAGGTCCACGCTTGTATCGGTGGTACTTCCTTTGTTGAAG
 ACGCTGAAGGTTTGAAGATGCTCAAAATCCGCTGGTGGTACTCCAGGTGGTGTGTTTGAACAACATCCAAA
 GACGTAGATTTCAGAACTGACAAGATCAAGATGTTTCATCTTAGATGAAGCTGATGAAATGTTGTCTTCTG
 GTTTCAAGGAACAAATCTACCAAAATTTTACCTTACTTCCACCAACCACTCAAGTTGTTCTATTGTCCG
 CCACCATGCCAAATGACGTCTTGGAAAGTACCACCAAAATTTATGAGAAACCCAGTTAGAAATTTTGGTTA
 AGAAGGATGAATTGACTTTGGAAGGTATCAAAATTTCTACGTTAATCTTCAAGAACAAATTCAAAT
 ACCAGTGTGTTGACCGAATTTATACGACCTATCTCCGTTACTCAAGCTGTCTCTTCTGTAAACACCGAA
 GAAAGGTGCAAGAAATGACCACTAAGTTAAGAAACGACAAATTTACCGTTTCTGCCATTCTTATCTGATT
 TACCACAACGAAGAAAGAGACACCATCATGAAGGAATTCAGAAGTGGTTCTTCCAGAATTTTGATCTCCA
 CTGATTTGTTGGCTAGAGGTATCGATCTCCAACTAGTTTCTTTEGTTATTAACTACGACTTACCAGCTA
 ACBAAGAAAACTATATTACAGAAATCGGTAGACCTGGTGGTTTCCGTAGAAAGGGGTGTTGCCAATCAACT
 TTGTTACTAACGAAGACGTTGGCGCTATCAGAGAACTAGAAAAGTTCTAUTCACACTCAAAATGAAGAAT
 TGCCATCCGACATTGCTACCTTGTGAACTAA

YJL138C, 395 aa (SEQ ID NO 224)

MSEGLTIDIEESQIQTNVYDKVYKFDDEMLDENILRGVPGVGFRRPSAIQQRAIMPTEEGHDVLAQAQSG
 TGKTTGTFISIAALQRIDTSVGAPOCALMLAFTRELALQIQKVVMLALPHMDIKVHACIGGTSFVEDAELSLR
 DAQIVVGTGPRVFDNIQRRFRFTDKIKMFILDEADEMLSSGFKEQIYQIFTLLEPTTQVVLLSATMPNE
 VLEVTTKFMRFVRILVKKDEITLEGIKQFYVNVVEEEYKYECCLDLYDSISVTQAVIFCNTRRKVEEL
 TTKLRNDKFTVSAIVSOLPQQRDTIMKEFRSGSSRLISTDLLARGIDVQQVSLVINVDLPANKENYI
 HRIGRGGNFRGRKQVAINFVTNEDVGAMRELEKFYSTQIEELPSDIATLLN

YKL060C, 1580 bp, CDS: 501-1580 (SEQ ID NO 239)

TGGGTCAATTACGAAATAATGATAGGAATGGGATTCTTCTACTTTTCTCTTTTCCATTCTACCAACCGT
 CGGGAAACGTGGCATCTCTCTTTTGGGGCTCAATTGGAGTACGGCTGCCGTGAGCATCTCTCTTTCC
 ATATCTTAACAACGAGCAGTAACCAATCGAAAAGCATGAGCTTAGCGTTGCTCCAAAAAAGTATTGGA
 TGGTTAAATACCAATTTGCTCTCTCTCTCTCTGACTTTGACTCCTCAAAAAAATAATCTACAATCAACAG
 ATCGCTTCAATTACGCCCTCACAAAACTTTTCTCTCTCTCTCGCCACGTTAAATTTTATCCCTCA
 TCTTGTCTAACGGATTTCTGCACTTGATTTATTATAAAAGACAAAGACATAATACTTCTCTATCAAT
 TACAGTTATTGTTCTTCTCTTGGCTTATTCTCTCTGTTCTTCTTTTTCTTTTCTCATATATAACCATACCA
 AGTAATACATATTCAAAATGGGTGTTGAACAAATCTTAAAGAGAAAGACCGGTGTCATCGTTGGTGAAG
 ATGTCCACAACCTTATTCACCTTAAGCTTAAGGAACACAAGTTCGCTATTCCAGCTATTAAAGTACCTCTT
 CTCTACTGCGGTCTGCTGCTTTAGAAGCTGCTACAGACAGCAAGTCCCAATCATTTTGCAAAACCTCTA
 ACGGTGKGTGCTTACTTGGCTGGTAAGGCTATCTCTAACGAAGGTCAAAATGCTTCCATCAAGGGTC
 CTATTGCCGCTGCCACTACATPCAGATCCATTGCTCCAGCTTACGGTATCCCAAGTTGTCTTACACTCTG
 ACCACTGTGCCAAGAAAGTTGTTGCCATGGTTCCATGCTATGTTGSAAGCTGATGAAGCTTACTTCAAGG
 AACACGGTGAACCATATTCTCTCTCCACATGCTGGATTTGCTCTGAAGAAACCGATGAAGAAACATCT
 CTACTTGTGTCAASTACTTCAAGAGAATGGCCCTATGGAACTAATGGTTAGAAATGGAAATCGGTATTA
 CCGGTGGTGAAGAAAGATGGTGTAACTAACCAAAACGCTGACAAAGCAAGACTTGTACACCAAGCCACAA
 AAGTTTACAAAGCTCTACAAGGCTTTGCAACCAATCTCTCCAACTTCTCCAACTGCTGCTGCTTTCCGGTA
 ACTGTACCGGTTTGTACGCTGGTGACATCGCTTTGAGACCAGAAATCTTGGCTGAACACCAAAAGTACA
 CCAGAGAACAAAGTTGCTTGCAGCAAGAAAGGCCATTGTTCTTGGTCTTCCACGGTGGTTCGGGTCTA
 CTGTCCAAAGAAATCCACACTGGTATTGACAACGGTGTGTCAGGTCAACTTTGGACACTGACTGTCAAT
 AUGCTTACTTTGACTGGTATCAGACACTACCTCTTGAACAAGAAAGGACTACATAATGTCCCAAGTCCGTA
 ACCCAGAGAGTCCAGAAAAGCCAAACAAGAGTCTTTCGACCCAAAGAGTCTGGCTTAGAGAAGGTGAAA
 AGACCAATGGGTGCTAAGATCACCAAGTCTTTGGAAACCTTCCCTTACCCTAACACTTTATATA

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YKL060C, 359 aa (SEQ ID NO 240)

MGVEQILKRKTGVIVGEDVHNLFTYAKEHKFAIPAINVTSSTAVAALEAARDSKSPITILQTSNGGAAV
FAGKGISNEGQWASIKGAIAAAHYIRSIAPAYGIFVVLHSDHCARKLLPWFDGMLEADEAYFKEHGKPL
FSSHMLDLSEETDBENISTCVKYFKRMAAMDQWLEMEIGITGGEEDGVNENADKEDLYTKPEQVYVYV
KALHPISPNIASIAAFGNCHGLYAGDIALRPEILAEHQKYTREQVGCKEEKPLFLVFIIGSSGSTVQEPH
TGIDNGVVKVNLDTDCQYAYLTGIRDYVLNKKDYIMSPVGNPEGPEKPNKKFFDPRVWVREGEKIMQAK
ITKSLETFRTTNTL

YKL097W-A, 779 bp, CDS: 501-779 (SEQ ID NO 245)

AGCTCCGAAGGGCAATTCCACAGGCCTCCGCGGGSCCGGCCCAAGGCCCAAGGCGTGGAATATCCC
CGTTTTTGGGGCCATAACACCCAGTACCACGCGCGGAACCGGCCATATAATAAGCTTTTCACTCTCAAGA
ATGCTAAACGTAAATAGGAACATCCCCTACCTTAGAAATTCGCGGAAATTTCCGCGCTTATTCATTTAGAAA
ATCTGGAAACCGTCCCTTTTTCCTCTTTCTTCCATTTCCCTTTCCCTTATTATTGCCATTTCTTTAACTGCAT
TTGGGGAAACCGTAGACCAAAAGGCCAAACAGAGAAATGTAAACGTTCTAAAAAAAACCAACGAAAAAATC
GAAAAATAAGATACAATAATCGTATATAAAACAGGCTTCCTCTCTCATCATTTTCAATTCTCTTTCTTGGC
ATCCCTTTTCTTACTCTTTTGTCTCTTTCTTCTCATATAATCAAGAAATAAATAAATTCATCAGATTGCGCTACA
CACTAACCAAGAAAAAAATGCAATTTCTCTACTGTCTGCTTTCCCTTTGCTTTTCTGCTTAACTTCTG
TTGCCCTGAAATCCGCTGCGCGCATTTCTCAATCTACTGACCGTCAAAATCCAAAGCTACTAUCCTGCTCA
CCACCGAAGCTACCACCACTGCTGCCCATCTTCCACCGCTTGAAGCTGTTCTCTCATCCAGCACCGGAA
CTATCTCTCAACAACTGAAATGCTGCTGCTAAGCCCCCTCTCCCTATGGGTGCGGGTGCTCTAGCTG
CTGCTGCTATGTTGTATAA

YKL097W-A, 92 aa (SEQ ID NO 246)

MQFSTVASVAFVALANFVAARSAAALISQITDQGIQATTTATTEATTTAAPSSTVETVSPSSTETLSQQT
ENGAIAKAAVGMGAGALAAAAMLL

YKL150W, 1409 bp, CDS: 501-1409 (SEQ ID NO 249)

CCCATCACATCGCATCAGATCAGATCACTCCCTATTTCTGCCCCTTTACAGCGCAAAGGAGTCCGTGTGTGG
GTGTGTGCTCCTTTTGACGATCATTAAGAGTCCATTTCTAGTATCCAGCTCGTAACAAATAGGTGAATGA
ATTAAGTTCTATTTTGGATGACCTTCACTATCCCTCCACGCAATGCTAAACTATCCCCCTCATATGACC
CCTATATCGTATAAGGAACTTTGTACCCCTGACAAATTCAACTTCAAAGGTCTAAGACCAACCAAGCGT
AGGAACCTATCGCTCGGAGTGTCTCTCCGTTTGAAAAAAGAGAGAAATAAGGGCCCTTGATTGGTGCTCT
TCTCCAGAGAGGTACGTATATAAGAAATGCAGTTTGTCTGCAATCGCCGCTTGTGTAAAGTACTCTTACC
TTTTCCCTCAATACTAAGCTTTTGAAGCAGCCAACTAACAATAGTATAACGTATATAGGTTAAAAATAA
TATTCCCAAGTCAAAAACATGTTTTCAGATTTATCCAGATCTCACTCAAAAGCATTACCGATTGCTCTAG
GTACAGTTGCTATAGCAGCTGCTACCGCATTTCTATTTGCAAAACGTAACUAAUATTTCTTTTGTCTTCA
ATGAATCTAATAAAGTGTTCAAAGGTGATGACAAATGGATCGACTTGCCAATATCTAAAATAGAGGAGG
AATCCACGACACCAGAAGGTTTACTTTTAACTGCTACCGAGACTCAGAAATCGGGTTGGTCTTAG
CATCTGCTCTGTTTGTCTAAATTTGTACACCAAAGGGATCCAAATGTGTGAGACCATACACTCTCTGTA
GTGATCTTTCCAGAAAGGTTCACTTCAAAGCTCTCTCAAGCATTATGAAGGTGGTAAAAATGAACCTCAC
ATTTATTTGGTCTTAAACCAATGACACCGTTTCTTTCAAGGGTCTCTATATGAAATCGAAGTGGCAAC
CTAATCAGTTCAAGTCAATCACCTTGTGTAGGTGCGCGTACCGGTATCAACCTCTGTACCAATTAGCTC
ATCATATAGTTGAAAACCCAAACGACAAAGCCAAAGTTAACTTGCTATATCGGAACCAAGACTCTCTCAGG
ACATTTTACTTAAGGAAGGAAGTGGATGCGTTGAAGGAAAAGTATCTGACAAAGTTCAATGTTACTTACT
TTGTTGACGACAAAGCAAGATGACCAAGACTTTTGAATGGTGAATTTAGTTTCACTCTCAAAGATTTTAAATC
AGGAGCATGTTCCAGGTCCAAAGGAAAGCACACATTTGTTTGTCTGCGGTCCCCCACCATTATGAAGC
CTTACTCAGGTGAGAAGAACTCACCTAAGGACCAAGGTGAATTTGATCGGTATCTTGAACCAATTTCCGCT
ACTCCAAGGACCAAGTTTTCAAATTTTAA

YKL150W, 302 aa (SEQ ID NO 250)

MFSRLSRSHSKALPIALGTVAIAAATAFYFANRNQHSFVFNESNKVFKGDNKWTDLPTSKYFRFESHDIR
RFTFKLPTEDSEMGIVLASALFAKFVTERGSNVVRFYTPVSDLSQKQHFQLVWYHYEGGKMTSHLPGLK
PKDPTVSFKGFIKWKWQPNQFKSITLLGACTGINFLYQLAHHIVENPNDKFKVNLLYGNKTPQDILLRK
ELDALKKKYFDKFNVTYFVDDKQDEQDFDGEISFISKFIQEHVPGPKRSCHLFFVCGPPPMWAYSGEK
KSPKDQGELICLENLGYSKDQVKKF

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YKL156W, 1099 bp, exon1: 501-503, intron1: 504-853, exon2: 854-1099
(SEQ ID NO 251)

CGAAGGTTTCGATCAAAGTTTGGCTCAATCACTGGACACTATTACTTCCGAAACCCCACTCCCGTTAAAC
AGAGACCGTGATGTCGTCAACAAGTATTTCAAGGAAAATGCTTACTATTAAAGAAAAATCTCTTTTCTA
GCCATTTTGGCTTTTATATAGTCAAGTATCTATATGTGACAAATACTTCTTCTAAGC/T/TTGGCTTCTG
ATAGGCTTAGCTTGCAGTGGTTGCAAACATACATAAATCAACAAAAAAGTACGGC/T/AAAAATTTTGGTA
TTCATTTATTTCAACCCGTGCACACTGGAAATAAATCTGTACATAACAGCATATTTTGTTTTGAAGAA
ATTTCTGTGTTCCCTCCGATGTCGGACCAATTTTACGATCCGCTAAATTTTCGTAAAGTATCAGTAACCTTG
GTATCTCTGTATAAGCGGAGTCTAATTTTCGATAACAAAGCAACTTTCATCCGTAAACACTTCCAAACAAAGCA
AAGATAGATATCCCAAAATGCTATCTTACTATCCCAATAAATTCAGCGCAACTTGCACCAAGTGAATAGAAC
AATACATATAGATAAGTTCGCAAAAGAAAAGAAACACATGTTGGTGGAAAATTTTTCACCAAGAGAGGCCAAG
AACTATGAAGAAAGACTTTTGAATATTTCAAGCGGTTGCTACATATAGTGGATAAGATTCAGGATCGA
CGTATGAGCTTACAGTTCATTGTTACCGGAATATTAATTTCTGATGATGGCGAACTTCATTCCAGCAAC
TCAAGCTTATGTTATTTTCTATTTCTGCACCGAGATGAGGAGAAAAAGGAAGTTTACTAACAGTTTACA
TTTATTTCTTTATTTCTGCTACAACAGGTTTACTGTTCAAGATTTATTTGACCCCACTGCACCTTCTGAAGC
AAGAAAGCACAAATTAAGACATTAAGTCCAAAGGTTCCAAAGATCGTACTTCCAGACGTTAAGTCCCGCAGG
TTGTTTGAACATCACTACAGTTTCTTCAACACGCCCAAACTTGCAGTTACCTGCGAATCCTGCTCAACAACT
TTTGTCCACCCCAACTGGTGGTAAGGCAAGGCTTTCTGAGGCTACATCTTTTCAAGAAAGTAA

YKL156W, 82 aa (SEQ ID NO 252)

MVLVQDLLHPTAASEARKHKLKTLVQCPRSYFLDVKCPGCLNLTTFVFSHAQIAVITCESUSTILCTPTGG
KAKLSEGTSPFRK

YLR029C, 1115 bp, CDS: 501-1115 (SEQ ID NO 265)

TGCACACTTACTTAATATGTTTTCGCGCCCTTCATAAGAGUGTGTTTCTAAAAATTTATTCGCCCAAGAACT
GAGATGGACTCGCACCCCTACATGACGTTTAAATATTTTACTGTTTAAAGGTTTCAAGACATGCACCAGGTTGUG
ACATGTGTTCGGATTATCATGACAATGTCTCTATCCGAGATGCATTTGTAGTATCAATTTGATGCGTATCT
ATGACATGACTTACATAGCATTACATCGTCAACATGATATTTATATTC/T/TTTTCGATAAATGTACCGGAT
TTAAAGCTGTCGAATATATTTTCTGAAATTTCTTGGAGCTGACGCAAAATTTTCAAGGTTGCTAAAACT
TTTCAAGATCTCTCACTTTTGGCTGGTAACAAGAAATCATCGCATTTCCAT/T/TTACCACCGGTACAT/T/
AACTGCTATCTCTCAGTTTCTTTCCCTATCCTTAAAGTAATTCCTTTTACAATCTTAAGAAAAACCGACT
AAACAAATRAATCAGCAATGGCTGCC/TACAAATAT/T/TTGGAAGAAATTCGCAAAAGAAAGAAAGCAATCTGATG
T/TTTCAGATCTTTGCAAAAGAGTCAGAGTCTGGCAATACAGACAAAAGAAATGTCATTTCACAGAGCCCGCTA
GACCAACTAGAACAGACAAGGCTAGAAAGATTCGGTTACAAAGCTAAGCAAGGTTTTCGTTATCTACCGCTG
TCAGAGTTTAGACGTGGTAACAGAAAGAGACCTGTTCCAAAGGCTGCTACTTACGGTAAGCCCAAC/TAAAC
AAGGTGTCAATGAATGAATACCAAGATCCTTGAGAGCTACCGCTGAAGAAAGAGTTGGTCTCTCGTG
CCGCTAACTTGAGAGTCTTGAACCTCTACTGGCTTAACCAAGATTTCTACTTACAACTACTTCAAGT/TA
TCTTGGTTCGACCC/TCAACACAAGGCTATCAGAAGAGATGCTCGTTACAACTGGATCTGTGACCCAGTTC
ACAAGCACCGTGAAGCTAGAGGTTTGAATGCGCACTGGTAAGAAATCCAGAGCTATCAACAAAGGCTCACA
AATTCACCAACACCAAGGCTGGTAGAAGAAAGACCTGGAAGACACAAAACACTTTTCTCCTTGTGGAGAC/
ACAGAAATATA

YLR029C, 204 aa (SEQ ID NO 266)

MGAYKYLEELQRKKQSDVLRFLQRVRVWEYRQKNVTHRAARPTRPDKARRLGYKAKQGFVIYRVRVRRG
NRKRPFVKGACTYGKPTNCGVNELKYQRLRATAEERVGRRAANLRVLNSYWNQDSTYKYFEVLLVDPQ
HKAIRRDARYNWICDPVHKHIREARGLTATGKKSRGLNKGHKFNNTKAGRRKTWKRQNTLSLWRVRK

YLR038C, 752 bp, CDS: 501-752 (SEQ ID NO 267)

GGAAAGCAAGCTCTAAATGATAACTCTACAAAAAAGTTACAGAGAAATTTGTGACTAATTTTATTGAAGCA
TGAAGAAATTAATGCTTAAAGTCTTAGAGCTTTTGGTGACAAGTCTGCAAAACGTCACAGACCCAAATPAA
AGCTACCGA/TTCGTTGGACATGTGTTTCCAAATTAATACGCTTACTCAAGCAATTAGACAGAGAAACAA
CACACAAATGGCTCAAAAAGCACTCGAGAGATTCAAATAAATCTATATGACACCAATGTATTTCTTTACCA
TATAGCTTCACAACATTTGACCAATCAATTTTCAGAAATGCGTCCGCGCGTAGTTTTTCCCGGATATCCCCA
TCCCTTCAGGACCTTTTAAAAGGTGATGAAGATGCACCAGATACAAAAGTTCCATPAAAAATGATTAGCA
GAGATATACAAATATTTTAGTAAGAATACATAAAGTATCTTTCGCTTTTCAACAAATAGGAACAGGCACATA
AATACAGTAATAATAGACATGCTGATCAAGAAAACCTCTCCACTACATACAGTTGGTTTCCATGCTAGAT

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TTCCCCCAACAAAACCAAAACAAAGCATTGTTGGCAATCTTATCGTGGAATTATCACAAGTGTGTTAATATGJA
AGGGCGAAGATTTTGGCTCCGTGCAAGGTCCTTTTGGAAACCTATAACGCCTTATGTCCCTAGACTCCA
TCGAAAAATGGGATGATCAAAGAGAAAAAGGTATTTTCGCAGGTGATATCAACTCAGACTAA

YLR038C, 83 aa (SEQ ID NO 268)

MADQHN SPLHTVGF DARFPOCNQTKHCWQSYVDYHKCVNMKGEDFAPCKVFWKTYNALCPLDWIEKWDD
QRPKGIFAGCINS

YLR312C, 1697 bp, CDS: 501-1697 (SEQ ID NO 285)

CATCAANTTAGGCCAACTTGAATAGTCAGCTAGGTGATATATTTAAAATCAATTAGCCCTATGACTACA
TTAGGTTTTATTGTTAGGTCTTTACGGCTGCATATTTGCTTTTCGCCGTTCCGGCGGGTCTCTGCCAGCAT
CTCTCCGCGGTCTTTGTATGGGTGGAGTTGACAGTTAAACCTCCCGACCCCCCTACCCCGGTGTGCCCCCGG
TCCATCTATCCATTTTTCGGTAACCCCTTTCCGCGACAGCTGCTTATCAAGGTAACCTGGATCGAGCCAT
AAAAATTGATCTACACAGATGAGATGGGGCATTGGGATATATTATTAGTCCGAGTATCATATAGTTAT
TCAGTTTATCCAGCTTACTGGCCAAAACGTTTTCCTTCATTGGAATAATCGTTTAGGAGCTACTGTTTC
CGGTATAAAGTAAACAAGCACAGTAGCAGAGTAATACCGCACTGACGATAATAGAGACTAGTAAAAACAGTC
GAGTTGTGCGGACCTAAAATGTCAGAAGAAGACGATCATCGAAGTCAGAAAATATCTTTGGATAGTTTGCATGAAAGCTCCT
AAGGGAGAGAAGGGGAAGAACAGTCAATCGAAGTCAGAAAATATCTTTGGATAGTTTGCATGAAAGCTCCT
TTCCAGGACAGGACGACGAGGACATTCGATGCAGATGTCCTATCGAACACTAGCAGTGAAGAGTCTGCAU
AGATCAANTCGTACTTTACGATTTTGAACATCTAATGAATTTAGTAATGCTGGAGTTAATATTGATCAAA
CTGGAGTTCCCACTATTTCAAGAGTCATTTGATACTTTGTCCGGCTCAAAATGTTGGCGGAACCGTATTGCG
CAAGTATGCAGCGGTGCAAACTGAAGGATAGTACGATAAGGAATTCAGCAACTATCGGATCATATCA
TAGATAAAAGTGAGGGTAAATCTGCTAAATGAAGATGTGGCATGTTATCAAGCTATCTTCATTGCTTT
CCATGACCTTTTTCATACCTCGCCCTCGAATATTCCCTGACTGGTGATGTGTGCGCAGCTTTTAAATCAC
AACAGTCATTACGTAATAATGAAAGGAAGCTGTTGTACGGCAATATCGATTTTGTGATAAAAATCTTT
ACGATTTCAACAGTGACTCTTTAAGTCAGTGGGCTCCTTCAGGAAAATACTAUGTTCGACCTTCGACAATC
ATATTGCAACCCATTAAAGGATGATGACCTAATCGCTGGAGACGATACAAACAGACTTAGTTATTT
TATGGTATACAACAAAAGCTCGAATGAAAGACGGTTGGCACAPAGAGAAATTAACAAATAAACCAGCAAA
GAATAAAGTTACACCTATTTCTCAAGAATTCCTTTAATCCGCTCAAGAAAGTTTAAGGGTATTGCATA
AAGAACAGAAACCCCGCTGGAAGAGGCTCTTTGTCTACTTCAATAATAAAATACAGGCAATTTTCTCCAC
ATATTAATAAAGGTATTTTCGATCATTTCTGCCAAAAGACAAACAAATGTTGCTCGGGATCCAGATTGCAGT
TGGCCAAAGCTTCGTTTCAAGTCAATGAAACCAATCCGAGTTTTTCAGTTTAAGGTTCCGAAAGATACCA
ACTGGTTTGTAAAGCAGCTCAAAACGGTTCGGATTGAAATTACAGCATTCGAGGATGTATAAAGCGATGT
CAGAATGCAGGAAAAAAATTTATTTTAAAGTCCAAACACTAG

YLR312C, 398 aa (SEQ ID NO 286)

MSEEDDHWNLVRLRLRKCRECEEQSSKSEISLDSLHSSSFAGEDDEDFDADVLNNTSSEPSAQMNRIY
DFRTSNFESNAGVNLDTGTVPTISESFDTLGSGNVGCTVLPMEGSKLKDSTIRNSSTLSPHIIDKSEG
KSARKLKMWHVIMLSLLSMTFSYJALEYSLTGDLVLAGFKSQQLRNNERKIJYGNIDFVEKKSYSDDSD
SLSQWAPSGKYVDFDNHIAYPELKDDFMGWRRYKTDLVILWYTTKARMKDGWHKRLNKINCGRIKLHL
FLKNSFKSAQESLRVLIKEQKRWKRJLFVLJHNKYRQFSPHIXRYFDHSCQKAKQCWSGSKLQLRKLRF
KSMKPFRRVFQFKVRKDTNWFVXQLKRFGLKLQHSRMKAMSECRKKNYFKCKH

YLR414C, 1292 bp, CDS: 501-1292 (SEQ ID NO 293)

TAGTCAGCCACACATTGACGTACACTGTGAACAGCCTATTTCCTTCCATGTATCTCAGTSCCCAGCTTA
TGAGAACTCTCACACCCCTCCCACTTGAACCTTCAGAGCCCTCTCCACTCCCCCTCTTTTCAACATCGCC
AGATAGCCCGCCCTTGAATGGTTCGCGACAAACCCGGCTTGGCTGGCCAGGCAAAAAGGACGCAGCAGC
CCTCGAGCGTTATTTCCCAATCGGGCCCTACTATCAOCCAAAGCCAGCTCGGTATTTTTAGCGCTTCTCG
CAGGAAAATTGGCTCACAGTATATATACGCGAGAATGTTGCTCTTCCATGTCTCACTACTCAATGAGT
GTCCAGTGGTGTTCATTTCTGACCACTTCTTTTGAAGTGAAGCAAAAAGAACTAGATCAAGATCATA
CAACCGCTGCGCAGTAGTGAACTTGATTAAAGCAATAGAGAACTATTAAGAAAAACAAACACATCAT
CGAACGACGCTATAAGCATGAGGAATTTTTTCAAGTTATTTTTCAGCTATATTTTCGCTAAGAACAC
TTATATTAGCCATTGTTCATCCCGACGATCAACGAAAAATACAGTCCCATAAATAAAATTTACTGTG
CAGAATTGGATCTGTCCAGATGAAGGTATCCAGCGGCTGCTCTCTTTGAGTTCTTCACGCTATCTT
CCTTGGGCGCTGCCCTCATATATAAAATATAGCGCTTTCGTCGTAATCTTACACTGCACTCCCTCGCATAACA
TCCAAATCATGTTCTTCGCCCTCACGGTATCCAGAATTTTAACTATCTGTCATTAGTGTATGACAATATCA

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ACAACAATGAGGCTCTGGAGCTTATGGATTCCGTGGCCAGTGTGTTTTTGCCCGAAAAACTAAAAAGTA
 AAATGACATACTACAACAATCTGGTCAAGTGTATGTTCAATTACCAATTCCTATTGGTATTGTCTTGAAUCC
 TTGTGAATCTAGTGTCAACGTATTGGCGCTGGATCATCCACATAAGGCCGCTAAACGTGGTCTTGGTGGCC
 TTTTTTCATTTTTTCGCCCTTTGGCGCCCTATTAGTCAGTATAGGTTGGTGTGTTGGGCACCTTACTCATACA
 TCAAATACATCCTAANGCATAACTATAGTCATTAACGGTATTTCAATGAGCATTGGTAAGGAACACCAGG
 GTTTGATGTGGGGGGCTGTGTTGGAGCATTACTGAATTTCAATTCATATGTTGTAGCGTGAGATCGAGGC
 CCACCGTCTATCTATGCGAACGCTCCAAATTGAGGAAAAACCATTGATTTGA

YLR414C, 263 aa (SEQ ID NO 294)

MRNFFTFFFAAIFSLGALILAIIVACAGSTKNYSPINKIYCAELDLSOMKVSTVLPSSLSSATLSSLGLPS
 YINIGLWSYCTVDSSHNIQSCSSPHGIQNFNLSSIVYDNIMNNEALELMDSVASVVLPEKLKSKMTYYN
 NLVKCMFITILIGIVLTFVNLVFNVLRWIIHIRFLTWFCAFFSFFAFALLVSIGSCLGTYSYIKYILK
 INYSDYGISMSIGRNYQGLMWGAVVGALLNFIKCSVRSRPTVIYANAPIEEKPLI

YMR251W-A, 680 bp, CDS: 501-680 (SEQ ID NO 317)

ATCCCGTTGAAGCAACCGCACCATGACTAAATGGTGCCTGGACATCTCCATGGCTGTGACTTGTGTGCTAT
 CTCACAGTGGTAACGGCACCGTGGCTCGGAAACGGTTCCTTCGTGACAAATTCCTAGAACAGGGGCTACAG
 TCTCGATAATAGAATAANTAAGCGCATTTTTGCTAGCGCGCCCGCGCGCGCTTTCCTTCCCAATAGCGAGGC
 ECAGTTTTATCGCGGAGCTCTACTTCTTCTTATTTGGGTAAAGCCCCCTTCCTGTTTTCGGCCAGTGGCTG
 CTGCAGGCTGCGCCGAGAACATAGTGATAAGGGATGTAACCTTCGATGAGAGAAATTAGCAAGCGGAAA
 AAAACTATGGCTAGCTGGGAGTTGTTTTCAATCATATAAAAGGAGAGAAATGCTGTCTCAUTATGTAC
 AGTTTTCTGGGACGCTTAACCTTTTATTGACAGGAGCTATCAATCATACAGATATTGTCAAAAAAAA
 AAGACTAATAATAAAAAATGAAGTATCTCAAGTTGTTGTTTCCGCCGTCCCTTCACTGGTTTTAGTAA
 GTGCTGCTAACAGTTCTAACAGCTCAAGCTCAAGAAATGCTGCCCAACCAAATGCGCGTTTAAACACCC
 CTAAGGTTCCACGCCCCGCTGGTCTTGGCTCTAGCTCGTGCTTTGCCCTTTTTGATTTAA

YMR251W-A, 39 aa (SEQ ID NO 318)

MKLSQVVVSAVAFTGLVSAANSSNSSSSKNAAQPIAGLNNKVVAGAAGVALAGALAFLLI

YNL030W, 812 bp, CDS: 501-812 (SEQ ID NO 323)

GTTTTGAACACCGAGCCATAGCCGTGATTGTGCGTCACATTTGGGCGGATAATGAACGCTAAATGACCAACT
 CCCATCCGTACGAGCCCTTAGCCCTGCCAATAGTTTCACGCGCTTAATGCCAAGTGCCTCGGAACCGA
 CAACTGTGGTCTTTTGGCACCGGGAAAGTCTACTACACCCAGACTTTCCGATTTCTATGGCAGGACGT
 TCTGGGAGCTTTCGCTCTCAAGCTTTTTCGGGCGGAAATGCAAGCCAGACCCAGAACAAAACAACCTGAC
 AAGAAGGCGTTTAATTTAATATGTTGTTCACTCCGCGCTGGGCTGTGTATTTCGGCTAGATACATACG
 TCTTTGTGCGTATGTACTTATATCATATATACTATATTAGGATGAGCCGGTCAAGAGATTTTTTTTTT
 TTTCTGCTTAATTTATTTCTTTCTCTACCTTTTTTTCCTACATCTTGTTCAAAAGAGTAGCAAAAACAACA
 ATCAATACAATAAAATAATGTCCGGTAGAGGTAAAGGTGGTAAGGTCTAGGAAAGGTGGTGGCCAAC
 GTACAGAAAGATTCTAACAGATTAACATTCAGGTATCACTAAGCCAGCTATCAGAAGATTAGCTAGAA
 GAGGTGGTGTCAAGCGTATTTCTGGTTGATCTACGAAGAGTCAAGAGCCGTCTTGAATCTCTCTTGG
 AATCCGTCATCAGGAGCTCTGTTACTTACACTGAACACGCCAAGAGAAAGACTGTTACTTCTTTGGATG
 TTGTTTATAGCTTTGAAGAGACAAGGTAGAACCTTATATGGTTTCGTTGGTTAA

YNL030W, 103 aa (SEQ ID NO 324)

MSGRKGKGLGKGGAKRHRKILRDNIQGITKPAIRRLARRGGVKKISGLIYEEVRAVLKSFLESVIRD
 SVTYTEHAKRRTVTSLDVVYALKRQGRITLYGFGG

YOL109W, 842 bp, CDS: 501-842 (SEQ ID NO 343)

GGAGGCTCTGCTTCAAGAGCGCGGTGTGCGCTAGTATTGCCCCGACGGTCCGCGTGCCTATCCCTAGAT
 TCCCTCGTSCCCCGACCCAAATAGTTAAACGTGTGGTTTTATGGGTCCACCAGGGCTTTATCCTGTTTTA
 TATCGATGGCGATTTGTGCTCCAGTGTATTTTTGTATATCCAATTAAAGTTTCTTACCTAATTTTAAAT
 TTTATCACTTTAGTTAATGCTGGTTTGTCTGATTTCTGCTGCTTTCTGTGCGGTTCTCCCTCTTCTCTT
 GTTTCTTCTGTGTGTCTCCCATCGCCGATGGGCTTATATGGGCTATATATATAGAGCGAGTTTTTACGT
 CBAAGATCATCTCAGTTTGCCTGATAGGCTTTCTACTTATTACTTTCTGTTTTTAACCTCATTATACTT
 TAGTTTTCTTTGATCGGTTTTTTTTCTCTGTATACTTAAAGTTCAANTCAAAGAACATACAAACTAC
 GTTTATATCAANTAAATATGTCTGAATTCAAAACAAAGCTGAAACTGCCGCCAAGATGTCCAAACAA

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AGTTGGAAGAAACCAAAGATCTTTGCAAAACAAGGGCCCAAGAAGCTAAAGGAACAAGCTCAAGCTTCTA
 TCCACAACCTAAAAAATGAAGCTACTCCAGAAGCTGAACAGGTGAPAGAAGGAAGAACAACATTCCTG
 ATGGTGTGCAACAAAAGAACCCGAAGCTGCCAACAAAGTTGAAGAACTAAGAAGCAAGCTTCCGCCG
 CCGTCAGTGAGAAGAACGAACCAAGAAGGAAGGCGGTTTCTTGAAGAAATTGAACCGTAAAATTGCTT
 CCATTTTCAACTAA

YOL109W, 113 aa (SEQ ID NO 344)

MSFIQNKAEAAQDVQKKLEETKESLQNKQDEVKEQAEASIDNLKNEATPEAEQVKKEEQNIADGVEQK
 KTEAANKVEETKKQASAAVSEKKETKKEGFLKGLNRKIASIFN

YOR285W, 920 bp, CDS: 501-920 (SEQ ID NO 365)

ACTAGCAAGATGATCGTCAGATATGGTGATTATTTTCCCTGTGCATGTACTTCAAAGATCATACAGCA
 TACTAAGCGCTTCCACGGGACACCTTCTGTGCGAAAATATCAGAAATTTTCTTGATTAAACGCAGCATA
 TTGAGTATATGAAATTAACGGGACACTGTGTGAAAAATTTGTAGTTGTACTTTTTTGTATCCCCCTTG
 GTAGACATATGGACGAATTACTACTAAGATTGGCTTCCATAAGGCCCAAATCCAGATATCACCTACCGT
 ATGTCCCTTTTCTTACTTGCATGACAAAATAATTTGTTATTTATCTTGGAACTATATAAGATTACATCTG
 ATTCCTTTTCTATCTTTTTCGAGAATATATTACCCCGCGGGAAGCAAGTAAGGGGAGAATTTTGTAG
 GTGTATAAAGAGAGTGGAGGCTTAATCAATCAAAGAATCTTTCTCGTTTATTTTCAGGGTTTGTGAC
 TAAGAAACGATATTAATATGTGGAAGGCCGTGATGAATGCTTGGAAATGGAACCGAGAGTCAAAGTAAGA
 ATGTTTCAAATATCAATCTTACAGTTTTGAAACATGAAAAGAATCGTTGGAAAGCATGATCCTAATG
 TGGTTTTGGTAGATGTTAGAGAACCATCTGAGTACTCGATTGTTTATATTCCTGCTTCCATCAATGTGC
 CATATAGATCGCACCTGACGCATTTGCCTTAGATCCTTTAGAATTTGAGAAAACAGATTGGCATCCCAA
 AACCTGACAGTGCCAAAGGAGCTAATATTTTATTGTGCTTCTGGCAAACGCGCCGCCAGAGCTCAAAAAG
 TCCCTCCTCAGATGGATATTCAAACACCTCACTATATCCTGGCTCTATGAATGATTGGGTTTCTCATG
 CGGCTGATAAACCTGACCTATAG

YOR285W, 139 aa (SEQ ID NO 366)

MWKAVMNAWNGTESQSKNVSNIQSYSPEDMKRIVGXIDPNVVLVDVREPSEYSIVVILPASINVFPYRSH
 PDAFALDPLEFEKQIGIPKFDSEKELIFYCASGKRGGEAQKVASSHIGYSNTSLYPCSMMLDWVSHGGDKLD
 L

YOR327C, 848 bp, CDS: 501-848 (SEQ ID NO 369)

GTGTATTATTAAATACGAACAAAATAAAAAATATGCCGACCAATTCTGTAGTAGTACTGTAATATATTGAA
 TATTAAAGCGTTTTTCTGCTCTTAGCGTATTCCTTTATACAGTCCGTGGAACAAAGCCACGGGCGGCTGTA
 ACAATGACCATGGAATCATTCACTCGCCCTAAAAGCGCATTCACGGAAGCTTTTATAGTGATCTTGGTC
 ACATGATATACGCGTGACTTTTTTTTACTTTTTCTCCCTGTCTTCCGCAAAAGTGGCTCAAAATCTTT
 CGGATTTTGGCATTATAGCGCGAATGGTGACGCCAACCAACCAACACCACTTCTCCACCCAAAAGA
 TGCAAAAGCGGGGAGCCAGTTAGTTTTCTTCAAGTTTGGTTGAAACAGCCTTTAATATTTTATAGAA
 AGGTAAACTATCTGCTCAGTGAATAGTATCTCTAAGTCAGGCATACATTGGAACACTTCCAAATACAA
 AATAAGAACGCGCAACGATGTGCTCATCAGTSCCATACGATCCATATGTGCTTCCACAGGAGAGTAACT
 CAGCGCCAAACCCAAATTCCTCAAAACAAGACTGCTGCTTTGAGACAAGAGATTGATGACACGGTGGGAA
 TAATGAGAGATAATATCAACAAGGTGTGCTGAACGTGGTGAAGGGCTAACATCCATTGAGGACAAAAGCTG
 ATAACCTTGGCTATCTCCGCACAAGGATTCAGAGAGGGCCCAACAGGGTCAGAAACCAATGTGCTGGA
 AAGATCTAAAAATGAGAACTGTTTATTCTTTAGTTTGTATTATTATTACTAGTGGTAATTATCGTTCCAT
 TCGTCTCCATTTTCACTAA

YOR327C, 115 aa (SEQ ID NO 370)

MSSSVPYDPYPVPPEESNSCANPNSQNKTAALRQEIDDTVGIMRDMINKVAERGERLTSIEDKADMLAIS
 AOGFKRGANRVRKQXWWKDLKMRMCLFLVVIILLVVIIVPIVVMFS

YPL037C, 974 bp, CDS: 501-974 (SEQ ID NO 377)

TCACGGCTGCTCTTCTCTCTTTTCGCATATCTATTTATCATCGACTTCCCTAAATTCGUACTCGTACC
 AAAAATGTTAAGCAGTAAGGCGAAGAACGTGGCGCGCTGGAGTCTGTGAATGTTTGGGTCCCTTGATGATCG
 ACTACGGTAGTAAGTATGTACTAGTTCCAACTTCATATGTTTACCTGATCCAAGGAAGAGCGGTTAT
 GAATTAATCTCTTGGCATGAGCGGACGGGTAAAGGGACACCGCCCTTCTTTCGATGGGAATCACCGCTAA

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TGGTATATGATGGATTATTTGTGGAATCATTTAGTAACGGCAGATGTTGAAAAAAAAGCAGAAAAATTTT
 GAATTTTTTTTCGTTGACATTGGAAGATTTCGTAGTGGAAACAGCTGCAATTGCTTGTAAAGTAGTAACC
 CCTCCTTTGTGCACAAGAGAGCGAATATTCTTTCTAGGGAGGTTTAAGAATAGAACATCTCACACCAGAC
 GCCACTCATAMTTCATATGCCCAATTGACCAAGAAAAATTAGCTTAGCTACAAAAGTTGTCTGCTAACA
 ACAAGTTGCTGCTACTAGAAGAAAGCTTAACNAGAAGGACAGGCTCTTTCTGCCGGTGGCAACAAGGATG
 ACACCAAGTTGCAAAAGTCAATTAGCTAAGTTGCACGCTGTACCATTTGACAAUCTGCCGAGCCAACT
 TTTTCAAGGACGACGGTAAGGTCTATGCACCTTCAACAAGGTCGGTGTCCAAGTTGCTGCTCAACAACA
 CTCTGTATTCTACGGTCTACCAACAGGAAACAACTTGCAGATTCTGTTCCCAGGTATTATCTCTCAAT
 TGGGCCCTGAAGCCATCCAAGCCTTGTCTCAATTGCTCTCCCAAATCCAAAAGCACCAGCCCAAGGCTC
 CAGCTGATGCTGAAAAAGAGGATGAAGCTATTCCAGAGTTAGTTGAAGGTCAAACCTTTTGATGCTGACG
 TCGAATAA

YFL037C, 157 aa (SEQ ID NO 378)

MFIDQEKIAKLQKLSANMKVGGTRRKLNNKACSSACANKDDTKLQSQLAKLHAVTIDNVAEANPFKEG
 KVMHFNKVGQVAAQHNTSVTYGLPQEKNLQDIFPGTIISQLGPEATQATSQLAAQMEKHRAKAPADAEL
 KEFAIPELVEGQTFDADVE

YFL079W, 1404 bp, exon1: 501-511, intron1: 512-932, exon2: 933-1404
 (SEQ ID NO 381)

AAATAGGACGAAGAAGCTTTTTATATACGAGCAATTCCTAATTAGTAGGAAGCGGAAATAATAATAIAA
 GAAAGTAAACGCAAAAGATAGGCTGACTGCCTTCATTCCACTAGGAGGTGAGGCGACATATTTGTCACC
 ATTCAAGTTACCGAGATGGTAGAGAGGTGGATGGCTCGGGTGAGCTTGATTGTACACTGCCAGCAACGAT
 GCTTTTTCTACCCATTTTATGAAGTTTAAACATCCGTACCTTTCCACCTCCAAACATTTTTTGTAACTTC
 CTCTTTTGAAAAATCAACAGTAATAACCTGTGCACTATACCCCGCTTGAGCCCGCAATATCCGTGAGT
 GAGGTAAGATCCATCCATACCTTAGCAAAATATGGTAGTGAGGAGGCCAACTGTATTGCGTTAAAGGCAA
 AAGGATTGGTATATACGAATGATTGGTAATTTGAAAAGTAGGTTTCGAATCAAAGAAAAGTGGACAGTC
 AAGGACACTAAACAAAAATGGGTAAATCGTATGTCCATATAACTTCAAAATGAAAATATAGCAGTTCAA
 ACATATCAATTAAATCATTATACATCTCCAATAAACATGTATGCRAGAGGAAAGCGTAAATATCTTCGA
 TTTGCACAATACCTTTGCTACTGAACTAAAAATGAAAATGAAGTTGAATTCTCAAAGGAATGTCTATGCAA
 GTTCGTTAAATTAATATGGTTTTTASTGGAAATTATACAGTTTGTGATAGATACACACGAGGAGTACGTA
 GCAAAGCAAGTGCACACAGCAATGATATGTTAGCAGGAAATAATATTATAAATTTGATATTGTGTGTTTT
 TTTGATATATGTTTGTGCGAAGCTAATACAGAATGACTACTAACTGGAATTTAAAGCACAATCATGCTC
 TTAGATGATTGATCTATTAAAAAAATATAAAACAGACATGGTTACAGATCTCGTACACGTTACATGTTC
 CAACGTGACTTCAGAAAGCATGGTGGCTTTCACATGTCCACCTACTTGAAGATCTACAAGGTTGGTGAC
 ATTGTCCGACATCAAAGCCAAATGGTTCTATCCAAAAGGGTATGCCACACAAGTTCTACCAAGGTAAGACC
 GGTGTGCTCTACAACGTTACCAAGTCTTCTTTTGGGTGTTATCATCAACAAGATGGTGGGTAACAGATAC
 TTGGAAAAGAGATTGAACCTTACAGATTGAACACATCAAGCACTCTAAATGTAGACAAGAATTTTTGGAA
 AGAGTTAAGGCCAATGCTGCTAAGCCTGCTGAAGCCAAAGCCCCAAGCTGTTGCTGTCCAAATTCAGAGA
 CAACCAAGCTCAACCAAGAGAATCCCGTATTGTCTCTACTGAAGGTAAGGTTCCCTCAAACCTTTAGCTCCA
 GTTCCATACGAAACCTTTCATTTAA

YFL079W, 161 aa (SEQ ID NO 382)

MGKSHGYRSRTRYMFQRDFRKHGAVHMSTYLLKIYKVGDIVDIKANGSIQKGMPhKPYQCKTGVVYNVTK
 SSVGVIIINKIVGNRYLEKRLNLRVZHIKHSKCRQEFFLERVKANAAKRAEAKFAQCVAVQLKRQPAQPRR
 SRLVSTRGNVFCTPLAFVPYETFI

YBL109W 836bp CDS: 501-836 (SEQ ID NO 383)

CATCGCTTGATTCCGGCCCTGCAAAAAATAAAGTAGTGGGTACGTAATTTCCGTTTTCATTTTCATTTGGTG
 CACACTATCTTAACTATCTGCTTAGTCCAGGAGAACCAAGATCTGTTCTGCTCAGCCGCTTCGTGG
 ATATTCTCTTGGATACTTTAAACATGGACCTACGTTCCGCTCTCGAAAAGACCAATATAACAAAAATTT
 ATAAATTACATTTCCCTTATTAGGTATACGACCTCGGCTTCGAAGTAGAGGAGCCCTTTCTGGCGTACC
 TACATATGGCGCTCACACAGACAACTTCCCCCAAAAATGTATTACCCCGCGAATAAGAAAAACAGAC
 CCAATTCACCCACGACGTATCAAGTTACTTCCCTTGGTGCAATGTCCCACGTATAAAAAAAATCCCTTGACGC
 TAGATCGTTGGACTAAAAATCTGGCTCACAAATCGCCTAAACAGGAAATATTGCCATTTTCGTTACAAAGCT
 TACTTCTTACATGCTATATGTCCCTACGGCCTTGTCTAAACACCATCCAGCATGCAATACAGTGACATAT
 ATATATACCCCTAACACTACCCCTAACCCCTAACCTATTTCAACCCCTTCCAAACCTGCTCTCAACCTTACCCCT
 CACATTAACCTTACCTCTCCACTTGTTAACCTTGTCCCATTTCAACCATACCACTCCCAACCAACCATTCUATC

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CCCTCTACTTACTACCACCAATCAACCGTCCACCATTAACCGTTACCCCTCCAATTAGCCATATTCAACTTC
ACTACCACTTACCCTGCCATTACTCTACCATCCACCATCTGCTACTCACCATACTGTTGCTCTACCCCTC
CATATTCA

YBL109W 111aa (SEQ ID NO 36)

MSLRPCLTPSSMQYSDIYLYPNTTLTLPVFNPSNLSNLPSHYPTSPLVPTLSHSTPLPPTTHPSTYYH
QSTVHHNRYFPISHIQLHYHLPCHYSTIHHLLLTILLFYFPY

YHR094C 2213bp CDS: 501..2213 (SEQ ID NO 205)

GCATTTGAOTCAAAAGTTTTTCCGAAGTGACCCAGTGCTCTTTTTTTTTTCCCGTGAAGGACTGACAAAT
ATGCGCACAAAGATCCAATACGTAATGGAATTCGGAAAACTAGGAAGAAATGCTGCGAGGGCATTCGCCG
TGCCGATCTTTTGTCTTTTACATATATGAGAAAAAGAAATATTCATCAAGTGCTGATAGAGAAATACUAC
TCATATGACGTGGGCAGAAAGACAGCAAAACGTAAACATGAGCTGCTGCGACATTTGATGGCTTTTATCCG
ACAAGCCAGGAAACTCCACCATTATCTAATGTAGCAAAATATTTCTTAACACCCGAGGTTGCGGTCTCCC
CCTCACGTTTTTAAATCATTTGAATTAGTATATTGAAATTATATATAAAGGUAAACAATGTCGCCATAATC
AATTCUATCTGGGGTCTCAAGTTCTTTCCCCACCTTTAAANTCTATAAAGATATCAATATCGTCAALTAG
TTGATATACGTAAATCATGAATCCAACCTCCCGATCTAATATCTCCTCAGAAATCCAATTCATCCAACCT
CATATGAATTTGAATCTGGTCTGTTCAAAGGCCATCAATACTCCAGAAAGGTAAAGGTTTTCAGC
ACAACCTTAAGTGAAAGTCAAGTGCAACCCGCCGTTGCCCTCCAAACACCGGAAAGGTGTCTACGTAA
CGGTTTTCTATCTGTTGTGTTATGGTTGCTTTCGGTGGTTTCATATTTGGATGGGATACTGGTACCATT
CTGGTTTTTGTGTTGCTCAAACTGATTTTTCTAAGAAGATTGGTAAGAAGCAACACGAGGTAAGTCACTACT
TGTCCAAAGGTGAGAACTGGTTTAATTGTCTCTATTTTTTAACATTGGTTGTGCCATTGGTGGTATCGTCT
TACCCAAAGCTAGGTGATATGATGGTGGTAGAATCGGTTTGATTGTGCTTGTAGTAATCTACACTATCG
GTATCATTAATCAAAATAGCCCGATCAACAAGTGGTACCAATATTTTCAATGGTAGAATTATCTCTGGTT
TAGGTGTCCGGTGGTATCACAGTTTTATCTCCCATGCTAATATCTGAGGTCCGCCCCAGTGAAATGAGAG
GCACCTTGGTTTCATGTTACCAACTCATGATTACTTTAGCTATTTTTCTTACGTTACTCTACCAATTTTTG
GTACCAAGAATTACTCAAACTCTGTCCAAATGGAGAGTTCCATTAGGTTTGTGTTTTCCGCTGGGCCCTTAT
TTATGATTGGTGGTATGATGTTTCTTCCCTGAATCTCCACGTTATTTCGGTTGAAGCTGGCAGAAATCGACG
AAGCCAGGGCTTCTTTAGCTAAAGTTAACAATGCCCACCTGACCATCCATACATTCAATATGAGTTGG
AAACTATGGAAGCCAGTGTGGAAGAAATGAGAGGCGCTGGTACATGCAATTTGGGCGAAATTTATTCACCTG
GTAAACCAGCCATGTTTCAACGTACTATGATGGGTATCATGATTCATCTCTACAACAATTAACGGTGG
ATAACTATTTCTTCTACTACGCTACCATTCTTTTTCCAGGCTGTGCGTTTAAGTCACTCTTTTGAAGCTT
CTATTGTCTTTGGTGTGCTCAACTCTTCTCCACTTGTGTTGTTCTCTGTACACCGTTGACCGTTTCTGGCC
GTCCTAAGATTGTTGATGTGGGGTGTCTGTGCGTATGGTCTCTCTGTTATCTTGTCTATGCCCTCTGTTGGT
TTACCAGATTATGGGCAAAACGGTCAAGATCAACCATCTTCAAAGGGTGTCTGTTAATGATGATTTGTTT
TCGCATGTTTCTACATTTTTCTGTTTCGCTACTACCTGGCCCCCAATTGCTTACCTTGTATTTTCAGAAT
GTTTCCCATTAAAGAGTCAAAATCCAAGTGTATCTCTATTGCCAGTGTCTCTAAGTATGATCTGGGGTTTCT
TGATTAGTTTCTTCAACCCCATTTATCACTGGTGGCATCAACTTCTACTACGGTTACGTTTTCAATGGGCT
GTATGGTTTTTGGCTTACTTTTACGTTCTTTTCTTCTGTTTCCAGAAACTAAAGGTTTATCATTAGAAGAAC
TTAATGATATGTACGCCGAAAGTGTCTTACCATGGAATCAGCTTCCCTCGGTTCCACTATCCAAGAGAG
GCGCTGACTACAACGCTGATGACCTAATGCATGATGACCAACCATTTTACAAGAGTTTGTTTAGCAGGA
AATAA

YHR094C 570aa (SEQ ID NO 206)

MNSTPDLISPKSNSNSVELESGRSKAMNTPGKKNESFHDNLSSESQVQPAVAPPNTGKGVVYTVSTCC
VMVAFGGFI FGWDITGTISGFVAQTDPLRRFGMKHHDGSHYLSKVRTGLVSLFNIGCAIGGIVLAKLGD
MYGRRIGLIVVVVIYTTGTTIQIASYNKWKYQYFIGRIISGLGVGGJTVLSPMLISEVAPSEMRGTLVSC
YQVMITLGIPLGYCTNFGTKNYSNSVQWRVPLGLCFAWALFMIGGMMFVPESPRYLVEAGRIDEARASL
AKVNKCFPDHPYIQYELETIEASVEEMRAAGTASWGLFTGKPAKFQRTIMMGIMIQSLOQLTGDNYFFY
YGTIVFQAVGLSDSFETSIIVFGVWNFFSTCCSLYTVDRFGRNCLMNGAVGMVCCYVYASVGVVWVW
NGQDQPSKSGAGNCMVFACFYLPFCATWAPIAYVVISCEFPLRVKSKCMSIASAANWTWGLTISFFT
PFI TGA1NFY YGYVFMQCMVFAYFYVFFVFPETKGLSLEEVKDMYAEGVLPWKASWVPVSKRGADYNA
DDLMDDDQPFYKSLFSRK

YBL099W 2138bp CDS: 501..2138 public: 1..2138 (SEQ ID NO 693)

CCCCGGTGATGCAGTTCCGGCCGGCCCTGGCCAATCAGATCCCTTTAAAPATGGGCCCCGGTGCGCTTTCT
ACCCCTTCAUGGCTTTTACGGCTTTTTCGAATCTTTGTATTTATTTGTAATTTATTAACATTTGGTCATATC
AATTTACATCAGACTTCATTTTTTCAATTCACCTTTCTGAATAAGAGCCCTTCCCTTTCATACAAGTAGA
GATATTATACATTCATAGCTCTTTCAATTGGCTTATTAGATTGCTCTCATCTTTTCCCATTTGACGTGTG
TACTCTCTCTCTTTTTCGTTTAACTGATTTCTCATATATTCCAAACAGGCATATATACTCGACG
CAAGAAAGAAAAGAAAAGAAAACCCCTCATAAAAACATAATCGACAACTTTTTTCTCATCCCAACC

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A:TAGTATAACAGATTGATCGTTCAAGCTCTCATAACTATCGCAAGAACAGTAACAAAATAAATAAAJAA
 AACACGCACATATAATAATCTTTGGCTCTGACTGCTGCTATTCCCTTCTCTATCGAGAAGCTCTAATTAACT
 CTACCAAGGCCGCAAGACCTGCCGCTGCTGCTTTGGCTTCCACCAAGAAGATTGGCTTCCACCAAGGCAC
 AACCCACAGAAATTTCCCTCATCTTTAGAGGAAAGAAATTAAGGGTGTGTCCGACGAGGCCAATTTGAACG
 AAACCTGGTAGAGTTCTTGCACTCGGTGATGGTATTGCTCGTGTTTTGGTTTGAACAACTTCAGGCTG
 AAGAATTGGTCGAGTTCTCTCTGGTGTAAAGGTATGGCTTTGAACCTTGGAGCCTGGTCAAGTCGGTA
 TCGTTCTTTTGGTTCCGATAGACTGGTTAAAGAAGGTGAATTGGTCAAGAGAACCCTGAATATTTGTTG
 ACGTCCCAGTCGGTCCAGGCTTTTGGTAGAGTTGTGACGCTTTAGGTAACTTATTTGATGGTAAAG
 GTCTTATTGACGCTGCCGCTGTTCAAGAGCTCAAGTCAAAGCACCAGGTATTTTGCCAAGAAGATCTG
 TCCATGAACCAGTCAAACCGGTTTGAAGCGGTTGACGCTTTGGTCCCTATGCTAGAGCTCAAAGAG
 AGTTGATTATTGGTGTGCTGTCAAAACAGGTAAAGACTGCTGTGCGCTTAGACACCATCTTTGAATCAAAGA
 GATGGAATAACGGTAGTGACGAATCCAAGAACTTTACTGTGTTTACGTTGCCGTTGGACAAAAAGAT
 CTACCGTTGCTCAATTGGTCCAAACTTTGGAAACATGACGCTATGAAGTACTCTATTATTGTTGCACT
 CTACTGCATCTGAAGCCGCTCCTCTACAATACTTTGGCTCCATTTACTGCCGCATCCATTGGTGAATGGT
 TCAGAGATAATGGAAAGCAGCGCTTTGATCGTCTATGACGATTTGTCCAAGCAAGCCGTGGCATAACGCT
 AATTATCTTTGTTGTTGAGACGCTCTCTGGTGGTGAAGCCCTACCTGGTGGTATCTTTTACTTGCATC
 CAAGATTGCTTAGAAGAGCCCGCTAAGCTTTCTGAAAGGAAGGCTCTGGTCTTTTAACTGCTTTGCTCTG
 TTATTGAAACCCAAAGGTGCTGATGCTCTCGCTTATATTCCAACCAATGCTTCTTCCATTACCGGATGGTC
 AATATTCTTTGGAAGCTGAATTATTCTACAAGGGTATCAGACCTGCCATTAACGTTGGTTTGTCCGTTT
 CTCGTGTGGTTCCGCTGCTCAAGTTAAGGCTTTGAAGCAAGTCGCTGGTTCCCTGAAATTGTTTGTGG
 CTCAATACAGAGAAGTCGCTGCTTTTCTCAATTGCGTTCCGAATTAGATGCTCTCCACCAAGCAAACTT
 TGGTTAGAGGTGAAAGATTGACTCAATTGTTGAAGCAAAACCAATATTCTCTCTTTGGCTACAGAAGAAC
 AGGTTCCATTGAATTTATGCCGGTGTAAATGGTCAATTTGGATGGTATTGAACATATCAAGAATTGGTGAAT
 TTCAGTCTCTCTTTTGTCTTATCTAAATCCAATCACAATGACCTTTTGAACCGAAATTAGAGAAAAGG
 GTGAATTGTCTAAAGAATTGTTGGCATCTCTAAAGAGTGTCTACTGAATCATTTGTTGCCACTTTTAA

YBL099W 545aa public: 1..545 (SEQ ID NO 594)

MLARTAAIRSI,SRTLINSTRKAARPAALASTRR,ASTKAQPTTEVESILEERIKGVSEANLNETGRVL
 AVGDGIARVFGLNNIQABELVEFSSGVKGMALNLEFGQVGVILVFGSDRLVKEGELVKRTGNIVDVVPVGF
 GLLGRVVDALGNPIDGKGF,UAAGRSRAQVKAPG,LPKRSVHEPVQGT,KAVDALVP,IGRGQRELIIGD
 RQTGKTAVALDITILNQKRWNNGSDESKKLYCVYVAVGQKRSTVAQLVQ,LEQHDAMKYS,VAAT,ASEA
 API,QYT,APFTAASIGEWFRDNGKHALIVYDOLSKQAVAYRQLSLLLRPPGREAYPGDVFYLLPRLLER
 AKLSEKEGSGSLTALPVIETQGGDVSAIPTNVISITDGGQIFLEAELFYKGRPAINVCLSVSRVGS
 AQVKALKQVAGSLKLFLAQYREVAFAQFGSDLDASTKQTLVRGERLTQLLKQNYSP,PLATEEQVPLIV
 AGVNGHLDGIELSRIGEFESSFLSYLKSNNHLLTEIREKGELSKELLASLKSATESFVATF

YDR504C 884bp CDS: 501..884 public: 1..884 (SEQ ID NO 695)

TAAAAGCCTTGCATATTGCTCAGAGTAAATTACAAGCGTTAAATGATAATTCAAATCTCAAANTACAA
 ATGACAGCTCTTCCCAATACTTTACGAATGCTGCAACTTATTCAAAGCCTAAATTTGAATATCAAGATT
 TAAACGCAGAAATTTCCAAATTTAATAGAAAGGAATTAACGTTTAACTAUGTTTGTGAGGAGAGAAATGATT
 TTAGAGACTTGATPAAAGAGCTGTTCAAATATTACAAGACAAGAATTTGGTTGTGTGCCATCCCGAATA
 ATCTGTCTATTCAATCTAAGTATTATGATAAACAAACAAAAGAGCTGAAATTATATCAAAACATAGTAA
 AAAATTACAATGCTGAAGATTTAATGAAGTCAATGAGTTTTCGCAGAACAGGGGAATPACAGAGTTA
 ATTTTGCACCTCCGTTGAACGAAATTGAACTCGACAACCTTCAGATTGCTGTGTATGAAGAATTAGTTT
 ACGAATTATTTTCAATTAATGATCTCTTATTTCTTGTGTGTAACATAAATTTCTTAAAGAAAAGACAA
 CCATTTGCCATTATTTTGTAAACATTTTTCATTGTTTTTCTTTTGTGTTTGTGTTTGTGTTTGTGTTT
 TTTTGTCTACTTTTATGTTATTTTGTGTTTATCGTTTCTGTTCCGTTGTTTACCTATTTTCTGCTCA
 ATTCAATTTGGTACTATCTTTCTATTATCAATATTTTCTTTCCCTTATGTTTTTCTCTATATGAAAACT
 TCACAGGGAGAAATACAGAGAAATGTTCAATATTCTGTTTACTTTGATAAAATTAATTTATACGCTCTC
 CCAATCATGGTTTTCATGGTCACTGGTAAGGAAAAATTCGAAAACTACGGGACTAA

YDR504C 127aa public: 1..127 (SEQ ID NO 696)

MICYFLVVTINFLKEKTTICHYFVNIFSLFLFLFVFEVVFIFVYFFVVLFYRFCSLFTYFPANSIWWY
 I,SIINIFFPLCFPI,YENFTGRNRRKCSLP,CM,IK,ITVTSRNSGFMVTKKKKPKLRD

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YEL032W 3416bp CDS: 501..3416 public: 1..3416 (SEQ ID NO 697)
 TATCTACCGGCTGCAAGCAGGCGGTGGGUAATCGGGCGCTTUUUUUTCAAAAAAAAAAAAAAA
 AAAAAAAAAAGGAACCTCTCAGAACGGGGAGGTTGAAGAGCAAGCCAAAGGGAAATATTAGTCTTGACCTA
 TGTGGGAAACAGAAATTTTCAATGAGTTATGGCAACTTGGCCGAGTGGTTAAGCGGAAAGATTAGAAATC
 TTTTCGGGCTTTGCCCGCCGAGGTTCCGAGTCTTCCACTTGTCTGTTATTCTCTCTTTTTCATTTTCC
 CTGTTTCGTACATCCGACCCCGCTAGAAGAAACAATTACTTTTCTTAAATGGGTAAAACTCGTGTTTTA
 GGAAAAAAAAAGAAAAATTTGGTCAAACTCCAAAGATAGGTTCTTAATCTTCTTTCAAGTTCGAAAGGC
 CTACGCTCTTTTCCCTGGAAGCATTTCATCCCTACTGCTCGTATTGAACTCCACTATAAGCGCACCCAAA
 AGATACAAACCTCAATTAATGGAACGCTCAACCGGATTTGATGGAGACGCTACTACTTTTTTCGCTCCAG
 ACCGCTGTGTTTGGTGACAGAGTGGCGAGATTTCAGAGATTTTTAGATACTTCCACCTCATACAGAGACT
 CTGTAAAGCTCCATACAGCTTTACAAACAGCAATTAACCGCGCCCAACTACAACGATGATCAAGATCAGCGAG
 ACCAACGAGATTTCGTAGGTGATGACGACCGGTTATGATCTTTGAAAAGGAAAAGAAAGCAGCATCGTCCA
 CCTCATTTGAATATACTCCCTCACAGGATTATCATCTCGCTTGATGACTTGAGAGAAATTCGACAGGTCTG
 TCTGGTCCGGCATTTTATGTCGAACCAAGCATACTTCATCCCGCTTGGCGAAAAGGGCGTTACTGACCTAG
 CAGATTCCATGGACGATGTTCCACATCCCAATGCGCTCTGCAGTATCGTCTCGCCATCCTTGAAGCTTT
 CCTTCAAGGCTCATTTGGTGACACGCAATTTCTCTCTGTACTCTAACGGCACAACATTTAAACAAAC
 TGGTCTCTGTTGAGCGTATCTGTAACCTAAGACTTCGTTGGTCAGGCCAAAGCTTATCAGATCTGTCCACT
 ACCGGGCAAGACTCGGTAGATTCCATTACAGAGATTATACAGATGCTACTACAACCTCACCAACCCGCA
 TCCCAACCGCTGCCATCTATCCAAACGGAGCACACTCAAGCTTAACAAACTAACCCAGCAATTTGGGTATA
 GTACGTTCAATAGACCATCAGCGTATCACTCTGCAAGAAATGCCCAAAATGGCCCCCGCTGGCCAACTTC
 CCAGCTTCATTGACGTCATTCTCGATGACGACCTTGTGGACAAGACCAAGCCAGGTGACAGAGTTAAGG
 TTGTCGGGGTATTCAAGTCGCTTGGTGTCTGCTGCCATCAACCACTCCAACCTCTAATACATTGATCGGGT
 TCAAAACTCTGATCCTAGGTAATACGGTGTATCTCTCCACGCCAGATCCACGGGTGTGCTGCGAGAC
 AAATGTTGACAGATTTGATATAAGAAATATCAATAAACTATCCAAAAAAAGGACATTTTCGATATCT
 TGTCTCAATCTTTAGCGCCCTTCTATTTATGGACATGACCATATAAAGAAAGCCNTTTTATTGATCTCTCA
 TGGGAGCTGTGGAGAAAAATTTAGAAAAATGCTTCCGATTTAAGAGGTGACATCAATATCCTAATGGTGG
 GTGATCCATCCACTGCCAAGTCCCAATTTGCTAAGGTTTGTGTGTAATACAGCACTCAUTGGCAATTGCTA
 CTACTGGTAGAGGTTCTTCCGGTGTGCGTTTACCCGCAAGCGGTCACTACTGATAGGGAAACAGGTGAAA
 GAAGACTAGAGGCTGGTCCCATGGTTCTTGGTGAACCGCGGGGTTGTATCTATTGATCAATTTGATAAGA
 TGACAGATGTGGATAGAGTCCCATTCATGACTAATGGAACAACAACCGGTGACGATTGCCAAAGCAC
 GTATTACACAACATTTAAATGCTCGTTGTAGTGTATTGCTGCCGCAAAATCCCGTTTTTGGGCGAGTACG
 ATGTCAATAGAGATCCACACCAAAACATTGCGCTACCGGACTCGCTGTTGCTCTCGTTTTTCATTTACTAT
 TTGTTGTGACAGACCATATCAATGAAATCAGAGATAGATCCATTAGTGAGCATGTCTTAAGAACAACA
 CATATTTGCCCTCCAGCTTATTTAGAGGGTGAACTCTGAGAGAGCGTTTGAATTTATCATTTAGCCGTTT
 GGGAGGATGACAGATATAAATCCCTGAAGAGCATTTCCAACTTCCGCGGCTGGTGTAGAAAATGAAGGAGAAG
 ATGATGAAGACCATGTCTTCCGAAAAGTTCAACCCCTTATTACAAGCAGGTGCTAAGTTAGCAAAAAACA
 AAGGTAACCTATAACGGTACACAAATTCGAAAGCTACTACCATCCCATTTCTTAAGAAAGTACGTTCAAT
 ATGCCAAGGAAAGGGTTATTCCACAGTTAACACAGAAGCCATCAATGTTATTGTCGAAAAATTACTG
 ATTTAAGAAACGATGATAATACCAAAAAATCGCCUATTACTGCCAAGAACTTTGGAGACTTTGATCAGAT
 TAGCCACAGCTCACGCCAAAGTCAGGTTATCCAAACAGTCAACAACGTCGATCCTAAGGTCGCTGCCA
 AATCTACCTAACCTTTTGCCTATTGGGTGAGGATATCGGCAATGATATCGATGAAGAGGAAAGTGAATACG
 AAGAGGCTTTGTCCGAGAGGTTCTCCACAGAAATCACCGAAAAAAGACAAAGAGTCAGACAACCCAGCAA
 GCAACTCTGGATCCCCAATCAAAATCTACTCCAAGAGGTTCAACGGCATCTTCCGTTAATGCCACGCCAT
 CGTCAGCACCCAGAAATATTACGTTTTCAGATGACGAACAGAACGCTGGTGAAGACCATTAACCATATAA
 TGTACCCGCTTCTGCGGATGAGGAAGCTGAATTACAAAGAAGGCTTCAACTGGGGTTGAGAGTGTCTC
 CAAGACGTAGAGAAATCTCTCAAGCACTTGAGGAAGGTTCTGTTGCGGACCTCTTACCGAGCTCCGTACTC
 CAGATTACTTAACGTATCTTCTGCGAGGTCAGATGATGAGCAACAACAGTCAGTTATTCTTTTGTACA
 ATGTCGAGCCCTCTACCTTTCTACTGGTAGATTGTCTTTAATCTCAGGTATTATTGCGCGCTGATGAC
 AAACAGAAATATTTGAAGAAGAATCCCTATCTGTGGCTCTTTGTTGGAAGAATCAACCAACAACTAC
 CGGAGGAGGAAAAATCTCTCGCTCAACAAATATTTAGCAGCTTTGAACATCATGTCGACAGAAAAAAT
 TAATGGTTGCTGACGATAAAGTTTGGAGAGTCTGA

YEL032W 971aa public: 1..971 (SEQ ID NO 698)

MEGSGCFDGDATTFAPDAVFCDRVRRFQEFIDTTTSYRDSVRSIQVYNSNNAANYNDQDDADEROLL
 GDDDGDDLEKEKKAASSTSLNIIPIRIIISLEDLRFPDRSFWSGILVBPAYFIPFAEKALTDLADSMDD
 VPHPNASAVSSRHPWKLSFKCSFGAILALSFRLLTAQHNLNKLVSVEGIVKTSIVRPFKLIRSVHYAAKTG

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RFHYRDYTDATTTTLTRIPFPAIYPTEDTGNKLTTEYGVSTPIJLQRLTVQEMFEMAPAGOLPRSIDV
 ILDDDLVDKTKPGDRVNVVGVFKSLGAGGMNQSNSTLIGFKTLILGNTVYPLHARSTGVAARQMLTDF
 DERNINKLSKKKDIFDIISQSLADSIYGHDKKATLIMTMGGVEKNHENGSHLRGDINILMVGDPSTA
 KSQLLRFVLNTPASLAIATTGRGSSGVGLTAAVTTDRETGERRLEAGAMVLADRGVVCIDFDDKMTDVR
 VAIHEVMEQQTVVIAKAGINTENARC SVIAAANPVFGQYDVNRDPHQNIALFDSLLSRFDLLFVVTDQ
 INEIRDRSISEHVLRTHRYLFPGYLEGEPPVRELRNLSLAVGEDADINPEEHSNSGAGVENEDEDDEHV
 FEKFNPLLQAGAKLAKNKGNYNGTEIPKLVITPFLRKVQYAKERVIPQLTQEAINVIVKHYTDLRNDQ
 NTXKSPITARTLETILRLATAHAKVRLSKTVNKVDAKVWNLRLFPALLGEDIGEDIDEESEYEPATSK
 RSPQKSPKKRQVRVQPASNSCSPKSTPRRSTASSVNATPSSARRILRFQDDEQNAGEDENDIMSLPA
 DEPARTQRRLQIQLRVSPRRREHLHAFEEGSSGPLTEVGTPLRLFWSSAGQDDEQQQSVLSFQNVPEPT
 ISTGRLSLSIGIARLMQTEIFEESYPVASLPERINEELPEEEKFSAQEYLAGLKTMSDRNMLMVADD
 KVWRV

YGR146C 1136bp CDS: 501..1136 public: 1..1136 (SEQ ID NO 699)
 CTTTCAGTTGGGCATCTTTTFTTTTTCACAATFAGCCCCCCTTTTTCQCAATTTGGCACTTGTTTGTA
 CGATCTTTTAGCTAGAACTGGAGACCTGAAACGTGGTGATTCTTATATTAAAGGAATACCGATCTTTT
 CCGTTTCAACACCCCAATCTGTAGAATCTTTACTTCTTGCCATTTCCGAAAATTTAGATACATTCACATCC
 ATACTTGGACACATATATATATACATATAATCATTGACACACCCCATCCGCATTGAGTAAACTGTCTT
 TGAAGTGTCTAAAGAACTTAGAACTATAGTGTGTGTCCTCAAGAACTTAAAAATTCACACTTTGTGAGAAT
 TATAAAACAGAGTAAGCAAGAAAGAAATAGAGAAACAATACTCCGCTACCGATTCTCTCTTTTPTCCCTT
 ATAAAAAAATTCGAGAATAATTACTTTATTCTTATUUCTUCAUUCTTTTCAGGTATTCTTTTACCGATT
 TGCATATCAATCATATAATGAGCACCGCATTCACCGATTACTGCACTGTTTGTGATCGCTCTCATTCCAA
 CATCTCCACACAAAACGAACATTAAATACCAGGAAGATCCAAAGGGACAATGAAACCAAGAGCAGTTTAC
 AATCAATAAGTTACATTGCTCCGAAGATTGTAAAGCTGAAGGATTCGAACCCCTTTAAATGAGAAATTAAT
 TATUUCUACTGCGATAAAAAATCAAAAACCTTCTCATTCGCCATAATCTCACTCCACCCCTTTTCATATTCTA
 AAAATTTAACTGCATCAAACTCTTCGAGCCGACTACCTCACTATCTTCATCTCCGAUATCTTCAACTA
 TCCCTTTTGACGAGTTGGAGAAGCTAGAGTCCCTATTAAATTTCAACCATTCCTTGCATACCTCAGGATGGTA
 TAGTCAATCTTAAGCAGGAGTCTAATCTTCTCGTCTTGACCAATATGATGAAAATGAACATTAATTGA
 ACTTAGCCGACTCTCTTAGACTCGATTCTAGTAAACAAATTCGATTCAAAACCCACATTTGGGTACGAAA
 ACAACTTCCACGATCAAAACGATCTAATTGATGATUATTGATCTCAGATCAGATCATTGAGAAVAACT
 ACAACCTATGGTTTAGACCATCTCCAGTTAA

YGR146C 211aa public: 1..211 (SEQ ID NO 700)
 MSTAFNDYCTVCDRLPTSPQKTNINTRKIQRDNETKSSLSQSNKLYCSEDCXKLKDSNPLNEKLLSHLHK
 KSKTSHSHNLTPLSYSKNLTPASNLPEPTTSLSSSPSTSTPFDLEKLESJLISPLLLPQDGIIVNPKQ
 ESNPSRVDEYDENEHYLNLADSLRLDSSYQLHSAHLGYEMNLPRNDLIDHITSDQTIENNYNLWFR
 LSSS

YHR135C 2117bp CDS: 501..2117 public: 1..2117 (SEQ ID NO 701)
 AGAGTATAACGACTACATTAATGAGAAAGATTCAAGTAGAGCGCAGCGTCAAAACCGCTGCGCCCGTTT
 AAGCAAGCTCGCCCATGACTTTTGGGAGAACGACTGTGTCTATTGACGAAGACATATTGGAAGATTGCTC
 TGACGAAGAACAATCATGATTGCAATCTCTAAATCGTTTACACATAUATACCTTCTACCTCTGTACTGTTA
 CATATGCAATTGACTTTACGATCTAATATAAATCCTTTTGTATGTTACCCCGCTGTGGGCTCGTTCTCTCT
 TTTCGTTTCTTACGATTTTTTTCGCGGAACAAGAAAAACAGAACAAAAACAATCAGCGATCGTATACAT
 GGGTCTTTGACTTCTGCTTGCTTCTTACAAACAACAAACGCAAAACCGTTTCAATTGAGTGCTCTGTGACTG
 GTTTTCAATGCGGATGCCATAGTAGAGAAAGACACATACAAAAATTTCCGCGCATTCGCTGGCCCTTTTC
 CTGCTCTCTCTTCCCATGCTCCATGCCCATAGCAAGTACCCTCTAGCAGTTAACAACCTCACCCTAATA
 TAAACGGAAACGCAATTTTAAAGTACPAAGCAACAAACAACCTCCACCACCAGGCTGTGAGCTCGCCCG
 CAAGATCTTUGATGACCGCCACGACCGCGCCCAACTCCAACAGCAACTCTCCAGAGATGACTCTACTTA
 TTGTGCGGCTACATTACAAGATCGGCCAAAAAATAGGGGAAGGTTCTTTTGTGTGCTATTTGAAGGTA
 CTAAATATCATCAATGGCGTACCGCTCGCGATCAAAATTCGAGCCCGAGAAAAACGGAGGCCCTTCAATTAA
 GAGATGAATATAAAACATATAAAATTTGAAATGGCACTCCCAATATCCCCIACCCCTACTACTTCGGCC
 AAGAAGGTTGGCAATATCTTGGTCAATTGATCTTTTGGGTCCCTCTTTGGAACATTTATTTGATTGGT
 GTGCAAGAAAAATTTCTGTCAAAACGGTTGTGCAAGTTGCTGTUCAATGATTACTTTGATTGAAGACT
 TCGAUGCACAAGACTTGATATACGTTGATATCAAACAGACAATTTCTTGATTGGAAGGCCCGGCCAAC
 CTGACGCAACAACATCCATTTGATCGACTTCGCTATGCCCCAAACAGTATCGTGATCGGAAAACTAAAC

AGCATATCCCATATAGAGAGAAAAATCACTCAGCGGCACTGCCASATATATGTCCATTAACTACACC
TTGAAAGAGAGAGCAGTCCAGAAGAGTGTATATGGAGGCCCTTGGGTACGCTTTTCTTTTATTTCTTGAGAG
GCCACTTACCCCTGGCAGGGTTTAAAGCTCCAAACAATAAGCAAAAATACGAAAAGATTGGTGAAGAAG
AAGATCTACTAACGTTTACGATCTAGCTCAAGGCTTACCTGTGCAATTTEGCAGGTATCTAGAAATCG
TCAGAAGTCTTTCTTTGAAGAGTGTCCCGATTATGAAGGCTATAGAAAACTATTACTATCTGTACTGC
ATGATTTAGGTGAAACCGCGGACGGCCAATATGATTGGATGAAACTGAACGATGGCCGTGGTTGGGATC
TAAACATAAACAAGAAGCCAAATCTCCACGGATACGGCCATCCAAATCCACCAAAACGAAAATCGAGAA
AACATAGAAAACAAACAGCTCCAAATGCAACAGCTCCAAATGCAACAGCTCCAAACACAGCAACAGCAAC
AGCAATATGCTCAAAAAACTGAGGCAGATATGGCCAATTCCTCAATATAAACCAAAGTTAGACCCCTACTT
CTTATGAAGCTTACCAGCATCAAAACCCAGCAGAAATACCTGCAAGAAACAACAAAGAGACAGCAACCAAC
AAAACCTTCAGCAGCAACAACCTCAACAGCAACAATTCGCAACAGCAGCAACAGCAACAGCAACAGCTAC
GTGCAACAGGCGCAACCTTCCATCTCAGCCTCAAGCGCAAACTCAATTCAAGCAGTTTGGGCTCTGTTATC
AACCACAACAAACCTTCTGCTGCTTTAAGAATCTCTGAACAGCACCCAAATGACGATAAATTCAGTC
TAGCTGCTTTCTCATAAGGGCTTTTTTCCAAAAATTAGTTGTTGTGCTAA

MEMPIASTITLAVNNLTNNGNANFNVPQANKQLHHQAVDSPAASSMTATTAANSNSNSSRDDSTIVGLHY
KIGKIGEGSGFVLFEGTINGMNGFVPAIKFEPKTEAPQLRDEYKYKILNGT'FNIPYAYYFGQEGLEHN
ILVIDLLGPSLEDLFDWCGRKFSVKT'VVQVQYKMITLEDLHARDLIYRDMIEKPDNFLIGRPGQPDANNI
HLIDFGMAKQYRDPXTKQHIPYREKKSLSCTARYKMSINTHLGREGSRDDMEALGHVFFYFLRGHLPWQ
GLKAPNNKQKYEKIGEKKRSTNVYDLAQGLPVQFGRYLEIVRSLSFEECPDEYEGYRKILLSVLUDLGET
ADQGYDWMKLNDRGWDNLNINKKPNLHGYPHPNPNNEKSRKHKNKQLQMQLQMQLLQOQQQQQYQYAK
TEADMNSQYKPKLDPTSIEAYQHQTQQKYLQEQCKRQQQKLQEQQLQEQQLQOQQQQQQQFATGQP
PSOPQACTOSQOQFARYQPOOQPSAALRTEPHNTNEDMSGLAASHKGETOKLGCC

TAGAGCAGATTGTTTTGAGTAGGATTTAGGAATCAAGACCTCCATCTTTGTGCGCATTATTCCCTAAATGT
AACGTAACCTCGTTTTGATAAGAGAATGTCTAATCGAAGAGAGTTAATAACTTAATAAGCTCTTTTAAAGA
ACGATGGCATTATATCGTCTCCTATGCCAAGATAATTACTCGCTCAAAATTCTTCAGCGTTTCATAAACT
TTGATATACCTTTCTGGCGCACAAAGCTAACCTTTATGTAGTTCTTACGTACATTCTTTTTAGCAAGTGC
CTGGTAGTGGTTATTACATAAAATGTATCTTTTCAATTTTGATAACAATTTCTTCAGTAGCATGTCTGTCT
AGCACGTGACGTAGAACCTGTGGCTTTTTTTGTGTCTATTATGACAATCAAGATACCAAATTCAGTCATG
TTTAAAGGGGAAGGTACCATAGAGATATATATAAAGTGTCAATTTACTATAATTGCGTATAGAAATCC
ATTGTTACTTGTCTCAATGAACAACGATTTCATTCGTCAATTTACGAACCTAATGTCTACTTCCAGAC
CGAAGTTGTTGGCAACAAATATTTCACTTCTAACACTGCCAAAGATGTTTTGGTGGCTAACCAATGAAG
CCGCTGCCAAAAGCTGCCAATAACTCCAAAACCCAGGCCCGAAGCTTATTTAATTTAGGCUAAGGCTTTT
TTTCATATTCCCTCTCAATTCGCCATTAAAGGAGGCTCAGAAAAGCCCTAGACATTCCAATGGTCAATC
AATATTCTCCAACTAGAGGTGCAGCTTCATTAAATTAATTCCTTGATTAAGCTCTATCTCTCTATTTATA
ACACAGAATTTGAAAGCGGAAAATGTTACCGTACAACACAGGTGCCAATGAAGGTACTACTTTCTTGTCTGA
TGGGCTTTTGAACGCTGGCGAAGAGTTATTTGTTTTTGAACCTTTCTTTGACCAATATATTCCAAATA
TGAACCTTTGCGGTGGTAAAGTTGTTTAUGTCCCCATAAATCTCTCCAAAGGAATTGCATCAAAGGAATA
CTAGACCTGAAGAAATGGACCAATTGACTTTGAGCAGTTCCGAAAAGCGATTACATCCAAAGACAAAGCTG
TCATTATCAATACCCCTCACAAACCAATTGGTAAAGTTTTACGCGCGAGCAATTAACCACTTTTAGGTA
ACATTTGGTCAAGCACAAAGTTGTGATTATATCTGATGAAGTCTATGAACACCTTTACTTCACTGATT
CTTTCACTAGAATTGCCACACTCTCTCCAGAAATGGGGCACTAACUTTAACGGTGGGTTCTGCGCGTA
AATCGTTTTGCTGCTACTGGTTGGAGAATTGGTTGGGTCTTATCCCTTGAACGCAGAGTTGTTAAGTTATG
CAGCTAAGGCACATACAAGAATTTGTTTTGCATCTCCATCCCTCTACAGGAAGCTTTGTGCAAACTCTA
TTAAGCAGCGCTTTAAAAATTTGGGTATTTTGAAAAAATGAGACAGCAATATATCAACAAATTCMAAATTT
TCACATCGATCTTTTCATCAATTTCCACTACCATATACACCTCCAGAGGGTACATATTTTGTCTCTGTG
ATTTCTCTAAAGTGAAAATTTCCGAGGAGATATCCCTACCCAGAGGAGATCTTGAATAAAGGAAAAGATT
TTCGCAATTTCTCACTGGTTGATCAATGAATTAGGTGTGGTTGCCATTCACCAACTCAATCTATATCA
AAGACACCGAAAAGCTGCTGAGAATTTGTTAAGTTTGCAGTTTGTAAGATGATGCTTATCTAGAAA
ATGCCGTAGAGAGATTAATACTACTCAAGGACTACTTATAA

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YJL060W 444aa public: 1..444 (SEQ ID NO 704)

MKQRFIRQFTKLMSTSRPKVVANKYFTSNTAKDVWSLTNEAAAKAANKSKNQGRRLTNLGGQGFPSYSPP
 QFAIKEAQKALDIPMVNQYSPTRGRPSLINSLIKLYSPIYNTELKAENVTVTTGANEGILSCLMGLLNA
 GDEVIVFEPFFDQYIPNIELCGGKVWYVPINPPKELDQRNTRGEWTIDFEQFERAITSKTKAVIINTP
 HNPIGKVFTRREELTTLGNICVKHNVVVISDEVYEHLYFTDSFTRIATLSPEIGQLTLTVGSAGKSFAAT
 GWRIGWVLSLNAELLSYAAKAHTRICFASPSPLQECANSINDALKIGYFEKMRQEYINKFKIFTSD
 ELGLPYTAPEGTYFVLVDFSKVKIPEDYPYPEEILAKGKDFRISHWLINELGVVAIPPTPEFYIKKHKKA
 AENLLRFAVCKDDAYLENAVERLKLKDYL

YKL123W 881bp CDS: 501-881 public: 1..881 (SEQ ID NO 705)

AAAATTAATCGATGTAACACAAAATATTCCGATTCGATCTTTTCATTCGAATTGGCGCGTTTAATGCCGC
 ATATACAAGAACATATACGAGGGATGGTCTATTGGAAGACCCGGATAATGTTAGCTTCCGTGAAGCTCT
 CTCTGAAGGCAAAGATATTGAAGTCGCCAAAGATCTTCAAAGAGTTCACGATCCACATGATGAAAGTGA
 TGAATGACGTCAGATGAGGTTGAATTACATGTTAATTGGGCCAAGTTGGGTTCTGCTTTATAGAAGC
 CAATGTCGAAAAATATGCGTTTGGGAGTGTTATGGCCAAATTCGAATTCCTCCCGGTATTAATGGAAC
 CGAGATCAAGAAGGATACTATTTTACAGAAAGGAGAGAATTCGCACCAAGATATGCTGACACTGATAA
 TTTCTTTGCTACTATGAAGCTAAAGAACCGCTTCTCTTACGATTTGACAGAGAAAAATTAATGTTACCGACAG
 GTGGTCTGTTGGGACGTATGAAGAATCTCTCTTAACTTTGACAGAGAAAAATTAATGTTACCGACAG
 TCTTGAACCCGACGATAACAACACCGATAACAATGTTAATAACAACGATGAGAAGCGCTGGTTGCAATGA
 AAATTCGCCATTATTGGAAGATGATGSCAATAAAGACCGAAAAATTCAAATACCCCCCGTGAAGTATC
 AGATGGAGCTATCAATAAGAACCCCTAGAAATAAATCTACTAAAAACGTCAAAGAAACAGAGGCAAAATC
 TTCTAAAAAGAAGAACAGATCGAGAAATAAGAGACATTATGAATTTGGTTTTTTTTTACAATTTACGCA
 TACACAATATATACATTTCTACTAGCTTTTTTTTTTCTCAATTCGATAGTTTAG

YKL123W 126aa public: 1..126 (SEQ ID NO 706)

MKESLLTLTEKINFTTVLKPTITTPITMLITMRTLVAWKIRHYWQMAIKDRKIQIIPPVKYQMELST
 RTLEINLLKNVKETEANLLKRRTDRENKRIYEFGGFFYNLRIHNIYIPTSPFFFPNSIV

YML028W 1091bp CDS: 501..1091 public: 1..1091 (SEQ ID NO 707)

GGTAACGATAGGGTGATACCCGCTGTGATAAAGAAGCTTCGTGCTCTTTTGGGTTACACTACTCCCTA
 TGTGAAGGAGAAAGCTGATGATATGTTTCACAGAGAGCAAGGACCGTGAGCAACCGGCTCCATCTGC
 CCAACAGCAGGAAACGAACATGAGGCCCTCATAATCCCTGACGAGGAAAGAACCCACCGCCACAGGTGC
 GCAACCTCATCTCTACATTCCTGATGAAGACTAATTCGAATCCGATGTGGCCACGTTATATAATGCGTT
 TAAGGTGTACGAAACCCATGCTGTTCTGGCCCGTGGGTTTTCTGACAAATTTGCTTTTAGGGATTTT
 TCGGTTTGGCTCCGCTTCGCAAGTCCGCTGCCAACAAACCAGGACATATATAAGGGAGGTAATTCGT
 CAGATCAATGCCGAACCGTCTCAACGGGCTTCCCTCCGTTCAATTCGTCACAAACUAAUCCAACTAC
 ATACACATACATACACAATGGTGGCTCAAGTTCAAAAGCAAGCTCCAACTTTTAGAAACTGCCGTCC
 TCGACGGTGTCTTTGACGAATCTCCTTGGACAANTACAAGGTAACCTAGCTTGTCTTACCTTTTATTC
 CATTTGGCCTTCACTTTCTGCTGTGCCAACCGAATCATTTGCTTTCTCAGAAGCTGCTAAGAAATTCGAAC
 AACAAAGGCGCTCAAGTTCTTTTGGCTTCACTGACTTCCGAATACTCCCTTTTGGCATGGACCAATAATCC
 CAAGAAAGGAAGGTGTTTGGGCCCAATCAACATTCATTTGTTGGCTGACACCAACCACTTTTGTCCA
 GACACTATGGTGTCTTGATCGAAGAAGAAGGTCTCGCCTTGAGAGGTTTGTTCATCATCGACCCAAAGG
 GTGTCAATTAGACACATCACCATTAAACGATTTGCCAGTCCGTAGAAAAGTTGACGAAGCCTTCAGATTTGG
 TTGAAGCCTTCCAATGGACCGACAAGAAGCGTACTGTCTTCCCAAGTAACCGACTCCAGGTGCTGCTA
 CCATCAAGCCAAACGTTGAAGACTCCAAGCAATACITCGAAGCTGCCAACAAATBA

YML028W 196aa public: 1..196 (SEQ ID NO 708)

MYAQVQKQAPTFFKKTAVVDGVFDEVSLDKYKGYVVLAFIPLAFTFVCPTETIAFSEAAKKFEEQGAQV
 LFASTDSEYSLLAWTNIPRKEGCLGPINIPLLADINHSLSRDYGVLEEEGVLRSLFIIDPKGVIRH1
 TINDLFVGRNVDEALRLVEAFQWTDKNGFVLPUNWTFGAATFKPTVLEDSKEYFEAANK

YOL052C A 686bp CDS: 501..686 public: 1..686 (SEQ ID NO 709)

TGGCCACTGAAAAATCCTGGCCAGACCACCCCTGAGCTAAGGGAGTTTAGCCGCTCAAGCTTTTATATTC
 CTCTGATGTAATAATATACACACCCAGACACGGTTGCCAAGGCCTCGACGGAAGGCCGCTTCAAGGCAC
 GCGGCAGTGGCTATCAGAAATACCTTAATATCATCAATATTTTTCAATCAATCGCAAGGTGTCAAACATC
 AATAAAGGATGATGCTCAAAGGTTTATGCCCGATGTTCTCTTAATCCCCCTTTCTCTCTAATAATAATCC

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TTT'TTTTACTCTTCTTCTT'TCCCC'GTTTTCCATTTT'TGTCTTTT'PUACCCCTTATGGGACATCAATA
 ATGCAAGTATGTTTATACAT'TTTTATATAAATGTATATATAAATGCCATTTCTTTACACATAAACCCTCCAT
 TCTTTGGTTAATTCTTTCTTCTTCTTTT'TTTTTCATTCTGAAAAAGCCCTCCAAAGCAAGCAGGCTAAT
 TTAATATCGATTTAAACATGAAAGTATCACAAGT'TTTCATTTCTGCCATCTCT'GCTTCGGGCTCGCTA
 CTAGCGTAAATGCTCAAAACGCATCCAAACCCACGAGTAACGCTGCTCCTGCTTTGCACGCTCAAAATG
 GTCAACTACTAAACGCCGGAGTCGTGGTCTGCTGTGTGGTGGTCTTTGGCC'TTTTGCATTTAG

YOL052C A 61aa public: 1..61 (SEQ ID NO 710)

MKVSQVFLSALSIVFLATSVNAQNASNTTSNAAPALHAQNGQLLNAGVVGAAVGGALAFLL

YOL099C 992bp CDS: 501..992 public: 1..992 (SEQ ID NO 711)

TGTCCAAATATGTTGATGAATTCIGTTTGCAAAGGGGGAACAACTTCAATGAATTGTATTTCGAAAGG
 TGCAGAATGTTACCAAAACAGATCTGAAAATGCCCATGCAGAAATATTTTGTCAACATCTTTGATTCCCA
 ATAAAAGCGTTGCC'TTTGTGAGCTGTCTCCAGCTAAATTGGAAATCAGTTCAAGAAATCTTTTGAAACTC
 AAGGTTTTCACCTGTGAAATAGAAGAGCTAGAAAGATGACGATGACGAAATCGATAGTGAAGAAGACGAAA
 ATGCGTGAATACATGACCTCCATTTTCAGCTTCACTTTTCAACACAGAAACAGTGCCTATTATCTGCAATC
 AATAAAATGACAAAAGGAGCATTTGICTCATTTCTTTTTCGAATTCGGGATCTGCCCTACCCCGCCTTTTC
 ATTTGATTGATCGAGAATTATTATTATFATT'TATATGAGTACTTGAATTCCTTCATATTTATTTTAG
 ACTATTTAAGTAGCTTGATGAAAACATTAGATAAAATTTACTAATTAUGAUCTCTTTCGATTTTGCAGATG
 AGTTTTTGAAATTTGTTTCTGTGTTTAGACCTAATCCACGCTAACCTTGTCTTTTGGCAATCCCGTTAA
 CTAATTTACTGGTTAACGGTACTGGAGCAGCGTGT'TTTTTSATTTTGTTCCTTGGCATTGATAAAGG
 TTTCAAAAATTTCTGCTTGATCTGTTCCTCTTAGCGCTATTATCGATTCAGAAAACGAATTTGTGCTTTTG
 AAATTCATGGAGATTGGCTATGCGTCTCTGGCTTTTGGCGAAGGAGACTTGGAACTTGGAGATCTTTAG
 GTATGCTCTTTCCCATCATGATCTTCTCTTTCAATTACCTTTTGGTTTCTTTTCAACAGTTCTTTTCT
 CTATTTTATTTGTATTGGAATTAAGAATTTTTTTTGAGAACASTAAACAATTTGCTCGTGGCTTTTATTAT
 CAGTTCUTUAAAAGAAATGACTTTGTA

YOL099C 163aa public: 1..163 (SEQ ID NO 712)

MKTLDKITNYDLDFDADEFLLKFVVFVRNPVTYTCLEGNPLTNLLVNGTGAACFFZFCSLALIKVSKILL
 ELLLLALLIDSENELCFEIDGDWLCLVLFGEGLLEVGRS)GMALPDDDVHLSITTFWFLCNSSFILFVF
 ELRIFLRTVNNLLVVFLSVLERNDL

YOL100W 3746bp CDS: 501..3746 public: 1..3746 (SEQ ID NO 713)

TTAACGATCGACTCGACACATTTGTTGATGGAAATAATTGCTUCCTAGTTAAACAGCCGAGAAATAGCCCC
 CCAGGATAAATUGGAGAAAAGTCACGTGCAAAAGAAATCATATTGACCGAAATAAACTAGAATAAATTT
 TGACGTTTAGCPATAATPACCCCAATGGAAGCGAACATTTCCCGATCCTTTTAGTTTTCCTTTPAAGGCG
 CTATTGGCAITTCATCTTCAAAGCTTUCGCAACACAGAAATTATATATTCACATTTCTGAGGCAGAGAAAT
 AGTTTTGACAACGAAACTGTTAATATTTTACTCCAGTTACCGCCTTTGAACTCTCATATTCGCTCTACB
 AAGCTACTTAGGGGTATTTAAGAACAAAGAACTACATAAAATAGTTTCGAAAAGGGAAAACAAAAGTAAC
 ATCTTGATGAACCGAGAAAGCCACTAACTAGT'TTTTAAAAAGCAAAAGAAAATTAATTCCTCCTTTTTTT
 TTTTTCATTTCAACCAAAATGTATTTTGATAAGGATAATTTCCATGAGXCCCTAGGCCGTTATTGCCCAGTNG
 ATGAGCAGAAGCTAAACATTAATCTTCAACGAAAAGCAGAAATTCCTCGCATTTAGACCCCCCATATG
 ACGCAAAAGCCACTCCACAAAGAAGCACTTCGAATAGAAACGTTGGCGATTTACTTTTGGAAAAAACAA
 CUGCTAAGCCTATGATTCAAAGGCCCTTACGAATACGGATAATTTCAATTSAAATGTACCAATATCAGC
 AGAGAAAAAATCTTGATGACGACACTATTAAAGAAAGTAATGATTAATGATTAAGAAACGGAAAAACTGTCC
 CTAGTACCAACGACGGCAGATATGACAACGATTACGATAATTAACGATATTAATGACCAAAAAAATTTGG
 ATAATATAGCGGGAAGTCCCCACATGGAAAAAAATCGAAACCAAAGPAAAGATTTGAACATGACTTUTTCAT
 UTCAAAAACCAATAGCTAAAGAGTCAUCCAAAGCCCAAAAAATAAATCAAAAAGGGAATCAAGGACT
 TTAAATTEGGTAGTGTAAATAGGTGATGGCGCGTATCTACTGTAAATCTTACCGACGTCGATTGATACCA
 AAAACAGCTACGCCGCAAAAGTACTAAACAAGAATATTTAATACGCCAGAAAGTCAAAATACGTTUA
 GCATAGAAAAAACCGCCCTTCAAAGCTCAATAATTTCTCTTAGTGTGTGCGATTATTTTCCACTTTTTC
 AGCATCAATCAAGCCTATACCTTCTCTTAGACTATGCCCCCAATGEGGACTTTCTTCTTTTAATGAAA
 AATACGCTTCATAGACGAAACCTGCGCAGGATATATGCTGCGCAATAATAGATGCCATAGACTACT
 TACATTTCAAACGGTATTATTATAGAGATAATAAAACAGAAAAATATTCTTTTAGATGGAGAAATGAAGA
 TCAAACCTGACTGAATTTGGTACTGCGAAGTTACTGAATCCTACAAATAATAGCGTTTCGAAAACAGAAAT
 ACGATTTATCAACAAGTTCGAAATCTTTGCTTGGAACTGCAGAAATACGTATCTCCAGAACTTTTAAATC

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ACAGTTTTACAGACTATCGTTGCGATATTTGGGCCCTTCGGATGTATACCTTTCCAGATGATTGCCCGAA
 AACCACCATTCAAAGCTACCAATGAATACTTGACITTCCAAASSTAAAGAAAGTTCAGTACGCCCTTTA
 CACCAGCTTTCCCACTTATATCAGAGATTGGTTAAGAAATCTTACTAAAAAACTTAGACCGGAAGAT
 TGACGATAAGCCAAATTAAGGAACATCATTTTTCAAAGATTTCAATTTTAAAGACGGCTCTGTTTGGT
 CAAAAACGCCCTCCAGAGATCAAACCATATAAAATCAACGCCAAAATCCATGCAGGCAATGCCAAGCGGAA
 GCGATACAAAACCTCTGAAGAAATCAGTCAACACACTTCGCCAAATCCCATCTACTGACTCAAAGGTUAG
 CTTCAAGTCCCTCTGTTGAGGAAACTACTCATTCAACCCCTATACAATAACAATACTCACGCTTCTACTG
 AAAGTGAAATATCAATTAACAGAGACACCCACTGATGAAAGAACACCGCAGATACTTGAAATATGCAAGAA
 AGGGTATAAACAATAGGAAAAATCAACCAGGCAAGAGAACACCAAGTGGTGCAGCTTCTGCTGCCCTAC
 CAGCTTCTGCTGCTTTAACCAGAAAAACCATGCAAGCTATCCAACTTCTAGTTCCGAAAAAGTAGCAGGT
 CAAGCTCTCTCGGACAAACATCAAGACCAAGCAACTTATAAGCGTACCTTCCTTCTACAGAAAAATAAACCAT
 TTGCCAAATCTCCACCTTTGTCTAGCATCAGTTTTATCGTCAAAAGTCCCAATGCCCTTCATACACACCTC
 CAATGTCCCCCCTATGCACACCATATGATACATATCAAATGACACCTCCCTATACGACAAAAACAGCAGG
 ATTATTCTGATACCGCAATTGCCGCAGCTAAGCCTTGATTAGTAAGCAAAATGTAAAAATAGCACAC
 ATTCTCCCTTGATGAACAAGCAAGATATTCATATGCTCCTTTTACCTGAAAAACATCAACGAACATGTAC
 TAAGGACGGA AAAA ACTGGATTTTGTACCACAAAATACGATATCTTAGAGAGAAAAATGCTTAAACTAA
 ATGGTTTATTTAGATCTTCAACTGTCTTGTAAAGCCTAGACATACTTTTTTATCCCAAGTACGCTAGGA
 GTGGGGGAGAGGTTACAGGTTTTCGAATGATCCAACTATGACTGCTTATTCCAAAAACAGAAGATACGT
 ACTATTGAAAAATATTTATCGATTTCAGCTCTTTCGAAGATGATTATCGAATTGAGGAGGTGACTTAT
 CGGAGTTGCTTACTAACAGAAGCGGAGAGGGGTACAAATGCAATCAAAACAGCTCACCAATGAAAGACG
 ATGATAAATCCGAATCTAACAAATAAAGGAAGCTCTGTTTTTCTGGAAGATTA AAAAATTAATTTTACCC
 CTACCTCAGCAGCTGAAACGCTCTCTTCTCTGATGAAAAACCAAGTACTATAAACCAACCATTGTAA
 TCACATCATTTGCAAGCTTTCTACTATTTCCCAAGAGGAGCCACCCAAATCCACTTACAAATTTAAAGT
 ATGAACTAGAATATGACATAAATTTGCGTCAACAGGGTACCAAAATAAAAGAACTAATCATTCCTCTGG
 AAATGGGAACATAATCATATAGTTGTGATTTCAGACACCTTACAAGTCATTTCTTTTGGAGCACTGATAAAA
 AAACCACGAGCAAAATGTTTTACTGTTCTCAAAAAATTCCTTAATTCGAATACAAATAAAATAGAGAAAG
 AACTGTTGCAAGAAACCAAAAGCTAATTTGAAGAAGAACATCATCATCCGGAAGAGCCATACCTAAAG
 ATCTTCCAACCTCCAAGTCTCTCTCGCCAAAACCCAGGACGCATAGCCAACTCCATCAATTTCAAAAC
 ACAATTCCTTTTCTGAATCGATTAAATAGCGCTAAGAGCAACAGATCAAGCAGAAATTTTGAAACCTTTA
 TCAATGCCAAGGAACAAATTCAAAAAACACGCTCTCCACTACCGTTAACCAAGTAAAAATAGTFAACG
 GATTGCCAAAAAGACAAGTTACCGTGGGATTAGGCTCTAACACAGGAACAAATTTCAAAAACTCATCTG
 CAAAATCGAAGAGTCTGTAA

YOL100W 1081aa public: 1..1081 (SEQ ID NO 714)

KYPDKDMSMSPRLLPSDEQKLNINLLTKKEKFSHLDPHYDAKATPQRSTSNRNVGDLLLEKRTAKPMI
 QKALTNTDNFIEMYHNQQRKNLDDOTIKEVMINDENGKTVA STNDGRVDNDYDNNNDINDQKTLDNIAGS
 PHMEKNRNRKVKLEHDSQQKPIAKESSKAQKNILKKGIKDFKFGSVIGDGAYSTVMTATSIDTKKRYAA
 KVLNKEYLIRQKKVKYVSIKLTALQKLNNSPSVVRLESTFQDESSLYFLLEYAPNGDFLSLKKKYGSLD
 ETCARYYAAQIIDAIDYLHNSGIIHRDIKPENILLDGEMKIKLTDFTAXLLNFTNNSVSKPEVDLSTR
 SKSFVGTASYVSPPELLNDSFTDYRCDIWAFCILFQMIAGKPPFKATNEYLTFCQKMKVQYAFTPGFP
 IIRDLVKKJLLVKNLDRRLTISQIKHHFFKDLNFKDGSVWEKTPPEIKPKYKINAKSMQAMPSSGSDRLV
 KKSVENTLQKSHLVTORSSSPSVBETHSTLYNNNTHASTESEISIKRPTDERTAQILENARKGINNR
 KNQPGKRTPSGAASAAALASAALTKTMQSYPTSSSKSSRSSSPATTSRPGTYKRTSSSTESKPFKSP
 LSAVLSSKVPMFYTTPMSFPMTPTDYQMTTPYTTHKQDYSCATAIAAPKPCISKQNVKINSTDSPLMN
 KQDIQWSFYLNINEHVLRTKLDFTNYDILEKKMLKLNGSLLDPLFGKPRHTFLSQVARSGGEVT
 GFRNDPTMTAYSKTEDTYYSKNIIDLQLLEDYRIEGDLSELLNRSGEYKCNQNSSPMKDDDKSES
 NNKGS SVFSGKIKKLFHPTSAETLSSSDEKTKVYKRTIVMTSFGRLVFAKRRQPNPVTNLKYELEYD
 INLRQQGTCKKELIPLFMGTNHTVVQTPYKSELLSTDKKTSKLFTVLKKILNSNTNKKIEKELLQRN
 QKVLERRPSSSGRALFKDLPTSKSPSKPRTHSQSPSISKHNSFSESINSAKSNRSSRIFETFINAKFQ
 NSKKHAAPVPLTSKLVNGLPKRQVTVGLGLNTGTNPKNSSAKSKRS

YOR302W 573bp CDS:501..578 public:1..578 (SEQ ID NO 715)

GTGATGATGTAATCCATCAACCCCTATAAAAAACACCTGTGCACCGCATATTTCCATAGCGCGTGACG
 CTAAAGTACAAGAACAGCGAGGGGCCGTTAACTCCAGGCTTTACCGAGGGCGCGCGCTGGCGCTTCCCG
 TGGAAGGGTGTTTGACTCATCATCGCATCGCATTTACCTCATGATGAGTAAATAGTTGUGATTTCACTTA
 TCACCTCTCGCGGAAAAAAAGCGGATGACATGATATATAAGGCTCTCTCGTAAGACACTTAACATCC

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AACGTCACCTAGATTATTCGGTCAATTTCTTTTTCATGCCCTCCTTTTTCTTTTCTTTTCTTGACTC
GTCGTTTCCTTTTCTTTTTTTTTTTTTTTTTTCTTCAGAACTATAACACATAGATACACTCGAACAT
CTAATTCCTTAAATACTGCAAAGAATACAAGGTAATCGACTCTTCTACATACCCCTTTTTCGAGATTIGA
AATAAAAAAACATTATATGTTTAGCTTATCGAACTCTCAATACAUCTGCCAAGACTACATATCTGACC
ACATCTGCAMAACTAGCTCCCACTAA

YOR302W 25aa public: 1..25 (SEQ ID NO 716)
MFSLSNSQYTCQDYISDHIWKTSSH

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Figure 2**Candida spp. homologues**

YBL002W_homolog 393bp public: 1..393 (SEQ ID NO 397)
 ATGGCCCCAAAGCAGAAAAGAAACCAGCTTCCAAAGCTCCAGCTGAAAAGAAACCAGCTGCTAAGAAA
 ACCGCTTCCACCGATGCTGCTAAAAAGAGAACCAAGCTAGAAAAGAACTTATTCTCATATATATAAT
 AAAGTTTTGAAACAAACACATCCAGACACTGGTATCTCCCAAAAGGCCATGTCAATTATGAATTCGTTT
 GTTAACGATAATTTTCGAAAGAAATTCGACCGGAAGCTCCAAATTAGCTGCTTACAATAAAAAATCCACA
 ATTTCCGCTAGAGAAATCCAACTGCTGTTAGATTAAATTTTCGCCAGGTGAATTGSCCAACATGCCGTT
 TCCGAAGGTACCAGAGCCCTCACAAAATACTCATCTGCTTCTAGTTAG

YBL002W_homolog 130aa (SEQ ID NO 398)
 MAPKAEKKPASKAPAEKKPAAKKTASTDGAKKRTKARKETYSSYIYKVLKQTHPDTGISQKAMSIMKSP
 VNDIFERLATEASKLAAYNKKSTISAREIQTAVRLILPGLAKHAVSEGTRAVTKYSSASS

YBL064C_homolog 732bp public: 1..732 (SEQ ID NO 399)
 ATGACGAGACAAAAACAAACAAAAAATACTTTTTTTTTCGCCACGCACACTACCATCTCGCAA
 CAACACCATTTACGTCCTCGATCTACCGACCTGATTTCAAAGCTGATACAACTAACGGGCTATATCTG
 TTTCACGAAATACATTCGTCATAGCTGGGCTATCTTCTTCACATCCCGCTGCCACACCACTGTGTGT
 AGCACCGAGCTTTCTGCGTTTCGCACGACTCGAACCGGAGTTTACCAAGAGAGGGGTGAAATTCGTTGCA
 ATTTACGCCGACCCCTGTGAAGCAAATTCGACTGGATTGATGATATGGAAGATTTTAGCGGATCCAGG
 CTCATATTTCCAAATTTATCGCAGACCCCTGAGAGAAAGTTTGCTACCTTGTACGACATGATCCATCACC
 GATGCCACCAATCTCGATGACAAAGGGCTTCAATTGACAATTCGTGCAGTGTATTATCATTGATCCAAGT
 AAGAAAATCAGATTGATCATGACCTACCCCTGCCTCGACCGGTAGAAACACCGCTGAAGTATTGAGAGTA
 CTCGACTCATTAACCTTCTTCATAAAACAAACCTTATCACTCCAATCAATTCGGTTCAGGTGACGAT
 GTTCTTGTCATATGGGTCTCCAGATGATGAGGCAAGAGTTTGTCTTCTAAATATAGGGCTATAAAG
 CCATATAATTAGATTGACTCCCTTCGAAAAGGAAGACAAGTAA

YBL064C_homolog 243aa (SEQ ID NO 400)
 MRDKKOTKKKSEFFATHHTMSQOPHLRLGSTAPDFKADTTNGPISFHEYIGDSWAILFSHPAAIHTSVC
 STELSAFARLEPEFTKRGVLLAISADPVEANSWDWIDMEDFSGSRVKFPILADPERKVATLYDMIDHQ
 DATNLDDKGLQLTIRAVFLIDPSKKIRLIMTYPASTGRNTAEVLRVLDLQLVDKQKVITPINWVPGDD
 VLVMGVPDDDEARVLFPKYRAIKPYIRLTPLEKEDK

YBR149W_homolog 981bp public: 1..981 (SEQ ID NO 401)
 ATGAAATTAGCCACTGAATTTGATTTCAAACCTCAACAATGGTAAACCATTCTGCTTAGGACTAGCT
 ACTGTTGCCCTCAAAAGATCCATAAGATGTAAAGGATCAAGTAATCACTGCTCTTAAAGCAGGATATCGT
 CATATTGACTACTGCTTGGTTTTATGGTACTGAAAAATATATTGGTGAAGCATTACAGAAATTAATTTGCT
 GAACGAATCATTAAGAGAGAAGATTTATTTATCACGACAAAAATTTTGGCCATCATATTGGGCTAATCCA
 GAAAATCTTTAGATCAATCTTTAAAGACTTCCAAATTCATTATGTTGATTTATTTTACAACATTTGG
 CCAATTTGTTTACATGCTGATGAAAATGGATTAACCGAAAATACCTAAGGATGAGAAATGGTGAATTCATT
 TATGATGATGATCCAACCCCAATGGTACTAAATATATCGACGTTTATCATAAATTAGAGGATATTTTA
 GAAACAACCAACAAAGTTAGATCAATTGGTGTTCATATTATCAATTCACAAACTTCGTCAATTTATTA
 CCTAAAGTTAAAAACATATTCTGTTTGTAAATCAAATTGAATATCATCCACAATTACCTCAACAGAT
 TTAGTTGATTATTTGACTAAAAATAATATCTGATTTCTTGTATTTCACCAAGTTGGTAGTTATGGAGCT
 CCAGTATTCAAAATCCCATTTAGTTAAGCAATTGGCAGAAAAATATCAAGTCACAGAGAATGAAATTCCT
 GATGCTTATAAATATTTTGAATGGTAGAGTTACATTACCAAGATCTTCTAATCTTGAAGAAATTAAGACC
 ATTATTAGATTACCACATTGACTAAAGGAAGATTTGGATGAATTCTATCAAGTTGGAGCTAAAGATCCA
 CAAAGATATATTTGTGATCCTTGGGGTATGGTATAGGATTCCCTTGGTCGAAAGCCCACTTTAAGT
 AAAGAATTTGATTAA

YBR149W_homolog 326aa (SEQ ID NO 402)
 MKLATEIDFKLNNKTIIPALGLGTVASKDPKDVKDQVITAVKAGYRHIDTANFYGTEKYIGEALQELFA
 EGITKREDLFITTKFWPSYWANPEKSLDESLEKDLQIDYVDLFLQIDWPICLIGDENGLPKIPKDENGELI
 YDDEPTPNGTKYIDVYKLEIDILETTTKVRSICVSNYSIPKLRQLLPKVKKHIPVCNQIFVHPQIQOOD
 LVDYCTKNNILISCYSPVGSYGAPVLKIPLVKQLAEKYQVTENFTADAYNIJNGRVPLPRSSNLERIEK
 IERLPHLTKEELDELQYGVKDPQRYICDPWGYGIGPFWKSDTLSKEFD

YBR289W_homolog 1389bp public: 1..1389 (SEQ ID NO 403)
 ATGAAACCAATGCAAAACGTTAAGGAGTGGTCAGAAAAATTGAAACAGGAAGGTAAAGATGACCTCTT
 CATTTGAAAGTGATATCAAGATTTTATTAAGAAAGATTAAGGAATTTGTGGGTAAATTGAATMAACAGCTG
 CACGACAACAAATTTATTATGGAAAATATTAACAGAGATATCAACTCTTATATCTMAATCAAAACAAATCG

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AGGATGAATTCATTCGGTTCCTCCAAACAAAGGACATTAATAACAGTATTTTGGGGGGAAGGATATCAA
GGTTATGGGCARTGGAATAACAAACTCCAGTACAAAGTTATTTATTTCCCAACAGGGATTTAACTGATAGA
ATCATCAATGAAGAGTGCATGAAAAACAAAAATAAACCAAAACATTATGTACCCATTCCGATTAGAGTTT
GACCAAGAAAAGGGATCAATTTAATTGAGAGACACATTTCTTTGGGATTTGAATGAAGAGATTATAAAA
GTGGAAGATTTCACTGCTCAATTGTTAGAGGAATATAAATTTATCTCCAAAGTTCATTATGAAACAATT
TTGTCATCTATTAAAGAGCAGATTGCTGACTATCTCCAGAAACCTAGCAAAACAAATGGGTCGAATTGAGA
ATTCCAAATTAAGATCGACATCACCATTAAACAATACACAATTAACCTGACCAATTTGAATGGGATATATTC
AADAGCCAGGAAGGCGATGCGAGAAGAAATTTTCATCTTACATGTGCGACGAATTTGTGTCTACCCGGGAGAG
TTTTCGCACTGCCATCGCGCATAGCATAGAGAACCAATCGCAGATGTACTATAAAGCATTGAATATGGTA
GGGTACGGTTTCGACGGTCCACCAGTACACGAAGATGAGATTAGAAATCATTTATTTGCCACCTTTAAGA
TTAGTATCATCGGACTTCTGGAAATCGTGGATGATTTTTCTCAATTTTAAGAAACCCATCAAGTTTGCCA
GACTTTTCACCTACGTTAGGTAAATTTGCCAATTTGGAAGTTGAAAGATTGGACAAGGAAATGGAGAGA
GAAAGTTAGAAAGGAAAAGAAGACACAATTAACAATGAACATCACCAACAGGGTTCTGGTCGAGGCTTCACIT
TCGAGAAGAATTCAGCTCATGCTGGTAGGGGAAACACCATTCCCGACTTGTTCAGACATACCCAAAGACA
TTTAGGACGCGCTGCCCGCTCATFCCATATTGCCAGGTGCTGTGATATGGGTGTACCTGAGGTGTATGAA
TACAAATGAAGTTTAAACAATAGAACTCAAGTTAGGAATCCAGATTATAGACCGCAACACCTTATTCGT
CTTGAAAATCAACTAGCGGATTATAACCATGATCCAATGAAGGTACTTTTATGGTTACAATCAAAATTA
CCCGTATAA

YHR289W_homolog 462aa (SEQ ID NO 404)

MKPMQNVKEWSEKLKQEGKDVPLDLKVYEDLIRKDKKEFVGKLNKQLHDNKFIMENLNKDIKSYNQIKQL
RMNSIALSNKGQYNNSSWCEGYQGYNGCITNSSTKLFIPNRDLTDRIINERVMENKPKHYVPIRLEF
DQERDQFKLRDTFLWDLNEELIKVEDFTAQLLEDYKFISKVHYETLLSSIKEQLADYSQKPSKTMGEIR
IPKIDITINMTQLTQDFEWDLLNSQEGDAEEFSSYMCDELCLPGEFTATAHSIREQSQMYKALNMV
GYGFGSPVYHEDETRNIJLPPRLVSSDSGIVDDFFSTLRNPSSLPDFSPTLGLSLQLEVERLDKEMER
ESRRKRHRHYNEDQQQSGRGFTSRRIAHAHAGRGNTIPDLSIPKTFRTAPSSILPGAVDMGVPEVYE
YNEVLINRTQVRNPDYRPPTPIRVENELVDYNHDPLEGTFMVTIKLPV

YCR004C_homolog 597bp public: 1..597 (SEQ ID NO 405)

ATGGCACAAAGGAAAAGTAGCAATTAATCAATTTATTTCAATTAATCAATCAATGTTTATGATTAGCGTTAGCT
GAAAAGCTCCAAATTCAGCTTCTGGAGGTGTTGCTGATATTTATCAAGTTGCCGAACATTATCTGAT
GATGTTTTAGCTAAAAATGCATGCACCAGCAAAACCAGATATTCCAATTCGAACATGAAACTTTAACT
CAATATGATGCATTTTATTTGTTATTTCCAACCAGATTTGGTAATTTCCCTGCTCAAAATTAAGCTTTTT
TGGGATAGAAACCGGTGGTTTATGGGCTAAAAATGCTTTAAGAGGCAAAATATGCTGGTGTTTTCGTTTCT
ACTGGTAGTCCAGGTGGTGGTCAAGAACTACCATTATTAATAGTTTGAAGTACTTTGGCTCAATCATATGCG
ACTATTTATGTTCCATTTGGGTATGGATATCTCGTATGACTGATTTAGAAACAAGTTTCATGGTGGATCT
CCTTGGGGGGCTGGTACTTTTCTTCAGCTAATCGCTCAAGAAAAGTTACTGATTTAGAAAAAGCTATTT
GCTAAACAACAAGGTGAAGATTTCTTTAAACTGTCTTCAAATGA

YCR004C_homolog 198aa (SEQ ID NO 406)

MAQKVALIITYSLYHHVYDLALAEKAGIEAAGGVACIYQVAETLSDDVLAKMHAPAKPDPIATHETLT
QYDAFLFGIPTFRGNFPAOIKAFWDRGTGLWAKNALRGKYAGVFSVSTGTGGGQJETTAINSLSTLAHHG
IITYVPFGYGYPGMTDLEEYHGGSPWCACTFASGNGSRKVTDEKAIKQQGFNPFKTVFK

YCR013C_homolog 450bp public: 1..450 (SEQ ID NO 407)

ATGATAACAATGTTACCATTTTCAGCAGATTTGACAGCAGCATCCAATAAGGATTTAGTACCCTTGGCG
AATTTTTCAAATTCGAAAACACCTGGTGGACCGTTCCAAACAATGGTCTTTAGCTTTGGCAACAGCTTG
TGGAAACAATTCGACAGATTTTGGACCACAGTCCAAACCCATCCAGTTGTCTTGGAAATACCTTCAGCATCA
GTAGCAGAAGAATTTTGGCATCTTTTGTGCAATTTATCAGCAGTGACAAAATCAACTGGCTAAGATCAAT
TCAACATTTGTTTTCTTAGCTTTTTCAACCAAGTGTTCACCGTTTTTAGCACCCGCTTCATTCGAAAAGA
GAATCACCAATTTGGCAATTTTGTTCAGATTTTCTTGAAAGTGAAGGCCATACCACCACCAACAATCAAC
ATATCAACCTTGTCCAACAAGTTGTCAATCAATTGA

YCR013C_homolog 149aa (SEQ ID NO 408)

MTLPLPFSADLTAASNKDLVPLANFSNSKTPGGPPQTMVLATATACWNNSTDFGPGSKPIQLSGIFSA
VAEVLASLSNLSAVTKSTGKINSTLFLAFSTKCTFLAPASSKRESPIGLFKIFLKVKAIDPFTIN
ISTLSNKLGIN

YDL147W_homolog 840bp public: 1..840 (SEQ ID NO 409)

ATGGGATAGGAGTTGGGTAGTAGGTGTGCCATAAAGGGTGGTTGTTTAGTTAGTTATGCCACATGTTGT
GGTAGTTTGATTTTPTTTTGTGGTUCACACGACATGGCCAAACATTTATCAAAAAATCGAGTTCAACTTT
TTTTTTTTTCCAGTTGCCACCACTACTTTTACCACCACTAACACATGTCAAGAGAAGATCCA
ATTAAGGCTGAAAAAGACTTTCTGCTACTTTAGATGAACAAATTTCCCATTTGATTGAAACATCTCTTGAC

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TACAAGCAAGCATTAGATAAGTATCTTGTCTCTGGAGAAACAAACTCGTCAGTCTTCCGACTTTGGCTTCA
 TCAAAAAGAGTTCTCAACAAGATTGTTACTGCAATTCSTTGGATAATAACGATTGGGAGTACTTGAATGAC
 TTGATAAATACTATCTTTGTCAAAGAAACATGCTCAGTTAAAGTCTGTCATTCAGCATTATCAAAAGATGCTG
 ATTGATAATTTTGGATAAAATTTGGATGAAAACAAACAGCAACAATTAGAGTTGAAGATGAAATTTGATTGAA
 ACTATTTAGAACAGTTCACAGACAAAAGATTCTTTGTTGAAAGTTGAAAGAGCCATTGTTTCAAGACAGTTG
 GCCAAATTTTATTTGAACAAATTGAAATGATTGGATAAGGCAGTGGAAATCTTGTGTGATCTTACAAGTA
 GAAACGTATTTCGTTAATGCCATTTCAGTGACAAGATTTCAGTATATCTTAGAACAAATTCAGTTGACTTTA
 CAAAAGGGGGACATATGGCCCAAGCCAAGATTCTTTGAGTCGAAAGATTTTATTTAAATTCGTTGAAGAATCT
 TGCCAAAGCTGA

YDL147W_homolog 279aa (SEQ ID NO 410)

MDRSWVVGCAIKGGCLVSVGTCCGSLTFPCGTHDWPNTYQKIEFNFFFTSSSPFTTFTTTRMSREDP
 IKAEDFSATLDEQFPLIEKISDYKQALDKYLVEKQTRQSSDLASSKRVLNKIVTALVDMNNWPFVND
 LITILSKKHGQLKSSIQAFIKDVIDNLEKLDENNKQQLKMKLIETIRTVTDKKIFVEVERAIVSRQL
 AKIYLNKLNLDLKAIVEILCDLQVETYSLMPFSDKIEYLEQLQLTLQXGDYGPSQDFESKDFIKIVEEL
 CQS

YDR253C_homolog 1752bp public: 1..1752 (SEQ ID NO 411)

ATCCAAAATACTAACCCTAATAATAGTAATAGTAGTAAGAATAATAGTGAATATCATCATCAACAACAA
 CAACGACAACGACAACACAAGTTGATCAATATCAATCTATTACATTACCACCATTACAATATCAATCT
 AATACTCACGAATCGATAGTACTACCTTCGCCAACACCTTAAAGAGGTCGATCTGAACATTTTAAATCCA
 CAATTCCAACGTAATATAAATTCAGACCACTGTTATTACCAAGTCTCGTGATAATAATAACACCACA
 AATATACCTATACCTATAAATTTACCAAGTAGTACCAATTTCTAACAATCCAATTAATTTCTAGTAGCAA
 TCAAGAATGTTTTTCAACCTAATCCTCTGAGTCCATTTATATCCCGTGGTCAACCACCATCATCAGCATTA
 TCACCACCAACACAACACCATCAACAACAACAGCAACAATTAATAAAAACTCAAAACATCBAATTC
 GGTTCCAAATACTCGATTACTGGTGGTGGAAATGGATCTCTTAGTACTACTAGTTATTTAGCTAATTC
 GCATAATATCAGTTATACTAGAGTCAACCATTTAAAGATAACCAACCAACCATCTTCCACAACTAAGGAT
 AATAATAACCGATAATTTGAAATGAAGACCAGAAGTTTTTCCGATTAGCAAAAGAGCATTAGTAGCT
 AUTCACCAAGGAGTTAAGACCANTCATTCCTAATAATAATGCTAATTTTCTAATTAATACTTTCTAAGAT
 GATATTAATAATCATAATAAGAACAAACAACAACTAATGATGGTAATGAAACCATACTTTGATTCTTACA
 ACTGCAGATTTATTAACAGATTTACAATATGCTAGTCTCTCATGGTAATCCCATTTGGCCAAATAAGT
 GGACTTCAAACCTAATTTCTAAGGATTTACTTGAAGTCAAGATCAATACTCTAATTTCCCTCATTTACAA
 AACAATAATTTTTCAAAGTTAATAATGGTGATAATAATAATACTAGTAATAGCAAGTTTATGTAATAT
 TATCATCATCATCAGGTANTGAACCAACATGGAAATTTTTTACTTCATGAAGCATCAACGAAAACAACA
 TCAAACAATACACGATCAACAGGAACAACAGGAACAGGAATAGGAGCAACAACCAATATAAATACAGAA
 TCAGAATCGGAATTTAAAGTGAAACGAGANTCAAGTATTGCCAATATAATCAATCCCTCAACAACAACA
 ACTTCCACAACAACCTAATAAGAAATAACAATAACACTTCATCATCTACTAAAACCTAGAAAATATTCTCAA
 GATCCACAAGAAAATTTCCCTTGTGATAAATGTCCTCATGTCATTTTCGTCGATCATCAGATTTAAACCT
 CACCAAAAACAACATTTAATCTATCCCACTTAATTTTGTCAATTTTGTGGTAAAGGTTTGTCTAGAAAA
 GACGCTTTTAAAAAGACATATTGGGACTTTACATGTTAAAGAAATGCTGTAAGAAATTTATATATTGAA
 AATTTAAATTAATTAATAATTTCAAGTCAAGTATGATGATGATGAAGAGGAGGAGGATGAAGAAAGAA
 GAAGGATTGGAACAGGATAGATTGTATAAGAAGAGGAGGAAGAGTAATAATAATAATCAAAATTAATTA
 GAAGAAGGATTTGAACATAATCATCAGGATGATCATCATCATCAAGAGGATGAAGTGAACGAGAAATTA
 CAACTTATGGATATCAACAGAATTGA

YDR253C_homolog 583aa (SEQ ID NO 412)

MQNTRNMSNSSKNNSDNHHQCCQRCRCQVQDQYQSITL PPLQYQSNTHESIVLPQQPKRGRSEHFN
 QFQRNINSREVLUPSSRDNNNTTNIPIPIILPSSTNSNNPITSSNSRMPSNPVSPLYPVVTPPSSAL
 SPPTQHHQCCQQLHKKFKTSNSGNTPTTGGGIGSPSTTSYIANSANTSYTHSQPLKDNNTQTSSTTKU
 NNNNTIENEDQKFFRLAKEALVATARKVKTNHSNNNGKFGNNTSKIDINNNHKNMNMKSDGNETILNST
 IADLLRRLQYASAPHGNFIGQISGLQTNKGLLEVQDEYSNPPOLOKNNFPKVNDGDNNTSNTSKFSNN
 YHHPSCNEPCWNPFLDEASTKTTSNKTRSTGTTGTGIGATTTNIISESESELKVKRESSIANIINPSTTA
 TSTTTNNKNNNTSSSTKTRKYSQDPTRKFPCKPCMSFRSSDLKRHEKQHLTIPPNICQPCGKCFARK
 DALRHHIGTLTKRNADKKLYIENLKYLNSSQDDDEEEDEEESSGLSQDRLYKKRKKSNNNNQCIK
 EECFEHNDDEDEDEDEDEVEKREFPTYGYQQN

YDR276C_homolog 516bp public: 1..516 (SEQ ID NO 413)

ATGTCGTTTATGTCTTTCCGATTTATTTCTTATTATTTCTTCAGTATTATTCCTACCATTAACCTGTTTGG
 ATTAGAAGAGGATGTTGTTTCATGTGATTCAATTAATTAATATTGCCCTATGTAATGTTAGGATACTTCCCA
 GGGTTAATTCATTTCATGGTATATAATAGCTAAATATTCTCTTATTTATTATCAACAACAACAACAACA
 CGTAAAGATACCATTTATTTATGCTTTTATTCGAAGTGATTTAGAAATCAAAACACCAAGAAGAGATGCCAGA
 GATGGGAGAGATGAATGTCATCATGACCACCACCACCACCATCATCATCATCACAACACAGGCAGAACTCA
 CAAAGTGCAGGATTAATAGTTTCTAACAATCATAATAATAATAATAATAATAATAATAATAATAATAATA

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GGTTCAATCATCATCGAATTTGACTCCTGTGGCTCCTATTCCCTGTTGAAAATGGAGCTCCACUACUAGUT
TATACTGAGATTGATAATAAAACACAACATTAA

YDR276C_homolog 171aa (SEQ ID NO 414)

MCLCLSDLFLIILSVLPPLPVWIRFGCCSCDSLINIALCMLCYFFGLIHSWYIIAKYSSYYVQQQQQQ
RKDTIYYVYRSDLENQTPRPDGRDGRDECHHDHIIHHHHHHHNRQABESQSAGLTVSNHNNNNNNNYGSSVVE
GSSSSNLTPVAPTPVENGAPPAYTEIDNKYQH

YEL039C_homolog 333bp public: 1..333 (SEQ ID NO 415)

ATGCCAGCTCCATTTGAAAAAGGTTACAAAAAGAAAGGTGCCACTTTATTTAAAACTAGATGTTTACAA
TGTACACACCGTTGAAAAAGGTGGTCCACACAAAGTTGGTCCAAATTTGCATGCTGTTTCCGTAGAAAA
TCCGGTTTACGTGAAGGTTATTCTTATACTGATGCTAACAAAGAAAGGTTGTTGAATGGACTGAACAA
ACCATGAGTGATTATTTGGAAAAATCCAAAGAAATATATTCCAGGTACTAAAATGGCTTTTGGTGGTTTA
AAGAAACCPAAGGACACAAACGATTTAGTTACTTATTTGAAGAAAGCTACTTCTCTAA

YEL039C_homolog 110aa (SEQ ID NO 416)

MPAPFEXGSEKKGATLFKTRCLQCHTVEKGGPHEKVGPNLHGVFGRKSGLABGYSYTDANKKKKGVEMTEQ
TMSDYIEMPKKYIPGTRMAFGSLKKPKDRNDIYPIYIKKATIS

YER112W_homolog 321bp public: 1..321 (SEQ ID NO 417)

ATGTCAGCAGGTATTCCAGTAAGACTTCTAAATGAAGCACAAAGGTCATATAATATCAATAGAATTGATA
AMTGCAGATACATACCGTGGGAAGCTATTGAAATGAACATTAATATGAATTTATCCCTATACGAGGCA
ACTATAACACAAGGCAAAATCGGGGAAAGTAAGTCATATGGACCAAGTGTTTATAAGAGGGTCAATGATT
AGATTTATATCTGTGCCCTGATATTTTAAAGAAATGCTCCTATGTTTTTATGAAACCTGGAGATAAACCA
AAACCTCCAATAAGGGGGCCCTCCACCAAAAAGAAAGAGAGTATGA

YER112W_homolog 106aa (SEQ ID NO 418)

MSAGIPVRLINEAQGHIIISIELINGDTYRGKLLENEONMNLSLYEATITQGKSGKVSHMUQVFIRGSMI
RFISVPDILKNAPMFFMKPGDKPKPPIRGPPPKRKRIV

YFR010W_homolog 1239bp public: 1..1239 (SEQ ID NO 419)

ATGGTTTTTAGGCACTCCAGACAAGAATTGCGCTTCAAGGCCAGTTGAAAAACAAGTTTTTCTCGAAGAT
TTGAATAAAAAATCAATTGGTTAAAGTTAGTAATGAACCTAGTGGGTTGACCAATTTAGGGGAACACTTGT
TACTTGAAGTCAAGTTTACAAACATATTTCCATATTTGATGATGTGAATAACAGGCTTGAAAGAATACACT
TTTTGGTGGAGCCAATCAAGCCAATAGTGCCCTTTGTGTTGTCTATTGAAAAGTATGTTCCAGCAATATGTCG
AAAAACAAGAAGTTATAACTCCTTCTACATTTTCTTTCTCTTTTTCAGAGAAGATCTTATCCTCAATTTGCT
GAACAACAAAATGGTATTTATAAACAACAAGACCGCTGAAGAAGCATTTTCCCAAAATTTTGAAGCTCTTGT
AGAAGCGAATTGAAAATAGATGATGTGTTCAAAATTTACATTTTACACCAAGACTCAATGCTTGGCTATG
CCAGAAGATGTCACAGAAGGGTTTGAAGAAGCATATAAAATTTGAATTTGTCATATCGCGCTCAAGACCAAT
TTTTTTGAGAGATGGATTGTTGGCTGGATTAAAGAAACGATTGAAAAACATAAATTCAACTTTTGAATGCT
GTAAGTGAATGAT
TTTTTCTGGAACGAGACATCAATAAGAAATCCAAGATTTTGAGAAAGGTTCAATTTCCATTTGAATTA
GATTTAGCAGAAATGTTGGATGATCAATTAAGGCAGATAAAGTTTCCATAGAGATACATTTAGAAAA
GTTGAAAAAGATAAATTTGGATATGATAAGAGATTTTCAAAAAAGACCAAAATTCACACCAAGTTTAAACCA
TTGGAACAACAAGAGGAGGATGAGATGAAAATAACATCAATCAAGAGTAAGTTTAAAGACGACITGAAT
AGCGCTTTGCCCAACGTTGATTTTACACCCACACAGAAAACCTTCTAGTGTGTATGAATTAACGCA
GTCATTACTCATGCTGCATCATCTGCCGATGCTGGTCAATTATAAAGCAATACGTCAAGGATCCACAGAC
TTGGATGGCGAGAGATGGTGGTTATTTAACCAGTATAAGGTGAGCTCCGTAAACAAGAAAAACATCGAA
ACTTTAGCTGGCGGTGGTGAAGCGACATCAGCTTTATTATTGATTTTACAAAGGTTTAGGGCTTTAG

YFR010W_homolog 412aa (SEQ ID NO 420)

MVLGTFDKNLPSKPVKQVFLEDLNNQLVKVSNPSGLTNLGNFCYLNSSLQFIFHLDDVNNRLKDYT
FGCANQANSFVLSLKSMFQQMSKKQEVITPSTFLSLPFRSYTPQFAEQQNGIYKQQDAEEAFSGQLLSL
RSELKIDDVFKITFNTKTQCLAIPEVDTEGFEEAYKLNCHIGVKTNFLRDGLLAGLKETTEKHNSTINA
LYEYELTKTTERLPKYLIVLITLRFWKRDLNKKSKILRKVQFPFELDLAEMLDVSIKADKVSNRDITRK
VEKDNIDMIRDPKRTKNEFSITPLRQQEEREMKCTSTKSKFKDDLNSALPNVDFTNTTENPSSVYELNA
VITHAGSSADGGHYKAYVKDPTDLDERKWLFDNDKVSSVNKEIETIACCGESDSATILLYKGLGL

YFR052W_homolog 834bp public: 1..834 (SEQ ID NO 421)

ATGTCTTTACAAAACTCACTGCAGAAATATACTCACTATTTCGAAAAGCAGATTATCAAGGTTGCCAA
CAATTAATCTGCTCCGATTAAACTAGAATTAGTCAAAACATGATTTGTTGGTTTACUATCCAACACC

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ACCGATAAAAACCAATTAAATGATTTTGAAGATTGCCCAAAGAAATTTTGGAAATTGGAGCATTATCGTCA
 TTATTAACCAACAACATATTCGGTTTTCAGAAATATTTTGGCTCAGTTGAGACCATTTTACTCTAACCCC
 AAATTACATAATTTACAAAAAGTCCATATCAATACCGATATAACAAAAATCATTTCATTATACCTTGTTA
 TACTTGTTGAGTCAGGGTTTGAATTCAAAAATCCATGTTGAACTAGAAGTGATTTATAATTCATCACAA
 TATGATGCCCAACAAGACAGTATTTACAAATTTCCAATAAATTTAGAAAACCAATTTAATGGAAAGGTAAT
 TACA/AAAAATCTGGAAGTTATTAAAAGAAGAGAAAAACTTACCATGTCAGAATAACACCAATTTTGT
 GATACCTTTGATAAATGCTTTACGTTTGGAAATGCCAAATCTTTGGAGAAAACCTACGATTGCAATCCA
 ATTTCTAATCGCAAGAATTTATTATATTTACCACAAGAATTGTCCGATCCTAACTTTGAGAAAACTTTTA
 AAGGAAACTTATCAAGTTGATAATTTGGAAATTCGAGGATGGAGTTATATATTTTCACTAAGAATGAAAA
 GAAACCAATGTTGATAACCAATCGGTTATAAGAATTTATTAGGGTACGCTGAACAAATCGAATCCATC
 GTATAA

YFR052W_homolog 277aa (SEQ ID NO 422)

MSLQKLTAETYSLFGKGDYQGCQQLAPIKLELVKHDHLLVPLPSNTTDKNQINDIRIAQRILEIGALSS
 LLTNNYSGFENYFAQLRPFYSNPKLHNQKVHINTDITKIISLYLLYLLSQGLISKFHVELEVIYNSSQ
 YDAQQDKYLQFPINLESNLMEGNYIKIWKLLKEKNLPCQETHTFVDTLINALRPETAKSLEKTYDSIP
 TSNCKNLIVLPQELSDANFEKTLKETVQVENVKPFEDGVTVFTKNEENETNVDNQSVTKNLLGYAEQLESI
 V

YGL080W_homolog 354bp public: 1..354 (SEQ ID NO 423)

ATGTCATCATTTAAAAAATTCACGATTTTATTTTTCAAAAACAATCCCTTAGATATGCTCTGTACAAC
 CATTTTGGGGTCCAGTATCAAAATTTGGGAATTCCTATAGCTGCTATTTTAGATTTGAAAAAGATCCT
 GATTTAATTAGTGGACCAATGACTGGTTCAATTAATCACTTTATTTCTTAGTGTTTATGAGGTCATTCAAATG
 GCAGTTACTCCTCAAAATTTATTTATTTTGGGTGTCAATTTTGTTAATGAATTGGCACAATTCAGTCAA
 GGATTTAGATGGGTTAAACATCACTATGATACTTCTTCAAATGATGGTGAAGATACCAAAAAGATAACT
 CAAAATTGA

YGL080W_homolog 117aa (SEQ ID NO 424)

MSSEKKFTDFLF3KQSLRYVCTTHFWGPFVSNFGIPIAAIILDLKKDFDLISGFMTGSLILYSLVFMRYSM
 AVTFQNYLLFGCHFVWELAQLSQGFVWKHHYDTSNNGSDTKKTTQN

YGR070W_homolog 4146bp public: 1..4146 (SEQ ID NO 425)

ATGTCGAGTAATAGTTCTTGGTCTAACCAACGATCTTTACCAACTGAGGAACAAATCCTAATAAAGGTAAT
 AACCATAACCCACATTTAATGTACACAACAACACTGCACATCTGTAAATATTTCTTCTCATTTTGTTCCT
 CAAGCATTTTATAGAACAACAACAACAACCACCAACCACCAACAATATCCGCCAAGACGGCCAA
 GCTCATAAACAACCAACCAATCAATANTCGTTTTCATCAATCACAAACCAACCAACTGCGCCATCAA
 TACATCCCATCCAAACAAGAACAAATGCACAACCTTACCCAACTGCCGAACAAAAATCAATCAACACTT
 CCTCCACCACAGGAACATCATATAGTTTTTCATCGACTATCGATCCTGGCTCACCAGCAAAATGAUG
 CCACCTAATTTTTCACAAAGGAACCAATCATTTTCTGGCTACCAACAACCAACCAACCAACCAACAC
 TATCCGCACTCACCCCATAGGCAATATAACCAACAACCCCACTCACCAAGGTGGACCTTCAACAGCCA
 TACATTTGGCCCAACCAACAACATGCCCACCTGGATATATTAACCAAGATCCATATTTCCAGCAAAATAGA
 TCAGTATCATCTTTGACTCAAGATAGGACAGGAGCACCACTACAACACCTTCCCTTATCCTGTCAACCAAT
 GATGATCCTGGATATCAACTACAACCACTGGCAATTCATTAACACCAACCAACCAACCAACCAACCA
 CAACAGCTTCCACTCCAGACAGGTAGCAACTTCGTAAAGGCCCTTCGAGCAACTTGCCCCCAATTTUAA
 ACTGATCAAGTTTACTATAGCCCTGATGCTAGAGAATTTGTTTCCACACCTTACACACCAACCAAGATTT
 CCCACTCCCATACCACCAAGCTAGAACAAATCACTTACTTCCGCATCATTAACACCAACCAAGAACAA
 CCACCTGCAACCTCTCCAACCATATTTCCAACCAATCTCTGAACCTGCCAGGTAAAGACAGCAACGCTCC
 AATCCCTCCAGCAGTTCCCTTCATCATACATTTTCCCTTAACCTCAAAATCGCGATCATTTACATCTATC
 AGCAAAATTTCTGCTCTTCACTCAACTAAGAAATTCGGTTCCCTCTTAACTCCGTCAATACCAACAAATTAGAT
 CGTTATCAATCCAGTGGAACTATTAGAAACAATCACAATCATAACCAACCAACCAACCAACTAGCCACAAC
 ATTCAATTTAGCTAAACCACTCAGTATATCCCGCAATTTTATCTGAAGTCCCAAAATTCCTTAAAGAGGCC
 ATCATTTTGAAGATCAACACCAAGGATGGTTTGGAAATACCATCAATTTTACUUGGCAAAATGGCAGCT
 CATATATTTATCTCCCATTTATTCGAACAATGATCGTAACTTGGCTTGTATTGGGAAGATCATATAGAC
 GCTCAGAAGTTTTCATGATGTTACTTACAATCATAGATTAAGGGATTCGGTACATGAATTTATGCC
 TTTAACAATGCTTATAATGAATTCGATTTTTCACCAAGAAATGGAGGAGCTGGTCTGGTTAGCAAT
 GGGGAAAATAGTGCATTAATTTCCAACATGGGTCTTTCTTGATAGCAGCACACAGTTACAGAAATGCT
 TTCAATGACCACATATCCGATTATCATACCTCACAAGCACTGCATCATTAACCTAAAATTCCTAGTAGT
 GCCACTGGTAATGGTTCAGTAGGTGTTGCTGGTAAAGGAGTTGAGTGCAGTCAACCAACAGGTGTTAAT
 GGAGTTTTCACAAATTTTACAGAATGTTAATTCGCCCAACATGAGCAGAAATAGTCTTTGTTACAGTATT
 GCTGTCCAAAGAGATTAGAGCAACAACCTAGATTAAATTTGAAACCTCAGGTTGGTTTGCAACGTGCT
 GTTTCAAAATTTATCAATTCATGATGAGGAAGAAACCGAACTTTATGGCACAAGACTGTACCTCAATCA
 GTTTTAGATAAATTAGACAAGCATGAAGAGACTCGACAAGAATTGAATTAAGAATTTGTTTATACCTGAA
 CGTGACTACCTCAAGGATTTGCAATTTATGACTGATTTCTACATTAAGCCCTACGAAATCCTGCCAAI

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AATATTATTCTGATTACCAAAGAGAAACNTTATTCAAACGTGTGTTTGGGGAGTGCCTGATTTGTG
 AGATTGGCCAAAGAGACTCAGTGAAGCATTAACCTCGAAGACACCAACAACAAAAGCCCGTTATTGAGACC
 ATTGGTGATGTATTTTATGATTATGTTGGTGATTTTGAACCTTTTGTGACATATTCTGCGAAATAAAGTG
 TTTGCTACTTTTGAAACATGAAAGACAACAAGTTAATATGAAATATGCTAGATTCCTTAGATGCGAATT
 GAAAAGAAACCAGAATCGAGAAGACAAGATTCATCTTTTTTAATTAAAGGGGTTCAAAGACCAGCA
 AGATACCAAGTTATTGTTATCGGGTATTTTGAACAATACCAAGCCAGAGTCAACCCGACTACAAGTATTTG
 ACCAAAGCAAAGAAGAGATTGAGAAATTATTGGTGAAATCAATATCCAAACTGGGGAATGTACTGAT
 CGACACAAAGTCATGGTTTTTCCATACCTTATTGGGCAAACAACCTTTTGGAAAATAGGTTTAAATTTCAA
 TTATCCTACAATAATCGTATTATCTATCAAGTGACCTTGAATAGAAAGAGGGGATACGAAAAAATTGAT
 TTATACTTTGTTTGAACATGCGTTGTTATTAGTGAAACACAAGATTCAAAACAAGCGTGAACAACATAAA
 GTATTTGAAAAACCAATCTATTACCATTGTTATTGTGCAATAGTGGTATGGAGATCCCCACTAAATAGA
 ACAATCATGCCTCATAGATACCATGGATCCTTGGTATCTGATACTAGTATAAGACCTCAAAAGACAGAA
 TCTAATATATATTGGTAATACTTTGAAATCTTTCATCAACACCTAAATTCCAATTGAATTTTGGGGTTA
 CGTAGTAATCAAGTTCACGCCCTCATTATTTGCTGATGACTTGACTATTGAGAACCAAGTGTGCTGCAA
 ATATCGGCUUACAGAGAAATTAATGATCCTAATGACATTTTTTCAATGCTTAAATTTGAAACGAGA
 AGATTCACTGGGAATAATAAATCAATGTCGCTGTTCTTTTATGGTGGGAAGAAATTCCTGTATGGT
 ACTGATTACGGGCTATGGGTTAGTACTGTTGTTCAATTAGTGGCACATCTAATGAAAAATCTGTAGT
 GATCCCACTATGGTCATTTCCAAAACCTATGTCACCTAAATGAACTGATTCCTTGAATCTCCAAGTTG
 TTAGTATTTGAGTGACAAATCATTATATCAATTTGATTTATCTTGTACCGATTCTTTGGATCATGTGAAG
 AATACCAAACCTGGGGAATTTGCTTTTGAATCATGTGCTCATTTTCAAAGTTGGTGTGTTGTAAGGAAA
 TTGCTAGTGATTTGGTCTACACAGGCTACTCTGCATTCATTTGTTATTTGAGCCTGTTAATCCATTT
 GATAAATCGAATAAGAAATGAACAAGAGATTAGAATTCAGAAATTAATTTCAAGTCTGTATCCAAAT
 TCCATCTCATTTTGAAGACTAAACTTGTATTGGGTGCTTAAAGCTTTTGAATTTTATCTTCTCAA
 ACAGGAACCAAAGAATCGATTITGGAGTGAAGCAGACCCCTTCATTAGATTTTGCACACAAAGAGAAAGT
 GTGACACCATTAGCAATTCATCGATTAGGACCTGATTTCTTATTTGTTTATTCTGAATTTGTATTTTGG
 ATCAATCGAAATCGATCGACAACAAATCATGATTGGGGGATATTTTGGGAAGGTAATCCACAAATGTT
 GCGATTTCTTCCCTTACTTGGTATCATTTGAACCTGATTTGTTGAAATTAGAGATTTGCATACAAC
 AATTTATTAAGAGCTTTAAACGGGAGAGAATATTAGATTTTGCATTGCAACGAACATGAAGCTATGTTT
 CTTTCTGAAGAAATGGATATGATATTATTATTTCCATTGATTTCTTGAATTTGAAAUCAAAGTCTCCA
 ACATAA

YGR070W_homolog 1381aa (SEQ ID NO 426)

MSSNSSWSMNDYSYQSRNNPNNGNNHNPFLMSQQHSQSVNIPSHLLPQAFTFQQQQPPQPPQPPQDGO
 AHNKNEPNNRHFQSQPPQSRHOYIPSKQEOMQPPYPTAEQNNQHFPFPQERSYSFSSMTDPCSPSKMT
 PPNFSQRNQSFSCYQQPPPPQQQYPPQSPHKAYNQTHHQGGLOQPYIAQRQNMPPGYINQNFYSQNNR
 SVSSLTQDRTCAPVQHLPPVNNDDFGYQLQPSAIIQSHHPPQQQQQQPPPLQTRRQLRKAPSSNLPPIC
 TDQVYYSIDARRIVSTPTHQQNFPTFIPFEARTKSLISASLKHQKQPSQPSQPPYQQQISESPGKDSNAR
 NSSSSSLHHTFSLTSKRSFTSTSKLSLETKRFGSSSSVNTNKLDRYQSSGTLIRNNHNNHNTINQTSN
 LHYAKPSVYPALLSEVAKLFKEAIICTNTKDGLEYHDTFTGKMAVDILCRIIRTNDRNLALJIGRSLD
 AQKFPHWVTYNHRLRDSVIEIYAFNNVNDVDFNEEENGAGSVSNGENSALSKHGSFLDSSQLQNA
 LNDHISDYHTSQSSGSLTKIASSATNGSGVGVAGKELASQQTGVNGVFTILTCEYSPTCNRNLSLCYSI
 ACPRRLEOQARLNLKPCGGLQRAVSKLSLHDQEEETETLWKTVPQSVLDKLDKHEKTRQELIYEFVYTF
 RQYVKDLEFMTDFYIMFLNPNANLCPDYQRETFIQTVFGGVPDLLRLAKRLSEALTRRQQQKPVET
 ICDVFLDYVQDFEPFVTVYSGNKVFACFEHERQQQVNMKYARFLDAIEKKPESRQDLSSFLIKGVQRP
 KYQLLLSGILKHTKPESPDYKYLTKAKEIEKLLVKINIQTCECTDRHKVMVIFRLLGKQPLENRFNFK
 LSYNNRJYQVTLNRKRONEKIDLYLFEHALLLVKKHIQNKRFQHKVFEKPMYLPFLFVNSGMEPTNR
 TIMPHRYHGSLSVSDTSIRPQRAESNYTGNTLNSSTFKPQLNFFGLGSNQVHASLPAADDTIQNOVLSQ
 ISAJQKKLIDANDIFSLCKFETRRFTGNMKINCAPCYGGKKLLYGTDGCVWVSTVRSISATSNKICS
 DPTMVISKTYVTQLLEVVEYSKLLVLSDKSLYEFDLSCDSDLDHVKNTKSGKLLLSHVSFFKVGVCUGK
 LLVIGARTGSSHSICTFEPVVPFDKSNKVKNRLEIQEINFSSDPISSFLKTKLCIGCAKGFEILSSQ
 TGTKEILDEADPSLDFATORESUTFLAHLGRDFLLCYSPVFLINRNGWRNTHDWGIFWEGNPQNV
 AIFFPYLLSEFEPGFVEIRDLHTTNLLRALTGENIRKLSNEHEAMFACEENGYDIIISIDFTNTKPKSP
 T

YGR132C_homolog 956bp public: 1..966 (SEQ ID NO 427)

ATGCTCATATTGACACCCAAATAATTTCTTCACTTTTATTTTCTTCTTTCTTTCTTCAAGACAACC
 ACAGTTTCTTCCCTCTGCTACTGCTAAACGCTCCAATCAAACTATGTCACAACGAATTCAGATTTT
 GTTCTAAAATAGCCTTGCCAGCTGGTATCAACATTCGATTGGCACAATCAGCCTTGATGATGTTCTT
 GGGGTAAGCGTGCAGTTATATTGACCGTTAAAGGGGGTCAAACAGGAGTTATTGGCGAAGGTACC
 CACTTTTTTGGTGCCATGTTTACAAAAGGCAGTGATATTTCATGTTAGAGTTGAACCACGAGTAATTACT
 ACCACTACAGGATCTAAGGATTTACAGAACTGTTTCATTGACATTGAGGGTGTGAGTAGACCGAASTA
 AGAAATTTGCCACTACTATTACCAAACCTTGGGGTGTGATTACUGGGAAGGGTGTGCTGCCATTGCT
 AATGAATTTTGAATCCATTGTGGCACATTTGATGCTGCTGAATTGATCACCAGAGAGAGGTTCCT

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TCTGCCAGAATAAGACAAAGAGTTGTCAAGAAGAGCGCGCAGAGTTCATATAGAAATTCGAAGATGTCTCG
ATTACACATATGACATTTCTAGAGAGTTACCAAGGCCGTGGAAAAGAAAACAAATTGCACAACAGAT
GCAGAAAGATCAAGATTCTTGTGGAGAGAGCAGAACAGGAAAAGAAGGCTGCCGATTATCAGAGCTGAA
GGGGAGGCTGAATCAGCAGACGTTGTTTCCAAAGGCGTTGGCCAAAGCTGGCGATGGGTTATTGATGATC
AGAAGATTGGAGGCATCAAAAGACATTGCATCAACATTGGCCAACTCACCAAATATCACTTATTTACCT
AATCTTGGCGCTGGCGGCAGCGATAGCGACGGGTCCAAAACCTCATTATTGTTGAATATTXGCGGTTAA

YGR132C_homolog 321aa (SEQ ID NO 428)

MLIDTKIISSPFFSSFSFFKTSVSSPSLSLNVQSNMTMSQRIADVFVSKIALPAGITIALAQSALYDVP
GGKRAVIFDRLKGVKQGVIGEGTHFLVPWLQKAVIFDVRVVEPRVITTTTGSKDLQNVSLTLRVLSRQLV
RKLFTLYQTLGLDYGERVLPALIGNEJLKSIVAQFDAARIITQREVVSAIRQELSRRAAEFNIEFDVS
LTHMTFGREFTKAVEKKQIAQQAERSKFLVERAEQEKKAATIRAEGEAESADVVSALAKAGDGLLMI
RRLAASKDIASTLANSPNITYLPNGGAGGSDSDGSKNSLLLNIGR

YGR135W_homolog 756bp public: 1..756 (SEQ ID NO 429)

ATGTCACGAAGATACGATTCAAGAACCCTATTTTTTCCACAGAACGCTAGATTATACCAAGTGGAAATAT
GCTCAAGAAGCCATATCCAATGCTGGTACAGCCATAGGGATATTTATCTCTCGAAGGTGTCTGTTTTAGCG
TGTCAGAAAGAAAGTCACCTCCAAGTTATTGGACGATGATGGATCAGCTGAAAAATTATACATTATCAAC
GATCAAAATGATTTGGCGTGTGGCTGGTATGACTGCCGATGCATCAATTTCTGTGAATTAATGCAAGAATT
CAAGCCCAACAGTATTTGAAGTTGTACGACGAAGACATTTCTCTCAAATCTTGATCAATCGTGTGTTGT
GATGTCAAAACAAAGGTTATACCCAAACATGGTGGGTGGAGACCATTTGGTGTAGTTTCTCTTATGCCGGG
TATGATGACAGATATCAATTCOAATTGTTTACATCGAATCTTCTCTGTAATTACAGTGGTTCCGAAGGCA
ACTAGTATTGGTGCTAACAATTTCTGCTGCTCAAACTTTATTGAAGAAAGATTACAAGGACGATTTGACT
TTAAAAGATGCGATGCCAAATGGCTATCAAGGTTTTATCAAAACATATGGATGCTTCAAAACATAAATAGT
GAAAAATTAGAATTCGCTACCTTAACTTTCGCCAAAGACAACAAAGTGTTCATAAAAATTTCGAACGAT
AAAGATATTGACATCTTAATTAAGGCTTCGGGGGTTCGAACGAAAAAATAGCGATGATGAATAG

YGR135W_homolog 251aa (SEQ ID NO 430)

MSRRYDSRTTIFSPDRLYQVEYAQEAISNAGTAIGILSPEGVVLACEKKVTSKLLDDUGSAEKLYIIN
DQMCAVAGMTACASILWMNARIQAQOYLKLYDEEIPCEMLINRVCEVXQGYTQHGGLRPFVGFYVAG
YDDRYQFOLFTSNFSGNYSGWATSIQANNSAAQTLLKKDYKDDLTLKDACELAIKVLKTMDSNINS
EKLEFATLSLGLKDNKVLHKIWNOKDIDILIKASGVLNEKNSDDE

YGR155W_homolog 1491bp public: 1..1491 (SEQ ID NO 431)

ATGACATCTACAAACAAACCACAGCCTTAAAAAGAAGATATTTAGAACTTATTGGTAATACTCCATTAA
GTCAAAATGAAACAAAATTCACAAATCGTTGGGAATTAAGCCAAAGCTCTATGCCAAAGTTGAATTATTC
AATGCCCGGAGGATCAATTAAGCATACAATTGCCAAAATATAGGTATTGGAGCCGAAAAACAAGGTAA
ATCAAAACCAGGCTATACTTTGATTGAACCAACCTCAGGTAACTACTGGTATTGGTTTGGCTTTGGTTGGT
GCCGTTTCGTGGATACAGAACCATCATTAACCTTACCACAAAAAATGTCAAAACGAAAAACTTTCTGTTTTG
AAACCTTAGGTGCTGAAATCATTAGAACTCCAACCTGAAGCTGCATGGGACTCTCCAGAATCTCATATP
GGTGTGCTAAAAAATTCGAAAAAGAAATACCAAACTCTATTATTTGGACCAATATGGTAACCCAGCC
AACCAGATGCTCATATTTATGGTACTGGTATTGAATTTGGGAACAACTGAAGGTAAAAATTACTCAC
TTGGTTGCTGGTGGTGTACTGGTGTACCATCACTGGTATTTCCAAATACTTGAAGAAAAAAATTCT
AAGATTCACTTACTGGTGTGACCCAAAAGGTTCTATTTAGCTGAACAGAACTTTAAATAATTCC
ACCGAAGGTTACTTGGTTGAAGGTATPGGTTATGATTTTATTCCAGATGTGTTGAACAGAAATATGTT
GATGATTGGATCAAAACAGATGATGCTGAATCTTTAAATTTGGCTAGAACAAATTATTAGACAGAACCT
ATTTGGTGGTGGTTCCTCTGTTCTGCTTAAAGCTGCTTTTAAAGTACCTTAAAGACTTACTGAA
GACGATACCTGCTGCTGCTGCTTTTCCAGATTCATCAGATCTTACTTGTCTAAATTTGCCGATGACCAA
TGGTTAATCTCCAATGGATTGAAAGTTGAAGATTCACCGGCTGCTAACAAAGCTGACGAATTTCTTGAAT
GGTAAGACTATCAAGGATTTGGTTGCTGGCAAGCTCCAGTTGCTCACTGTCACTTATCTGACACAGTT
GCCAAGACTTTTGATTTATTGCAATCCAATGGGTTTGATCAATTTGCCAGTTTTCGAATAACTCTGCAAGA
TTAGTTGGTTTGATCACTTATCCAAGATATTGAAATCTTTATCCACTAAAAAGATTCAAAACGACCAT
TCAATCAGTTTCGATCATCATGATTTACAGAAAGTTGGCTGATTTTGAATAACTTTTACCATCACTAAA
AAATCAGGATTCACTAAGAGCAAGTTATGAACCAATCAAGTTGGACACCCCACTAGCTGCTTTGAATAAA
TTCTTTTGAACCAATTCAAATGCTATAATCACAGATGATGAATTTGAACCAAGTTCAAATTTGTTACTAAG
GTCCATTTGCTTTCCATATTGACTAAAAACCTACTTTTAA

YGR155W_homolog 496aa (SEQ ID NO 432)

MTSCNKPFAI KFDJLELTGWTPLVKNKIQSLGIKAKVYAKVELFNACGSIKDRIAKNMVLEAEKQKK
TKPCYTLIEPTSGNTGIGLALVGAVRGYRTIIPPEKMSNEKVSVLKALGAEIRTPTEAAWDSPESHI
GVAKKLEKEIPNSIILDQYCNPNPDAHXYGTYGEIWEQTEGKITHLVAGASTGGTITGTSKYLKEKNS
KIHVTGADEFKGSILAEPESELNNSIPGYVRGIRYDPIPDVNLNRYVDWIKTDDAESFKLARRIIREEG
ILVGGSSGSAALQALQVAKDLTSDDFVVVVFPOSTRSYISKFADDEWLTSGFEVEDSPGANKADEFLN

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GKTKKDLVAGKAFVVTVTLSDTVAKTFDLLOSNQFDQLPVLNNSGRLVGLITLSKILKSLSTKKIQTIN
SISIIIDFRKLADFEKSEFTITKKSGFTKRSYEPKIKLDTPLAALNKFFETNSNAIITDDELKEFQIVTK
VDLTSYLTKNASF

YHR138C_homolog 384bp public: 1..384 (SEQ ID NO 433)
ATGAATCAAAATAAGAAATTAACCTGGTCTTAAATATTATTAGCGATTATATCAATCATTACTTTATTC AAC
TTTAAACAATTTCCCAATAACTGCCATCAGATCATTGTCTCCCTGCCCTCTCCACCGCTACTAAT
ACTAATACTAAATCAACAATGTCAGATTCCAAAGGTTACATTATCACTTTGAAAGATACTTGTGCTGAT
TCCGAAGCTAGTTCAATTAATCAAGATTACTGAATTGGGAGGTAATAATCACTAATGAATTTAGTTTA
ATCAATAGCATTTTCTGCTCAATTGCCAATATCCATGCTGAAGCTTTACCTAAAGATTTTGTCTGGTATT
GCCAATATTGAAGAAGATGCTGAAGTTCGTACACAATAA

YHR138C_homolog 127aa (SEQ ID NO 434)
MNQNKKLTLGLILLAIISITLFPNFKTISQITAIKSPVSPASSTATNTNTKSTMSDSKGYIITLKETCAD
SEASSLRKSLTELGGKLTNEFSLLIKGPSAQLPTTHARALPKDFAGTANTFERDGRVRTQ

YHR179W_homolog 1212bp public: 1..1212 (SEQ ID NO 435)
ATGACAAATCGATAACGAAGGCATTGTCATTAACCATTTGGGTTCAACAAAATTATTCCAAACCAATAAAAA
CTTGGTTTTAACACTPTTATCACAAGAATAGCATTGTGCACCATCCACACGTTATAGAGCAACCAAAGAT
AATATCCCTACCGATTTCATTTAGAGTATTATTCTCAACGATCAGAATATCCTGGAACTTTAATCATT
ACTGAAGCAACTTATACATCACGTCAGGTTGATTAGTACCATAIGTCTCTGGGATTTATAATGATGCT
CAAACTAAAAGTTGGAAGAAAATTAATGATCGGATTTCATGCCAATGGAAGTTTCAGTTCACTTCAATTG
TCGTTATTTAGCTAGAGTTGCTAATCCTAAAATTTGAAAGATGCTGGATTACCATTTGTTGGAGCCTCA
TCAGTTTATTTGGAATGAAGAAAGTGAAAAATTTGGCCAAAGAAGCTGGAATGAATTGAGGGAATTGACA
GAAGAAGAGATCCATCACATTGTTGAAGTTGAATATCCGAATGCTGCTAAACGTCGCATTGAAGCAGGA
TTTGATTATATCGAAGTGCATTACCTTCATGGTTACTTGTAGACUAACTTTTAAATCTTGCCTCTAAT
AAAAGAACCTGATAAAATATGGTTTGTGGTAGTATTGAAAATCGTGCTCGTTTATTATTAAGAATTATTGAT
AAATTGATTGATATAGTTGGAGCTGAAAGATTAGCTATCCGTTTATCACCATGGGCCACGTTCCAAAAT
GTTGACCTCGAAGGAGAGAAATTCATAGTTATGATTGATCAATTACAGAAAGGGCAAATTTCTGCT
AATGAATTAGCGTATATTTCTCTTGTGTAACCAAGCTGTTCAAGCAAGTTGGGATATTGCTAAAGAGAAT
CAAGTTGGCTCAAATGAATTTATTTTGAACATTGGAAGGGGAAAGTAATTAGAGCAGCTACTTATGCT
CATGAATTAATAAATAATTAATGAAGATATTAATAATGATAGAACTTTAATTCGCTTTTCAAGATTTTTC
ATTTCTAATCCTGATTTAGTGAAAAAATPACATGATGGGATTTCTTTGACTCCTTATGAAAGAGCAACA
TTTATTAATCATGATAATTTTGGATATAATACTTGGATTAATATGAGATAAATATGGAGAAAATAAAGTTTTCAATCAA
CAAGAAGAAAGGAAAAAATTTGGGTAAACCTTTAGCTTAG

YHR179W_homolog 463aa (SEQ ID NO 436)
MTIDNEGIVIKPLGSTKLFQPIKLGFNFLSQRIAFAPSTRYRATKDNTPDLQLEVYSQRSEYPGTLII
TEATYTSROGLVPYVPGIYNDAQTKSWKKINDAIEHANGSFSSVOLWYLGRVANPKNLKADGLPVPQAS
SVVWNEESEKLAKELAEAGNELRELTEELIDHIVEVEYFPMAAKRAIEAGFDYIEVHSANHOYLLDQPLNLASN
KRTDKYVCGGSIENRRLRLRLIIDKLIDIVGAERLAIRLSPWATFQNVVEGEEIHSYIIDQLQERANAG
NELAYISLVEPRVQASWDIAKENQVGSNEFLKHWKGVIRAGTYAHENLNKINEDINNDRCLIAFSRFF
ISNPDTAKKIHOGFSITPYERATFYNHDMFGYNTWIKYGENKVFNEQEERKKLGKPLA

YIL074C_homolog 1392bp public: 1..1392 (SEQ ID NO 437)
ATGTCATCTCCTCAACAAATTCCTCAACTCATTCCAACAAAGCCTTCGAATTTATCAACCATCTCCAAAATGCT
GTTTCTACATCACCAACTCAATCATTTCTTGAGTCAATATGTTCCAAAGCAAGCCAGCTAAAGCTTTGAAA
CCTTTTCAAAACCTGGTGAATATCAAAAATTTTATTTATTTGCAAAATGTTAAACCAAACTGCCAATAAAATTTTC
AAAAACCAAGGTTACCAAGTCTGAATTTTATAAATCATCATTAACCCGAAGATGAATTATTAGAGAAAATCC
AAAGATGTTTCATGCCATTGCTATTAGATCAAGAGCAATAATTAACAGAAAAAATCCTTAAGCTGCTAAA
AACCTGGTGGTATTTATTTGGTATTTCTCTGTAATGCTACCAATCAAGTTGATTTGGAATTTGCTGCCAAATCA
GGTATCGCTGTTTTTCAACTCTCCATTTTCAATTTTCAGATCAGTTGCTGATTTAGTCATTGCTGAAATCC
ATTACTTTGGCTAGACAAATTTGGGTGATCGTTCAATCGAATTTGCACACTGGTACTTGGAAATAAGTCAGT
GCCAAATGTTGGGAAATCAGAGGTAAACCTTTGGGTATTGTAGGTTATGGTTCACATTGGTTCCCAATTA
TCATGCTTTGGCTGAAGCTATGGGTATGAATGTTATCTATTATGATGTCATGACCATTATGCTCTTAGGT
AATCTGAAACATCTTCAAACTTTGGACGAATTTGTTGAAAAAAGCCGATTTCCCTTACTTTGCACGTCCTCA
GCTACTCCAGAAACCAAGAACTTTGAGTGTCTCCCAATTTGCCGCTATGAAAGATGGTGCCTACGTT
ATAAATGCTTTCTAGAGGTAATGTTGTTGATATGCCAGCTTTTCTGTTCAAGGCTATGAAAGCCGGAATAAT
GCTGGTGCCGCTTTAGATGTTTACCTTCATGAACAGCAAGAATGGTGAAGGTTTATTCAGTGATAGT
TTGAATGAATGGGCCAGTGAATTTGTTTCATTGAGAAATGTTGATTTTCACTCCACACATTGGTGGTTCTT
ACCGAAGAAGCCCAATCTGCTATTGGTATTGAAGTTTGGTAATTTCAATTGAACCAATACATCAACGAAGGT
GCCTCTCAAGGTGCTGTTACTCTCCAGAAGTTTCATTGAGACCATTAGACTTGGATCAACAAAATGTT

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GTCAGAGTATATATATATCCATCAAAAACGTTCTCTGCTGTGTTGAAAACGTCACAACATATCTTATCCAAAT
CATAACATTCAGAAACAATTTCTCCGATTCTCAAGGTGATATTGCTTACTTAATGCCCCATATTTCCTGAT
GTTCGATATCAGGATATACAGTCATTATATGAACAATTAGAACAACCTCCATATAAAATTCCTACTCGT
TTGTTGTATTAA

YIL074C_homolog 453aa (SEQ ID NO 438)

MSSPQQIVNSFQQALNLSGSPNAVSTSPQSFLSQYVPSKFAKALKKFFKTGDIKILLLENVNOTAINIF
KNQGYQVEFYKSSLPEDELLEKIKDVHAIGIRSKTELTEKILKAAKNLVVIGCFICIGTNQVDLEFAAKS
GIASFNSPFSNSRSVAELVIAEIIITLARQLGDRSIELHTGTWNKVSARKWEIRCKTLGTVGYGHIGSQL
SVLAEAMGMNVIYYDVYTIMSLGNSKQVESLDELLKKADFVTLHVPAFPETKNLLSAPQFAAMKDGAYV
INASRCTVVDIPALVQAMKAGKTAGAALDVYPHPPAKNGEGLFSDSLNEWASELCSLRNVLTPHIGGS
TERRAQSAIGLEVGNLSLTKYINEGASQGAIVNFPEVSLRPLDLDDQNVVRVLYIHQNVPCVLKTPVNNILSN
HNIEKQFSDSQGDIAYLMADISDVDISDIOSLYBOLEQTPYKLATRLLY

YIR037W_homolog 436bp public: 1..486 (SEQ ID NO 439)

ATGTCTCAATTTTACGAATTAGCTCCAAAAGACGCCAAGGTGAACCATATCCATTTGAACAATTGAAA
GGGAAAGTTTCTCTTATCCTCAATCTTCTTCCAAATGTGGATTCACTCCTCAATACAAGGGTTTAGAA
GAATIGAATAAGAAATTTGCTGATCAACCAAGTACAAATCTTGGGTTCCTCATGTAATCAATTTGGCCAC
CAAGAACCAGGTAGTAACGAAGAAATTGGATCATTCTGTTTCATTGAACCTACGGTGTACATTCCTCACTC
TTCCGATAAAATTTGAAGTCAATGGTGACAATACCGATCCAGTTTATAAATATTTCGAAATCACAAAAGAGT
GGTGTTTTCGGGATTGACCAGAATTAAATGGAATTTTGAAAATTCCTTGATTTGACCAAAATGCTAAAGTT
ATTGAAAGATTTCAGTTTCATTGACTAGTCCAGAAAGTATCGGTACCAAGATTGAAGAATTGTTGAAGAAA
TAA

YIR037W_homolog 151aa (SEQ ID NO 440)

MSQFYELAPKDAKGPYPFRQIKGKVVLTWVNAASKGGFTTQYKGLEELNKKFADQPVQILGFPCNQFGH
QLFCSNEELGSSFCSLNYGVTFPVLDKIEVNGDNTDPVYKYLKSQKSQLGLLTKWNPFKFLIDQNGKV
IERFSSSLTSPESIGTKIEZLLKK

YJR096W_homolog 849bp public: 1..849 (SEQ ID NO 441)

ATGTTCATATCGATTAAATCAAACCTCAATTCUGGTCATACCATTCCATCAATTGGATTAGGATGTTATGAT
ATCCCAAGAAATAAAACGGTTTCCGGTAGTTTATGAAGCTTGTAAAGTTGGATATCGTCATTTTGATACCT
GCAGTGTATATGGAAACGAAGAAGAAGTCATTGAAGGTATAAGTAAATCTTACCAGAGAACCCCAAT
ATACCACGATCTGAGTTTTTTACACCACAAAGCTTTGGGAATTAATCAATTTGGGTACTTCAAGCACTAAA
CAAGCCATTTCAACAATGATGGCTCAAGTTGGTGCATAAATTACAATATATTTGAATTTATTTGATTTCAT
TCTCCATTACCAGGTAAGACCAAAACGTTTAGAAAGCTGGAAAGTTTTCGAGGATGCTGTGGAAAAAGGA
TGGATTAAAAACATTEGGGGTTTCTAATTATGTTAAACATCATATNGAAGAATTGTTTGACCAATGCAACG
ATCCCTCCAGCTGTCAATCAAAATTGAAATTAGTCTCTTGGTGTATGAGACACCAATTTAGCTTACTTGGTGT
TTAAGTAAAGGTATCAATGTTGAGGCATATGCACCATTAACCCATCGCTAACAAATTACAAGTCAACAAT
ACTGAATTTCAAGAAATTATGCAAAAGTATAATAAATCAGCTGCTCAAAATATNGATTAAATGGTCACTTA
CAAAAAGGTTATATACCATTACCAAAAACAAAACCTCCATCTCGATTAAAGGAAATCTTTCTGTTTGAAT
GATTTTGAATTGACTAATGAAGAAATTAAGGCTATTGATCAACCTGATGCTTATCAACCAACAGATTGG
GAATGTACTGATGCTCCATAG

YJR096W_homolog 232aa (SEQ ID NO 442)

MSYRLIKLNSGHTTPSTGLGCDIPRNKTVSVVYEACKVGYRHPDTAVLYGNEEEVIEGLSKFLRENFN
IPRSEFFYTTKLWNNQLGTSSTKQAISTMMAQVGDKLEYIDLILLHSPLFGKTKRIEHWKVLQDAVEKG
WIKNIGVSNYKGKHIEELLFNATIPPAVNQIEISPWCMPQDLATWCLSKGINVEAYAPLTHGNKLQVNN
TEFQETMQKYNKSAQILIKWSLQKGYIPLPKTKTPSRLLKENLSVDDFELTNEEIKAIQPDAYEFTDW
ECTDAP

YKL196C_homolog 603bp public: 1..603 (SEQ ID NO 443)

ATGAAGATTTATTACATTTCCTATTTTAAACATCAACTGGAGACAAGGCTTTAGAGTTAACTTCAGCCAGA
GATTTATCACAGTTTTCTCTTTTCGAAAGAAATGGGGTATCCCAATTCATGACTTTTTTCGCAGAAACC
GATCCCCAAGAAGCTCAACCTGGACAGAGACAAGTGTGTAAGAAGGTAATTATATTGGTTCATACTTAT
ACCAGATCACAAAGGAATTTCTGGTATCATTATATAACGGACAAAGATTACCCGTGAAGACACGATATACA
TTAATAAATAAAATCTTTGGAAGAATATTTATCATTTGCATCCTAAATCTGATTGGGAAACATTGATAAA
GCAATGAAACTTTACAATATGGACAATTAGAAGCATATTTGAAAAATATCAAGATCCCCTCAAGCT
CATTCATCATGAAAGCTTCAACAACAATTACATGATACTAAGGTGTGTTTACACAAAACCTATTGAAGGG
GTTTTACAAAGAGGAGAGAAATTAGATTTCATTGGTTGACAAATCAGAAGCATTCCTCAAGTTCTTCAAGA
ATGTTTTATAAACAAGCAAGAAAGAAACCAATTCCTTCTCTGATTATGTGA

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YKL196C_homolog 200aa (SEQ ID NO 444)
 MKIYYIGILRSSGDKALELTSARDLSQFSFFERNQVSOQMTFFAETVSQRCPGQQRQSVLEGNVIGHTY
 TRSEGISGIIITDKDYFVRPAYTLINKILSEYLS*HPKS*MENTDKANETLOYGQLEAYLKKYQDPQTQA
 DSIMKVVQBLEDTKVVLHKTTEGVLRGEKLDLSVDKSEALSSSSSRMFYKQAKKTNSCCVIM

YKR676W_homolog 771bp public: 1..771 (SEQ ID NO 445)
 ATGGATGACAAAGCCTCGACATTTCTACAAAGGAAGAATTGAAGACATTAAAACTGAAGACGACATT
 TCATTAGGTACACCTGACCATAACTATGATTTTTTCCCGTCTTAGAGAATTGTACTTTAAGGCTGAACCA
 GAATACGAGGGAAGATTACAGATTCCAGTATTGTGGGACAAAAAGAAGGTACAACTCGTAAACAATGAA
 TCTGCTGAAATCATCAGAAATCTGAATACTGAATTCATAGTACTTTGCCAAGTGAATATGCCGAAGTT
 GATCTTGTTCUAAAAGACTTAGAATCTCAGATTGATGAATTGAACAGCTGGATTTACGATAATATTAAC
 AATGGTGTTCATAAAGCTGGATTTCGATCCAAGCAAGAGGTGTACGCCAAAGAATGTCAAAATGTGTTC
 GATCATTTGGCACAAGCTGGAAGCCATTTTGAGAAAAAACCACAATGGGTCCAAAGAAGGAGAAATTTTG
 TTGGGCAACCAATTGACTGAAGCAGATATCAGATTCTACACACAATTATTAGATTTGATCCTGTCTAC
 GTTCACACCTTTAAGTGTAAATATTGGTACAACTCAGAACTCACTATCCATACATCCACAATTGGCTCAGA
 TTATTGTATTGGAAGATTCTGTGTTCUAAAGAACTACCAATTTTCGAGCACATCAAGTACCCTACACC
 AAATCTCATATCAAGATTAATCCATACCCCTNTAACACCATTGGGTCCAGTACCAAAATATTTTACCATTG
 CAAACAAAAGTAA

YKR675W_homolog 256aa (SEQ ID NO 446)
 MDDKGRFPPTKRELKTLKTEDDISLGTDPDHNYPFSRLRELYFXAEPEYEGRPVFPVLWDKKEGTIVNNE
 SAEIIRMLNTEFNSLLFSEYAEVDLVFKDLESQIDELNSWIYDNIRNGVYHGGFASKQEVYAKECONVF
 DILDKVEAILEKONHNGSKKGRFLTAGNQITFADIRLYTTTIRFDPVYVQHFKCNICTIRTHYPYIHMLR
 LLYWKIPGFQETTFEHLKYHYTKSHIKINPYGITPLGPVPMILPLEEK

YKR092C_homolog 1287bp public: 1..1287 (SEQ ID NO 447)
 ATGGGTGAGCTGTGCGCTCGGGACAGGCAATATTTACACCCAGAGGAAAGAGACCAAGATTCTGTTTTT
 GGGCTCATCT
 TTGGAAAAAATTTTTTTTTTAAATTTCTTTTTTCACTCTTAAAGAGTCAATTATTACAACCTACTACCA
 ATACCAAAAGATGAGTTCCAATACTCAAGATTTAGTTTTTAGCTTATATTAATGATTATGTTTTCCAGAAAC
 GAAGAATTGTCAAAAGTTGAAGAAGGCATTATCGAAATTCCTTAGCAGGCAAGAAATTACCAAAAGTTCT
 AAACAGTTTGGAAATCCATTATTGATGAAGTGGAAAATTAAGAAAAGAAAAGCAACCAAGAACTCATCA
 TCTGATACTGAAAGACTCTTCATCTGAGAGTGAAAGCTCCACTTCCGACAGCGAAAGCTCCTTCTCAGAC
 AGCGACAGCTCTCTCTCTCAGACAGTCAAAAGTTCTTCTCAGACAGTGAAAGTTCTTCATCAGACAGTGA
 GACAGCGATGACGAGGAAGACAAAGCAAGACAACCAACCAACCAAGATAACAAAGACAGCGAACACAGC
 GAAAACGAAAAAGTGGAAAGACAAACAAAGACACCAACCTCTGNTTCAAGTTCCAGTTCCGACTCMAAA
 TCTGATTGAGACTCAGACTCAGACTCCAGCTCTGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG
 GACTCCAGCTCCAGCTCTGATTCAGACTCCAGCTCCAGCTCTGATTCAGATTCAGACTCAGATTCAGAT
 AGTGACAGTGACGACAAATTCCTCAGAAAGTAGTTCTGAAGACGGAAGATCATCTAGTGATTTCAGAAAC
 AAGAGGAACAAAAAUAUCCAGAAAGACAAAGAAAAAGCAACAGATGATATCAAGAGAGAAAAACCA
 GTTAAAAAGTTCAAAAACGAGTCCAGAAATCATCAGCTCATCTCTCTACTGATTGATTCTCTCCAACTCCA
 CAAACAGAAATTAAGGCCAGGCCAAAGAAAAATTTTTCTAGAAATAGATAGAAAGTAAAGTTAACTTTGAA
 AATTCAGTATTACAAGACAATACTTACAAGGGAGCTGCAGGAACCTGGGAGAGAAAAGGCTACTGAAAA
 TTATTACAAGTCCAGAGGTAAAGATTTCAAAAGAAATAAAATAAAATGAAGAGAGGAAGTTATAAAGGA
 GTACTATACACTTTAGCTAGTGGGTCTATATAAATTCGAAGATTAG

YKR092C_homolog 428aa (SEQ ID NO 448)
 MCECGWEGIFSSQKXRPREFVGLISLSLSYSHKRRATIKVCPNGLEKNFFFNFFHLLKSQLLQLLP
 IAKMSSNTQDLVLAYINDYVSRNEELSKLKKALSKFLAGKELPKVSKQLKSTIDEVHQEXXSKPRNSS
 SDSDSSESSESSTSDSESSESSESSESSESSESSESSESSESSESSESSESSESSESSESSESSESSES
 ENKVERDNKDTSNDSSESSESSESSESSESSESSESSESSESSESSESSESSESSESSESSESSESSES
 SDSDDNSSESSEDESSSDSESKEEQKQFEDKKRKHITDILKEKPVKFKNESESSESSTDSIPATP
 EPFLKPGQRKHITGRIDRSKWNFNSVLQDNTYKGAAGTWGEKASEKLLQVRGKDFTKNKNKMKRGSYKQ
 GSTTLASCYKFED

YLR043C_homolog 312bp public: 1..312 (SEQ ID NO 449)
 ATGGTTACAGTTGTCACTGAAGTTAAAGAAATTCCAACCCCTTTTAAACCAAACTTACTTATTGTT
 CACTTTTTTCCCACTTGGTGIGGTCCAATGTAAAAATGATTGCTCCATTATTAGAAAAATTCAAAAATGAA
 TATTCTAATATTAAATTTTTGAAAATGATGTGATCAATTTGGGTTCCTTTAGACACAAGAAATATAAGTT
 AGTTCTATGCCAAGTTTGATTTTATTCAAAAATGGTGAAGAAGTCAATCGTGTCAATTGGTGTCTAACCA
 CCTCCTATTAAACAAGCTTTGGCTTCTCTTGCTTAA

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YLR343C_homolog 103aa (SEQ ID NO 450)

MVHVVTVEVNEFQTLLENLIVDFFATWCGPCKMIAPLLEKFNQNEYSNIKFLKIDVDQLGSLAQEYINV
SSMPTITLTKNGEPVNRVIGANPAATKQATASIA

YMR273C_homolog 4938bp public: 1..4938 (SEQ ID NO 451)

ATGTCACTGCCCCAACACGGTCAATCCATAGUGAATCAAAATTTTGAATCAGCTGTACAAGATCTTGAACAA
GAGAAGAAAATGGTGGCAGCCCTTAAAGAGACTATCTATAGGTCATATGATGCCAATATGATCCCGACTTG
CCACCCAGGCAGTATGGATGATATTGATCCCTTTGCCAAACAATAACAACAACAGCAATACCGCTAGTAAC
AATAACCACTATAATGGTCATACCAGAGATCACACCAGCAACAACAACAATACACACAATCATCTCC
AACTCAAAATTTGAACCACTATCGTGGTCAAAGTCCCTTATGATGAAAGATTTAATTCACACAATATCCAC
AGATCACACTCAACTCGATCAGCATCAAAATCAGATTCAACTTCTCCTTCTACTTCCGCTCAACACAAAG
CAACAACAACAACAACAACCCGCAACCTTTTCCACATGAACCCACAGACTCCCTCCATATAACAATTCACCA
AGCCCACTCAAGAGAGCTAGTTTTTACGACAAATTCAGCTGTGTGACCTCAGAAGTCACGGATATTTT
TTCCGATGCCGAGGATGAAGTTTATGATAGTTTCATCCCTTTGTGTGGGTACCAGCTAACCTCTCATCCT
CAAGTGAATCCCTGAATCGTTCAAGAGTTTAAATCAAAATCAGTGGAGAGATATTGGAAAGAAAGCTA
TCTCGAAAGTCAACTATTTCAGAAAGTCAACTTTTATCACCGCACTCCCTCAACCCAGTAAUAAAGAGACA
TTAGCCCCAGAACCCAGAAATAGTCCAGAACTGGAAATGTGATGTGTACCTCCTTCTCCAGTAAGAA
TCTTCTCTGTCTCTGTCGTCACAAACAATCAAAATGAAGACGTTTCTCGAAATCGTCTCTCTCTCT
TCTTCAACTTCTCCACAAGATCCAGCTAAGAGAGAAATCTTGGTACCTTCAACCACTCAAAAAGATAC
CTGAATCCATCATTTCCACAGCTAACTTTCAGAAATGGAGCAGTTGTCAAAATGGCGGGGATGGACAAG
AATGACGCGAGTAACCTTTGGCAAGAACTTTGTGGCCACAATCACTGGGGTATACAGATGTCCAAAAAATA
GCATTTGACGAATTAGATAGTTTCACTAACCAACCCCTACTGCAACAACACCCCAATTCACCTGGGTCTCCA
GGAAGTTATGACTCTGCAAAUCCACCTCGCAACCAAGACCTTGCATTTACAACAACGATTAACAACATCAA
TTTCAACAAGCTCAAAATCAAGGCAGAAAGGGAGGCAGAAAGATCGACAAGACATCAACAAGCGAACA
CAGTGGCCAGTATCGAATGACGATAGTCACAAATCTCTGTACAGTTTACAGCAAGTGAAGGAGCTTCT
ACTGCTAATGCTTTTACCAGTGTCTCCAGTCTGTCTGACTTTTCCCTTGAACCGAAGTAGAAGAACTGAT
TACCGGAAAAAGGAAACAGATTGGAACAACAAGACTTTTGAATAATTCGCTCTTACAACAAGTACAAT
GTCCGGAATTTCCAGTTGTATTATTAACCTACAAGAAACCCAGTAGATTCTCTCTCTGTCTCTCACTTCACTT
TCACCATCTACATCTCAAAGCATGATGGGTACAGGGGTGAACACAAGAAATCTCAAAGCCATTGGAA
GCAGCAATGGCTAAUCCAAATGAATGGATGGTTCAAGATATTTACATAAACCCGATATCCCACTTCAACCC
ACTATTGATTTTCACTGCTATGGGTGCTAAGAAATCAGCCAGACAAATCACTTACCTTCCAGAGAATGCAATG
GATGGCAGATCTCGAACAAGCCCAACAAGACTCTCTGCTGCTATCTGCATCAAGAAAGCTCTCAAT
CCTTATCATCAACAACCCACAGCCTCAAGTGCACCTTCAAAACCCGCCAACCACTTCCACCAGCACAACAA
GCTCATAGACAAATCGACGAGACAAACCCACAATCATCCGAGCACAGGAGTTGAAAGCACTCACCGACAG
GATAACAAGCGTGTAAATGCTGTACAGCTTTCTAAATACAGACATAAATGATTTTATGCTCAACTGAATCAA
TTTCAGACTAATGCAACAAGAAACCAATCGATATGACAACCTTCUATAAAAAGGATAAGACTCCATTTTGTG
CCAAATGAAGACCAACCAAGCTAAGTCCCATTCGACAAGAAATTCAAATGTAAGAAATTTGTCTTCTCTCG
TCTCAACAGCAATTTACATCAACCCGATCTGACAACTTCTGTCTTCCGCCCCAAGTCAAGTCAACTACATCAA
AATTTAGACAAGTTGAGATCCGAGATCAATGAATTTAAGGAAAGCTTGAATTAATCGGAATTACCTGGT
GAGCAATCAAAAGAGAACACACACTGCGTCAAGACCAAGCACCACCAACAACGACAAACGACCAACCA
TCACAGCAACCACTTGAAGCCTCGCAATTTACAACTCAATAGCACTCAACCAAGCACTCAAGCATGAACA
GTACAACCCCAACAAGTCCAGCCCTTACAGTCAAGATACTAGTTTGTGATATCAGTTTATCAAGATTTTACG
CTTCAAGATCAATTTGGTATTGTAACAGGAAGCATTTGAGAGATTTAGGCAAGGAAAAGGGGCACTTCTCAT
GAGATTGATATGATGATGATTTTGTGATGAATTTTAAATTTCTGCTATCAATGAACGACATGGCTCT
CAATTCACACTTGTATCATGACATTTTGGACAGCTTTAATTTGGTGAATTAATCAGTTGGTGTGATCTGCA
GATGAAGGAATTTGATAATTTTCAAGGCTAAGAAATGAATATCCCTTGGGCGACAACAACCAACAACAA
CGTCAACAACCAAGAGCTGTCTTCCCAACCTCTCTCACAGCAGTACTTGGGCGCATCATCAATTGCACCTTG
CAACAAGGTAAAGATACAAATAAAAAAGTTGGTCTCTGTTTAAGTATTGATACATTTGCAGAACAAGCC
ATTCACCCCTGACGAAACCTGCAACTGGATTTGGAAATGAATGCTTACCTTCCCTTACCTTGCATTTAGAT
GAATCTCAAAATAGCACTCTCTGGACATCTGAGAAAGGCAAGCAATTTCTGCAAGCTACGACGATTAATAC
AATATAGCTGACAAATCATCTACTGCGGGTACCCCCAAAACAAGAGAGACCAACTTAAACCGAA
TATCTCAATTAAGACCCCTAATTTGGAGATTAATAGCACTCTGATAACTATAAGGAACAAATGGGCAATTCAG
ACATCTAACAATAAAAAATTTGAAABGAAGAATCTTTTGGTTTCTTATGATACAAATCATCTGTGGGA
GCAAAATGATACATTTGAAATTTGAAGGGGCAAGAAATTTGAAABGAAGAAGTCTGTGGGCTCTGTGCGG
GAGGCTCTTGGCAGTGGCTCTGTCTGACAGATATCAACAAATTTCCGCTCTTGGCTCTTGATAAACTACCT
ACAAGATCATTTCTCAATTTCCGAAACCTCAACCTGACCAACACCCAGAAACATGATCTTGAGAACGGTTCA
GATCTTGAACGTTGAATTTGGAACACCAACCTTGAATTTGAATTTGAGTTGGAGCTGGATCTTGAGTTTGA
TCTGAGCAACCAAGGAAAGCAAGGATGCTTCAATGGTAAATGATTTCAAGCTTTTGGATTTGATCTTAC
TCTATGAACTCCACAGACAAAGGAAPACCTGTCTTCCAAATTTTTCAGAAAAAAGCAAAAGGTACCGG
TCAAGCTCACAGTCAATTTTTCATTTGAATCAAAAGCTTCAAGGCTCAGCTGTGACTATGAATCCGAC
AAAGACCGCAACCTGATCAAAAGGAAGGGCAACAATAGCAAGCACTTTCAGAAAGGAATCAAGGSCC
AATTTGTGAGAACCAACAATTTCACTGAATTAAGGAAAGCTTCCAGCTTTTGAATTTTGTGTCACCAAGAA
TCCAGAGCAGATCGAAGGAAAGAGAAATTTGUSACAACTAATCCCACTCGTAAGGCAGAAAGAGCTGAG

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AGTCAAGAGCAACAGGAGGAACAGTTCCTGTAACTCGTCCGGATACATCAATTCAACATTGAACA
 UTCAACACGACTTTCTCAGCTCTTGGGGAGAACCGACGATGTTTATAGATTCTCCTACTGATGACTTGGGTT
 GAAGAATGTAAGATCTCGTAACATTCAGAGCACAAATAGTTATTTGTTGATGAGGATGAAACTCTCTATTCAA
 AATAACAATGATAACAAGATTGTTGGGGATGCTAAAAAGTTGACGAATTGTCCAAAAAGAAATCAATTAGC
 AGGMAAAACCGGAACAATATCCAAAAGAAAGACCTTTCTACTGAAGTTACTGATACAAACAAAGAGGTA
 GTAGAGGAGGTTCTTGCAGCTGAGCAAAGTGTCAAACCAAGCCAAAGGGGAAGATCTTTTGTCTA/CAAT
 GAAGATAAAGAGAAATTAGATATCCAAGAAAAGTTGAAGAAATCAAT/AAAACGTACATCAAGGGCCAC
 CAGCCTATTGAGTTTACTGATTGAGCCTTTGGGTTCCCTTGCCACCACCATCTCAATCAACTTTAGTG
 ATGCTTGACTACAGATTTCAGCTTCATCTTGAGCGTCCCATTTATAGA/TGT/CACACTTGAAACTTGCT
 AACCTTAAGCGTTCACTAAGAGAGCAAGTTTGT/TTGTGAAATTTTATGATGCTACCTCAACTTAGTT
 GATCATACATTACATTTAGAGCAACAAAATATGAGCAAGTGAAGATGGCGATCAGATGGAACGTTGACGAC
 GACGACAAAGAAGAAATGACTGACACTGATGACAAAGACATGATTTTTGACACAGTAATATTGCCGAT
 GAGGATGATCTTATTCCTGAAGAAGCAATGGTGATTGCGATTGGGATTAAGTTAGATATGCGATCTTTA
 CATAGGAAACAGCATCATCAATCTGGAA/TCGAAGTTAT/AG

YMR273C_homolog 1645aa (SEQ ID NO 452)

MSSPNTSFHSDSNFESAVQLEQEKKNVAALKRLSLGHMMQYDFDLPPGSMDDIDPFANNNNNNSNTASN
 NNHYNGHTRDHTSNNNNTHNHSNPSKINHHRGQSPYDEDLTPQNIHRSHSTRSRFSKSHSTSPSTSPQHK
 QQQQQPQPFPHEPQTPFPYKSPSPVKRSPYDNSSVLTSESHDIP/DAEDEVSSSPLLWV/PANSH
 QVNPESFKSLIKTOVEEILERKLSRKSTISRKSTLSRSSSTSTKETLAPEPEISPESECDVSPSPSVRK
 SSLSSSSQNNQNEVDVSRKSSSVSSTSPQKPAKRESWYFNNSKRYSNP/SLRELTSLEBQ/SLK/MAGMDK
 NDAVTLARTLSAQSLCYTDVEKLAFCLELSSQMTATATT/NS/SGSPG/YSANFPRTTTLHLQQR/LQHQ
 FQQAQ/IKAREALERT/HQ/SEQQW/PVSN/DSHKSSSQ/LTASEGGSTANA/TSAGSGADPALKRSRR/TD
 YRKKETDSKQKTSNNSP/PTRKYNVRNSQLL/FNYKKPVDSPSSSPSPSPST/SQSMGHRV/KHKKSQK/PLE
 AALANPHMDGSDMSHNPYPTASTTILFSRMGA/KKSARQSLSPEN/AMDCR/SRTK/PENKTHRCYSHQFRSII
 PYHOOP/POPOVOPOTRQQLPPAQQA/HQ/STRO/THNHPSTGVEKHHRQ/DNK/RV/MSSAS/N/DINDFMAQSNQ
 FQTNGTNRNHRVDNLHKDKDTAFLPNEDIQRKSHSTRNSNVRNLS/SSSQQLH/QPYST/TSVAPKSRQLHQ
 NLDKLRSEINEFKESLNKSELPGEE/SKREHRSR/HQ/HQ/RQ/RPAPSQ/HQL/PRMY/MHNDRHQR/QQHEH
 VQPPQVQPLQSD/TSFDLSYQDLSVEDQLGIEQ/ALRELGKEKHSHEIDIDDAFDENL/KXSPINERHGS
 QFTLDHDILDSFNLVNQLVGSAD/EGIDMLKGKNEIPVGRQQPQQQRQ/PRAASPPSSQOYLGHDELHL
 QQGKDTNKKVGPRLSIDTLCKNPIHP/ETATGFG/MNALPSP/TLHLEDSQNSTPGHSRKASNSASYDNY
 NIADR/STAGTP/KK/ETKVKTKL/FNKUPNLEIDSDNYKEKMG/LET/NNK/LKKKSPGLLSTTSSVG
 AND/PSNEG/PKK/KKKKSWG/LRERSASASSAD/INLPP/ELDKLPTR/SF/SNPETSTDQIQKH/DLENGS
 DLERELEHEFELELELES/DELFDYEQQRKH/QDASMVNDSSFAVDSISMKSTDKENVLSK/PFKKAKVPG
 SSSQSVFSFESKSGSASVDYESDND/AKSIKKGNNSR/LFKKKSR/K/SEQ/NSV/NKEKLRPLNLVSNE
 SQTIEEKENLRSNGTRKAE/RVESQEQ/EEQFPVTS/SP/HLQFNIEHLKDD/VPLGEKDDVLD/SGTDLDV
 EDVRSRNIQ/STIVIVDEDETPIQNNND/NKDLMLK/VDEL/SKKK/ISRK/RNM/MQ/KNLSTELTDTNREV
 VEEVLATEQSVKPSQGEDLLSKNECKE/KLDIQEKL/KKSIKRTSRANOPIEFTDSAFGEPLPPPSQ/STLV
 MLDYRFPVHVERATYR/LSHLKLANPKRSLREQVLLSNFMYAYLNLVDHTL/SL/EOQNM/SS/EDGTQMERDD
 DEEBENTDTDEKDMIFGESNIADDEELIPEE/ANGDSIGINLDM/DGLHRKQ/HQ/SGTEV

YNL112W_homolog 1332bp public: 1..1332 (SEQ ID NO 453)

ATGTCATACAATAACCGAGGATATAATAATAGAAACCGAGGTAGTTACGGTGGAGGCTACCCCCCTGGT
 GGTAGCAGAGGTGGAAGAGATGGCTACAGTGGTGGTGGCAGAGGCGGTGCTACGGTGGTGGTGATAGA
 GATCAAGCTGGATACAGAGGTGGAAGATTCAAGTGGTGGTGGCCCTGGTGGTGGTAGATT/TAAT/GAT/UCT
 CCAAGACAAGAAATTAATGCTTCUACAATGGGATTTAGAACAAATTC/CAAAAATTTCAAAAAAAATTTCTAT
 TCAGAACATCCAGATGTTGCTGCCAGATCTGATAGAGACATTGAACAAATTTAGAAAAGAAAATGAAACG
 ACAGTTAAAGGTCATCATATCCCTCATCCAATCACCACTTTTGATGAAGCTGGTTTCCAGATTATGCTT
 TTACAAGAAGTCAAAGATCAAGGTTTCCCTAAACCAACTCCTATTAGTGTCAAGGTTGGCCPATGGCT
 TTTAGTGGTAGGATATGAT/UGGTATTGCGCGCACTGGTTCCGCTAAAACCTTTATCTTAAT/TTGT/TTACCA
 TCCATTTGTCATATTAATGCTCAACCACAATTACAATATGGTGTATGCTCCAATTTGCTTTTGGT/TTTAGCA
 CCAACAAGAGAAATTTGGCACTGCAAAATCAAACTGAATGTTC/CAAAATTTGGTAAATCATCAAGAATTAGA
 AACACTTGTGT/TTATGCTGGTGCACCAAAAAGGTC/CC/CAAAATTAAGATTTAGCCAGAGGGGTTGAAAT
 TGGATTTGCCACTTCAGGACATTAATGATATGTTTGAAGCTG/STAAAPCTAATTTGAAAGAGAGTCACT
 TATTTGGTTTTAGATGAAGCTGATAGAAATGTTAGATATGGGTTTGAACCA/CAAAATTAGAAAAATTTGCT
 GAT/CAAAATTAGAATGAT/TC/CAAACTTTGATGTGGTCTGCTACTTGGCCAAAAGAGTGCACAACATTC
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 ATTA/CTCAATTTGCTTCAACTCATTCATCAATTTTCCAAAGAGAGATAGATTAGT/TAACATTTGGAAATCC
 GCTTAAATGAAAAGATAACAAAATATTTGGTTTTTTGCTTCTAC/TA/TAAGAACTTGTGATGAATCAACC
 ACTTATTTAAGATCAGATGGTTGGCCAGCATTAGCCATTATGTTGATAAAGAGCAAAATGAAGAGAC
 TGGGTTTTAGATGAATTCAGAAAGGCTAA/AACTTCTATTATGTTTCCAACTGACGTTGCTGCTAGAGGT
 ATTTGGTATGTATAATTTTAA

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YNL112W_homolog 443aa (SEQ ID NO 454)
 MSYNNCGYNNRNGGSYGGGYGGGGSRGGRDGYSGGGRGGGYGGGDRDQGGYRGGRFSGGGRGGGRFND
 PRQELTAQWDLEQLPKFEXMFYSEHPDVAARSDRDIEQFRKENEMTVKGHDIPHPITCFDEAGFPDYV
 LQEVKDQGFPPKFTPTCCQGWPMALSGRDMIGIAATGSGKTLSTYCLPSIVHINAQPOLQYGDGPVILVLA
 PTRELAVQIQTECSKFGKSSRIIRNTCVYGCAPKGPQIRDLARCVELCIATPGRLIDMLEAGKTNLKRVT
 YLVLEADRMMLDMGFEPQIRKIVDQIRPDQITLMWSATWPKEVQQITREYLNDFIQVTCGSLLELAASHT
 ITQLVEVIDEFSKRDRLVKHLESALNBKDNKILVFAS TKRTCEITTYLRS DGWTPALAHGDK EQNERD
 WVLDEF RKCKTSINVAEDVAARGIGMYNF

YOL151W_homolog 1032bp public: 1..1032 (SEQ ID NO 455)
 ATGTCAACACCAATTACTGTTATTGTTTCTGGAGCCACAGGATTTATTGCTCAACACCGTCTTTAAACAA
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 TTATTCAACAATCCACAAAACCTTATCTTATGAAATTTGTTGAAGATGTTTGGAACTAAAGGTGCTTTGAT
 AAAGTATTACAAAAACATGGAGAAGCAAAAGTGTTCCTTACATTTAGCTTCAACCATTCCTATTAAATGTC
 ACTGATGTTGAAAAAGAATTGTTATTGCTGCTGCTGTTGATGGTACTAAAAATGTATTACAACCAATTTAT
 AATTTTGGTAACAACTTGA AAAAGTGGTTATCACTTCATCTTATGCTGCCATTAGTACCGCTTCTTAAA
 GAAGCTGATAAAAAATGCAATTTATTACAGAAAAGGATTTGGAATGAAATCAGTTGGCAAGATGCTTTACTT
 AATCCAGTTAATGGATATCGTGGATCCAAAAATTTGCTGAAAAGCTGCTTGGGATTTTATAAAAACTT
 AATGATAAGGTTAAAACTTTCATTGTCGACAAATTAATCCATCATTTGTATTGTTGGTCCACAACTCATTTGGT
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 GATTCCAATTCCTTGGCTCAAAAGGAGGTTGGGTTGATCTAAGAGATGTTGCCAAAGCTCATATCATTTGCC
 TTTGAAAATGAGGATGCCAAAATCAAGAATATTGTTGAATTCAGGTAGATTTACATCTCAATCACTTT
 GTTGATATTATTAAATGATTAATTTCCAGATTTGAAAAGGAAAAATACCGATTTGATTAACCGAGTTTCAGAT
 AAATCTGTTATTGCTGAAAGTTTGGCTACTATTGATGATACCAATCTCGTGAATTTATTAGCATTTGAA
 TATTATAACCTTGAACAATCAGTTTATGATACTGTTGAACAAATTTGTTAATGCTCATAAGTTGTAA

YOL151W_homolog 343aa (SEQ ID NO 456)
 MSTPITVIVSGATGFIAQHVVKQLLAKNYQVIGTVRSTAKGDHLLKLFNNPQNLSYEIVEDVGTKGAFD
 KVLQKHGEAKVFIHLASPFHFNVTDVEKELIIPAVDTGTONVILQATYMEGNNTREKVVITSSYAAISTASK
 EADKNAILTEKDWNEISWQDALLNPNVNGYRGSKKFAEKAAWDFIKSNDNVKPSLSTINPSFVFGPQSFG
 SEIKQSLNTSSEIINSILKLPND SIPASKGNGVDVRDVAKAHIIAFENEDAKNQRIILLNSGRSTSSSL
 VDIINDKFPDLKGKIPVDEPGSDKSVIAESLATIDDTKSRELLGFVYNLEQSVYDITVEQIVMAKKL

YOR286W_homolog 546bp public: 1..546 (SEQ ID NO 457)
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 GCATTAAGAACTACACCAAGATTTTATAGTGTATTGACTGAAATCTCCAGAGGCCAAAGTATATAAATAT
 GCGGATGTTAAGGATGTGGCCGTACACCCCTGAAAACCAACCCCTGATTTCTGTTTACTGGATGTTAGAGAA
 CCAATCGAATTTGGAGATGGTCAATATACCAGGAGCTTTGAAATATTCATTAAAAAGTAGTTCUUGGUCBA
 TTGCAATTTGTCACAAAGAAGATTTCCAGAACATTTTGGCATTTCCCTAAACCAAGTACTGATAAAGAACTG
 ATPTTCTATTGCTCTTGGAGGTGTTAGATCTACTGCAGCTGAAGAATTGGCCCAATACTTTTGGTTATAAG
 AAAAGAGGAAATTATCTTGAAGTTGGGAAGATTTGGGTAAACATGAAAATAAAAGAACTAA

YOR286W_homolog 181aa (SEQ ID NO 458)
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 ADVKDVAVHPENHPUSVLVUVREPTTFQDCHIPCALNIPFKSSPGATILSRKDFQEHGFPKPSYDKEL
 IFYCLGGVRSATAEELANTFGYKKRCNYLGSWEDWVKHENKKK

VPL078C_homolog 702bp public: 1..702 (SEQ ID NO 459)
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 CCAATTGGTTTTCAGATACTTGTCTGCTCCACCTGACCCAAAAACAAAAGGCCAAATTCUATTCATTGATCCA
 TTACCACGTAACAACTTATTAATCTAAGACTGGTCTTTTGGCTACTTCAGCCGCTGCTGCCATCTATGGT
 ATTTCCAATGGATTATTTATCTATACACGATGAACCCATTTTGTCTGTCACTTTTGCAGTTTTCACAGCT
 TTGGTCCGCAAAATTCGTTGCTCCTTTATACACTGAATGGGCCGATGGTGAATCAAAAAAGTCAACGAT
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 TCATTTGAATTA AAAACAAAATTTGGCTGTTTCTCAGCAAGCTAAATCTGTTTTCGACTCTTGGGTACGA
 TTTGAACAACAACAAAGACAAATGGAACAAGAACAAATTTGCCAAAGAAGTCAATTGATAAAGTTGACAAA
 GAANTTCTAATCCAAATTTCCAAGACAAAGTATTGGCTGAATCTCTTAACGAAATCGAAAATTTGTTT
 GCTAAAAACCTAG

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YPL078C_homolog 233aa (SEQ ID NO 460)

MSMINRIALRSARFAMGMAFRPAPIGLRYLSAPADPKQKANSIIDALPGMNLLEKTCVLATSAAAAIYG
ISNGLFIIHDBTILLVTFASFTALVAKFVAPLYTEWADGEIRKVNIDILNOSRTNIIIEAVNKRIETVSEL
KNVVATTEDLFALSKETACFTEDSFELKQKLAVSHEAKSVLDSWVRFEQQQRQLFQEQLAKEVIDKVLK
EIANPKFQDKVLAESIINFETKFAKN

YPL085W_homolog 2490bp public: 1..2490 (SEQ ID NO 461)

ATGTTCTCCTTAAAGTNGAAACATGCATTGACCTTAGCTGATTATGGATTGATCAATGAATCACAGAGA
TATATTGATCATATTAAATCTAGTATCARGACATTGGGTAAACAAATCACCTTTTGGTCACGCCCTAATTTTG
CTTCATGAGTTTTCAGAAATTGATTATGAGAATCACTGAAGCTGGATCTGGAGATCGATCAAAACAACTGG
TTTCCCGCTAAGATTAGTCGACTCAATCTTGATAAGATCTGGGGACAAATTGATAAATTTATTGTTGGT
GGAGATGAACCTGAAAAATGCTAACAAATAACGATGGTAAATGGAACTGGCAATGCCAAGTCTACTGTTTTC
AATAAAATTTAGCCCCCTCCGTGTUGAGAAATGCATCAAGTGTGAATTTACACAACCTATGTACAACCTTCA
ATGATTAGGCAACCATCACATTTACCATATCAACCACAACAACACCGCAACCGCAACAGCAATTATTG
GATCAAGTTCCACATTGAAAGAAAACCTACAACCTGGATTCACCTCCGCAACACCAACCACTTAGTTGGTCA
CCATCAACGACATCAGTTAATAAATATTCTCCAAGTATTAAATCGAGTCTCTCGTCAAGCACACTGAAT
AAGTTTGA AAAATATGCCCCAAGCAACAATTCATCTCATCAATAATCTTAGTCTTGTTGAAGAAAGGTCA
GCTGTTACTACTGCTGATGGTCTCTGAATACCTTCACCAACCAACACCAACAGAGTATCAATGCCGTCAACA
GTTCCCGGTGCCACTTCCACCCACCAACACCCCGTAAGCACGCCACAACATGTATCTAGGTCTCCACGT
AGCCATCAACTGCACCAACCAACCAACATTAACCACTGCATTCCATCATGTTCAACAACCATCTGAGA
GATCCGTCACCAATTAGCGACACCAATCTACCTTTATAGCAATAGTGTGGCGGACAAATTTCTACTACG
TCAGTGGGTTCCTATTCTTAGTCAAATACCACTTGTGACAGACTCATGGGAAACAACCTTCTATTTC
AGTGTAAATTTCTGGAGATAGTATTGCAACAGTGTGGTTTAGGAGAACAAAGAGAAATGTTTTACCCCATCA
ACCGGACAAACAGGGAAACCTCTACAAGTGAAGTGAATACAAATGAGGAAGGTTATGGATTTCGCCGT
CACTATCATCATGATCAACCTGAAACATAACCGGAATCTCCAGAAATTAAGAGGCTTACAAACAACCAAG
TCCACCTAACCAAGAAATAGTAAAGACATTTCAATGATGTAGCATTGGATAGTGCTAAGATAACAGAA
CCTTCCACAGGAACCAAGAAAGAAACCGAAGCAATCAGGTAACTGTGGCAGCTGCTCCACCACCTCTAGCT
GCTCCAGTTTCACCTCTAGAAAAACAAATCTTCTAGATCTAATCCATATGCTCCATCTACAGATATT
GGTCTTATCACTAATGCAACCATCAGCAATAGGACAAACACCTAGTGGGAAACCAAGTGTAGAAATCA
GGAUCAAGAACTAACAGATATGGACCACCAACAGGAGTTGGTAAATAACCAACCACTATTGATGTTTCG
CCACCTTCCTGCTACTAATAATACTGGTAATGAAGATTCCATTACTATCTTTTCTATGGTGCCTATCAA
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GATGTTTGTGATGAAATAGTTTACGAGCTGATACATTAACAACITACAATAAATAATATGGTAAATATA
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GGAGCCGGAAGCTGTTACTGGGACTGGTGGAGCATTGATGGATTTCCTATACCAGGATCACTTGATGAA
ACTACTCGACCAAAATTTCTATATTGGTGGTCTACTAGAGGATTATTTTCTTCAAGATTATCAGAATCA
CAAAGTGTATTATATCAACAATATGCAATTGCTGATGATACAGTTGGTGTATTATTTCTATTATGGA
GAAGATGTGTAGATGATGAAGATGAACAAGCTAAGCAACAGAAACAAAAAGAAAGAGGACACAAGAA
CAAGAAATGAAAGAGAAAGCAGCAACAACAACAACAAAAAGCTGCAGCAAGGATAACAACAATAAGTGGC
GGTGGTGGTGGCAAATTTCTTAGCTTATTGGTGGTGGTGGTAATAATAAGAAACACATAATGATGCT
AAAGTTTATAAGCTCATTTAGGACAAAAGAACTTTTGTATTATGATGAAAAATTGAAACGTTGGATA
GATTAA

YPL085W_homolog 829aa (SEQ ID NO 462)

MLSLKLKHALTLADYGLINESQRYIDHINSSIKTIGNKSPEVTPNELLHEFQNLIMRITVVGSGDEONNW
FSGKISRVLNLDKIWQQIDKFLVGGDESKNGMNDGNGTGNCGSGSVFNKFSPSVSRNASSVNLHNYVQPS
MIRQPSILPYQPQQQPCFQQLLDQVHIERKPTTGFTFPQPPPLVGHPSSTSVNKYSPSIKSSPQQAQSN
KFEKYAPSNKSSHHNLSLVEERSAVTSADGPEYPIIHQHQQSINASTVFPVPLPPTFTVSMPOHVSRSR
SHQSHQPTLPPSHSHVQPPSRDRSPLATRIYPYNSVGGQISTTSVGSIPSQIPLGRQTHGKQPSYS
SVISGDSIAAVGLGEQLNVLPPSTCQPIGKTATSEVNRNEEGYGFGGHYHHDQPETITESPELRGTQQDQ
SSEAEISXDTSNDAVDSAKTPEASQRPREFYDSGNVAAAPPPLPAPVAPPRKTKSSRSMPYAPSTDI
GATSNAPSAIGQTFSGKFSVRKSGSRTRNGYGPPEGVGNKQPTIDVSPPSATMNTGNFDSISMFYSYGAYQ
NESSPPLKQPSQFDQTAVASAPAPHPPLQPOLAVFERVPTKTVANIDDSFDENSLAADTLTTYNNMFMNF
PYGSSPMGPTVATNGPGSVTSTPLILNQGSANMKLSNLSTLSVLTGAGTVITGIGGAFDGFPIPCSPDE
TTRPNSIFGGHTRGLFSSRLSESQSVLYQQYATAADTVGDYIPIMEFENDDEDEQAKQKQKEKEAQE
QELKRKQEQCCQKAAAKNNMNSGGGGGKFFSLPFGGGGNKKQDNEAKVYKAHLQKQNTFVYDEKIKFWI
D

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YPL190C_homolog 396bp public: 1..396 (SEQ ID NO 463)
 ATGCCAAGTACAAAAAGATCATCATCTACTGAATACTCCCATAAAGACTCTAAAAAGAAAAGTCAAACTA
 GATTATGTAAATCTCAAACCATCAAAACCTTATATGTCAAAAATCTAAATACCAAAATCAATAAGAAA
 ATTTTATTGCATAATTTGTACCTATTATTTCCTGCATTTGGAGATATCATTTCTATATAATCTACAGAAAT
 GGTTTTCGCCTTTATAATATTTAGTAATTTAAATCTGGCTACATTTGCCGTTGACAAATTTGAAAAATCAA
 GATTTTTTTGACAAACCACTTGTATTTAAATATGCTGTCAAGGAATCTAAAGCTATTTCTTCAGAGAGAAA
 CAAAACTACACATGAAAATGATGAAGAACTGATGCCACTCTATGAATAA

YPL190C_homolog 131aa (SEQ ID NO 464)
 MPSTKRSSSTEYSHKDSKKKVKLDYVNLKPSQTLVYKMLNPKINKKILLHNLVLLFSAPGDIISINLQN
 GFAFIIFSNLNSATLALRNLKNQDFDKPLVLNYAVKESKAISQEKQKLQDENDEEVMPSPVF

YBR112C_homolog 3243bp public: 1..3243 (SEQ ID NO 465)
 ATGTATGCGACAGCCCATACAATTAAACAACAACAACAACACACACACACACACATCCACCACCACCTTTTA
 AACGGTGGACTACATGCAAGTGGGGCTCCTCCAAATCCCATGAAGCAGCAGCTATTCTCAGCAACAA
 CAACAACAGCAGCAAAACUACAAATGGTCTTGGTATGATTTTTCGCCGAGCTGCAGCTTCTGCTAAACAA
 CAGCTGTCCAAAGCCAGCCCAACCAACAACAACAGCAGCAACCAACAGCGATTACCTAGTTTCAGCTTCT
 CTTAATGAAACTACAGTATCAACTTGGTTAGCCATTGGTTTCATTAGCCGAGAGTTTAGGTCACATTTGAA
 CGTGGCAAGCTTTCTTACAAATTCGGCTTTGAGCAATTCACCAATAACCCAGATATTTTAGTCAAAATA
 GCAAAATACATACCGTTCAAAGATCAGTTTCTTAAGGCTGCTGAATTTGTATGAACAAGCTCTTAATTTTC
 CATGTTTGAGAATGGTGAACCTTGGGGATTATTTGGGTCAATTTACTTTCATGTTGGAAATTTGCAAGA
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 ATTGGTATTTTATATACACATATAGGCTCAATTAGAATATGCTGAAGAAGCCTTTGTGAGAGTPTTGGAT
 TTGGATCCAAAATTTGACACAAGCCTAATGAATTTTATTTCCGTTTAGGGATCATTATATAAGCATCAAGGT
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 CATCTTTCTGTTTCAAATTTGGTTTCACTGTATGAACAACAAGGATTGGAATGGTGCCTAAGGATGCTTAAT
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 GCAGAAATCAAATCCATCAACACCAGCTAATGGTGTCTGCACCACCAACATAAGCUAATTCUAAACAGATTTT
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 TTGGTTAGAGTAGAATGATTAGAGGTGATTTTCACTGCTGCTTATTAAGCTTTTCCAAACAACTTGTCAAT
 CGAGATGCAAGAAACCCAACTTTCTGGTGTTCAAATTTGGTGTTTTGTACTATCAAATAAGCCAAATATCGT
 GATGCATTTGGATGCTTATACAGAGCCATTAGATTTAAATCCTTATATCAGTGAAGTATGGTAATGATTTG
 GGGACTTTTGTATGAGACTTTGTAATTAATCAAATTAGTGTATGCACTGGATGCATATAGACAAGCAGAAAGA
 TTGGATCCAAAATTAATCTCTATATAAGGCAAGATTGAAACAATTTGACAAAGTATCAACAAGAAGGTAAT
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 ACTCAACAACAACAGCAACACAAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC
 CTGCAACTTCAACCTTCAACCAACAGCAACCAACCTCAAACCCCAATCAACAACCACTTCACTTCAACCA
 TCTTCAATTTGCTCTCTCAACAATCCAAACCAATTAATCAACAACCTTCAAGCTTCAAGCTTCAAGCTT
 CAAAGTTCAACCAACCACTTCACTTGTATGAACCTTGGGACAACCCGGGGCAACCAACCAACCAATTTGCCA
 CATCTTCCACACATACCCAGCAACCTTCTCAAAATCAAGAAAGCCTCCAACTTCAAGAAUAAACCAAT
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 CAACAACATCAAAAATCAACTGCTTCAATTAGCTCAATTTGCCACCTACACCAATTTCTAAATCTCCAGCTAAG
 CCACATGGTGCACCTCAACAAGAACTGGTTTACCCGATTTATTACAAACTCTGCTAATATCATATCA
 GCTTCACTCAACATACCTCAACCAACAACAATATCAACAACCAATATTGCACCTGTTAGACAAGAA
 CAAGTTAACCATGTTCTTCAATTTATCTGGCTCTTAGACCAACTGAGACCAACCTTCTTCAAAATCAAC
 AACCCAAATGAGTCAACCAACAACAAGTTCCACAACCTCAAAAGCAAGCAACCTTAAACCAAGAGGCTACT
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 GCAGCAGCAGCAGTGTACGACCAAGCTTCTGCTCCAGTTGGTGTATATAAAAAAGATACTGTATCTACT
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 AATGTTGTTCAAGACAAGAAAGTTCCCGACACCGAGCAGATCGTTTCAACAAGTTGAAAAACCCGTGGAG
 TCACAACCAAGAGTTACACCAGCTCCAAACCAAGCTCCAGCTCTTGCAACCAACCAACCACTGAACCTGCA
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 AATGAAGAAGAAAAATTTTAAAGAGGCCAAGCTGTTGAAACGACTACTGAATCTTCAACCAATTTAAACCA
 CCTGTTGAGAAAGAAAAATGAAAAAGTTTGAAGTTACCACCGCCACTGGAAACCAACCAAGTTTCAAGAAAGACA
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 TCATCAAAATCAACAGCTCAAAATGAAGAAGCAAAATCTGGAGAACAACTAAAAAAGATACACCAAG
 ACAAGTCCAGCAAAACAAAGGGAAGTTAAGGAAGTAATACCAATCATCTACAGAACTGTATCAAAACCA
 GATGTTGAAAAAGCAATTAAGAGAAACAAAGATGAAGATGAAGTTGAATGGCTGATGAAGATGACCTC
 AAAAAAGATGAAATCCAGAACCTCCATGAGAAAGATTGAAGAAAGATGAAATTTATGATGATGAATAG

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YBR112C_homolog 1080aa (SEQ ID NO 466)
 MYATAHTIKQQQQQQQQCHPPPLNGGLHASGAPPNSHEAAAIAQQQQQQQQQHNGPQGMIVAAAAASANQ
 QAVQARAQQQQQQQQRLPSSAALNETTVSTWIAICSLAESLCDIERATASYNSALRHSPNNPDILVKI
 ANTYSKDKQFLRAELYEQALNPHVENGETWGLLGHCYVLMCLNLOKAYAAAYORALFYLENPNVPKLWHG
 IGILYDRYGSLEYAEEAFVFEVLDDPKNFDKANEIYHRLGIYKHQSKLOPALECFQYILNPNPHPLTQT
 DVWFQIGSVYEQQKDWNGAKDAYEKVLQINPHHAKVLQQLGCLYSQAESNFPSTPANGAAPPPIKPFQQDL
 TIALKYLKQSLVDQSDAHSWYVLCRVEMIRGDPFAAYEAFQQAQVNRDARNPTFWCSTGVLYYYQISQYR
 DALDAYTRAIRLNPYISEVWYDLGLTYETCNQISDALDAYRQAEERLDPNPHIKARLEQLTKYQQECN
 THFPQFPSSSQPRFLQGHVLESTQQQQQQQPPPPPPQQQQQQLOHQSSQSPQPPQTSQSPSLLQHO
 SSLPQCIQPLHQQAAPLVNQQQSFPPPHLMNLGQPCQQPQQLPPLPHPTQQPSQIQEKPPTQEQPH
 YQPPPPPPHQQQSSQSPQPPHQFQHTQNSPQLAQPLPHHSNPPAKPHGAPQQTGLPDLHNSANIIS
 APSQVFPQQQYQOPHIAFVRQEQVNHVPSIYSAPRFTETTLPOIMNPNESITTOVPQLKKEEPKPEAT
 VSAPVFEATKVQDQVTIQESAPAAAAAVSAPASAPVGDIKTITVSTTTTATSTTADAVPVSVSQVGEAP
 NVVQEKKVPDTEQIVSQVEKFVESQPEVTPAPTAPALATAPEPAPTDKDVVMAPSASATPVTQSIVE
 QNTRVSEATKAPESNGKHLEDKNDDEKILKRPTVETTTESVVPVNPVEKENEKVEVPPPPSEQPSSEKR
 EKEVNGSLKKPLENESKVDLPOFSSNLTACNEEAKSGEETKKITPKTSPAKQGEVKEVIPSSSTETVSKP
 DVEKDNKEKDKDEDEVMADDDVKKDLENPEPPMRKIEEDENYDDE

YDR145W_homolog 1536bp public: 1..1536 (SEQ ID NO 467)
 ATGGAAGAGTTCAATCAAAATTAGACAAAACCTCACTGAAGTTCAAAGGAGGGTTCAAGTTGTTGGAACAA
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 GCAAACTTCCAACAGTATCAAAAAGTAGGGATTATATATAGAAATCAGTTGGTTCTTCAAGCTAAAGCA
 CAACAACACAGACAATTCACACAGCGACAGCAACAACAGCAACAGCAACAGCAACAGCAACAGCAACAGCA
 AAATCAGCTCAGAACCAGAACCCAGAAATCAAAACCAAAACCAAAACCAAAACCAAAACCAAAACCAAAAC
 CAATACAAAGGAGTGCAATCTGCTGGACAAACACCTTCAGCAACAGAGCTTTTCGCCACAGTTGCAGGCT
 GTACAACAACAACAATTTTGGGCAACCTGCAACACACACAGCAGCAGCAACAACAACAACCTTAGAAAT
 GCGAATAAAAGTGCACTTCAAGGTCAAGCTCCTTCACAGCGCGCCACTCCTTTACCTCTTCGGCCAAACA
 CCTCAGAGTCAACCTACAGCACAAGCGGGTGTCTTCACAGGCAGCTACACCCAGGATTTCAGAGCTTCT
 CAACCCACACCATCGCAAACTTCGAGAACTGGATCAGCTCTACAACAAGGGCCACCAAGTCGACAGGCA
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 TCAGAAAAGGCCACTTCCCCAACAACCTGGAAGCGGAACAGCGAAGAGTCTTAGTGTTGCTGCTACTCCT
 CCTCAGAATAATGGCACTGTAACTGCCCGGTCTGCATCACCCTGTTGCAACTACTACAGATAGTGCTACA
 ACTGGAAGCTCAGGAACCTCCCCAACAACAATCAAGGTCACGATCTGGATCATCGTTGAATTTGCCGCGC
 ATTACAGCTCAGTCTGTCCCATCATTCGCCAATTTTCGAGTTCATTAATGTAACAACCCCCACAATCACC
 ACAATTAAGTAGTATCAATGATACGAGACCCAGTTTGAGTCGCAAGCAGCTGCCAATCCTATCAGTATTTTA
 TTAGATACACCAGCGATCACAAAATTCCTTACTTTTGATATCGAAGGACACACTGCTGCTCATTGATTCT
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 GGGGATGGTAACACCAAGTATTCATCGCAATCTCGAGCAATTTTTCTTGGATTGCGCTGATGAATTTAT
 CATTCACTGACAAGTTTTGCTTGTCCGTTAGCAAAACATAGAAAGGTGGATAGTATAGAGGCAAGAGAT
 GTTCAACTACATTTGGATAAGAATTGGAATATCAAGATTCTGTTTATGCAATGGATGAGATTTCGAAAC
 ACAAGAAAATACAACTAGTAACTATTATAGTCAGAAAGTACAAAGCTCTCCAAAGTTTCGAAAGCTGTG
 AATGATGATAATGCTTAA

YDR145W_homolog 511aa (SEQ ID NO 468)
 MERFNCIRQKLTEVQRRVQLLEQTKKTGNVTPEIQIQIDKEIIECKAKFQQYQKVCYIRNQLVLQAKA
 QQRLQQRQQQQQQQQQNNNLKSAQNQNQNQNQNQNQNQNQNQIQGVQSAQPTPQQQSFSPQLQA
 VQQQFMGNSQQQQQQQQQLNANKSALQGQAPSQAPTPLFVVRPTPQSQPTAQAGVASQAATPGERAS
 QPTPSCTSRGTSALQORAPSRQASSTPQSQFPPLPSESRIIPSAITSEKPLPQQPGSGTAKSPSVAATP
 AQINGTVTARSASPVATTTDSATTGRSGTPQQQSRSRSGSSIMLAGITRQSVPSLPISSSINVKQPTIT
 TFNSINDTRPSITGGGAANPMSITLDTPTTKLPTFDIEGDTGVLDSSSTSGRVLNKRKLGLDLINPLQVDE
 GDGKTSIDGNVEEFLDLADEFIHSVTSFACRLAKHRKVDSEARVQLHLDKNWNKIPGYAMDEJRN
 TRKIQPSNSYSQKVGQVEVSKAVNDDNA

YDR154C_homolog 333bp public: 1..333 (SEQ ID NO 469)
 ATGATGTGCTCCAAAGACTGCTCAAAATTCAGAGCTTTATGTACTGGTGAAAAAGGTTCTGGTTACA
 AAGTTCTATCTTCCACAGAGTCATCCCACAATTCATGCTTCAAGGTGGTGATTTACCAACTTTAAGC
 GTACTGCTGGTAAAAGTATTTACGGTACCAATTTGCTGATGAAAACCTTTGTCAACACACATGACAGAC
 CAGGTTTGTGTCTATGGGCAATGCTGGTCCAAACCAATGGTTCCCAATTTCCATACCACCGTTTC
 CATGCCCATGGTTGGATGGTAAACAGTTGTTTTCGGTGAAAGTCACTGATGGTTTAG

YDR154C_homolog 110aa (SEQ ID NO 470)
 VMMSFQRSSKISELYVSVKKVLVTKVLPSTESSHNSCFKVVISPLITVSVVAVFTVPNLSMKTLSRDYTD
 QVCCLPMSVQCPMVPNSSLPFPHAGWVWNTLFSVKSSNV

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YDR216W_homolog 4257bp public: 1..4257 (SEQ ID NO 171)

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 GCGCCCTACCTCCCGCTTCGACTACCAAGAATTATAAGCACAAAAACAGAATACCAATACTGGAACATCC
 ATGTGCGCCAAAGTAATTCAATAAATTCACAAACAACAATGCCAGCAGCAGCAGCAGCAGCAGCAGCAGC
 TCAAAAAAGTCCAAAGACATCCCATTAAGAGTGAAGTGCATTTTGCTACAACCCCTCTGGGAAACCAAG
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 CACACAAGGAAAAACCATTTAGTTGTGGTGTTTGTCAAACGCAAGTTTATGTCGTGAGATTTATTGCTA
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 AATCTCAGGATGGGGACGATGATGATGACGATGATGACGACGATGAAGAAATGCCAAATTTCTCAAGAC
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 ATTCTATCAGCTACCAATTAC TGGAGTGTGATAACTCCAACAAGGCTCTAGAAGAGGTGCATCATTTTCT
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 GTTGAATTTTCAACCCCTCAATTTCTTACCATCTTCATTGGATAATGAAATGACGTGGCTAAATAATATT
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 TCAGCTACCGATATGGGACAAACAAGATCCGAAAGTGTAAACAGTTTAAACACCTCCATTTGATGGTTCC
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 GTTTTGGCAATTATTAACAGCGACCAATGGGGGCTTCTTGGCCCAATACAAAAACGATGCTGAACATCT
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 ACGAACTTTTTTGTGATGATGTACAATCTACCGTTCACTTTCTCAATCAATGATATTAATTTGGCA
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 GCCTTTGATACTGATTTTGGATATTTGAATATGGTAATTAATGGTTATGCCAAAAAAGAAAGATTTTAA
 CGATTCACTCATCATGAGTTGGGATATGATAAAGAAAACACGATGTCAATTTTGTATAAACAATATTTAA
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 TTTTGAATTTGAGATATCAAACTCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG
 GCCTTATTTATAAAATTTAGAACAAGAAATTCACAAACTTTGATTTTCAAAATGGGAATGATTTATCTTCA
 QATCATAATACAAATACAAATACCAACCAATACATTTACTACTACTACTACTACTACTACTACTACTACT
 CAAAATCAGCATCATTACAAAGATTTGGATTGAAGAAAGACTTTATATATCTTAAAAATGGGAGAAAT
 GTTTTGAATTTATATTTATGATTTAAATTTAAAGTTTTCGGTATTTAAGAAATTTGGGAGATAGTTTATCA
 GAAATTAGAAAAATTTTAAATTTGATAATGAATCTACTTTGAATGGTTAA

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YDR216W_homolog 1418aa (SEQ ID NO 472)
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 MSPSNSTNSTNNNAAAAAATTTTSKRSKNTPIRIATAGTTTSGKPRI.FVCQVCTRAFARLEHLRRHERS
 HTAKKPFSCGVCCQKFSRRDLLLRHACKLHAGCTDAITRLRSKSIKKSQDGDGDDDDDDDDDEEMANSED
 ENHDHDESGNASTKNGKKDKKDPPEFNLNLFNSKQKPTKANTTKSKVAKLS.ITTSRKNSTNPTKNSSS
 LHKQVLDQRQKAAVNPKIVSESTKIVSGTWSGVSIPTFSRRGASFSAQSGANYAINIPEFNDIYPOSDW
 VEFSTPQFLPSSLDNEMTWLNNIPNIEGLSDSVSAANLMRQNSITNSADIVEPPVNVSQHGSPFSHQSTF
 SATDMGQTRSESVNSLNTPTFDGSYMMPTVTITSNQETQNGVAAHHHHQOQQQHQOHHNHQHPNQSSSLGLS
 RNDMLSEDHYGYSFYDIPENILNFMESISTTSNAMSSGPIONFKPLSPITQETIEHEITPRIDGRIGDF
 QNNNNNTNDNP.IHQNINYDINFIHTIDSIGQDVTSKEMPOCYSFYCDMNVSAATSSANDYNSPNNIVSTSQ
 QMNOFALHNQSSHPSCASPHLNQAMNMKMLKNVSSNKLFTNHIRKHMINKALGKYPISGIMTPTIPTSNF
 KIDPYLSVFIQSPFLAILPFIHPKLNVEIMAMTGMEDINNESARVCLPLLTATWGALLANNKNDAEHL
 YFASRRTYHYTLESRKTNTSTNDKNYKNGKDKSSSGNPLWLLQSLMLSVLYGLFSINENNVIIVLRQLNA
 LNSLVKTSIKNKGPIFFSNNGEDEELYNKLNSHDNGTSLFSNNLNDEMRYKNMINMQSQTRIVFIYRL
 TWPLMMYNVPLTFSINDINGLAVISKDEETLWNPKNYQEFQEFSHKNNKTLDDYLNKNKNEPIIFRELL
 LTVTKPGTISDSNISPETEKKVTHQLQNLCYGFNCLVREGLYELKQYQEMKEVDITFKVLDDYLTKFYPTND
 GLGFNCFRLPANKDLEKIDYALLVEFTKISSIIDLKLKKEQSWLKNYQDLTQNYHRELLDAHSTGNPLNS
 INDYDYLKLADUCISVLKLILFKVEDSNNSNSRNSKNDPTNEINNKLNMMNNNNNNNNNSNGDQLIS
 AFOTDFGYLNMNDNGYAKKEEFLRFTLDELRYDKENTMSYFDKILKLIIFEEVEKSSNLIQAQMLFHAF
 SVLSIFSVMRKNDNNSSPFANTGLIFELNHRYSMVLRLLERIETFIKLRVQTSAGGGGGGVNNNNNN
 ALSIKLEQEFINLYLYNGNVLSSDHNTNTNTNTITTTTTDNGTKQNHHSQDFGLEKTLYLKMGEN
 VLNYIYDNLKVCVFKKLGDSLSSEIRKYLIDNESTLNG

YDR224C_homolog 393bp public: 1..393 (SEQ ID NO 473)
 ATGGCCCCAAAGCAGAAAGAAACCAGCTTCCAAAGCTCCAGCTGAAAAGAAACCAGCTGCTAAGAAA
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 AAGCTTTTGAACAAACACATCCAGACACCTGGPATCTCCCAAAAGGCCATGTCAATTATCATATTCCCTT
 GTTAAACGATATTTTCGAAAGAAATTGCCACCCGAGCCTCCAAATTAGCTGCTTACAATAAAAAATCCACA
 ATTTCCCGCTAGAGAAATCCAAACTGCTGTTAGATTAAATTTGCCAGGTGAATTGGCCAAACATGCCGTT
 TCCGAAGCTACUAGAGUCCTCACAAAATACTCATCTGCTTCTAGTTAG

YDR224C_homolog 130aa (SEQ ID NO 474)
 MAPKAEKKPASKAPAEKKPAEKKTASIDGAKRKPKARKEFYSSYIYKVLKQTHPDTGISQKAMSIMNSH
 VNDIFERATEASKLAAYNKKSTISAREIQAVRLILPGLAKHAVSEGTRAVCYSSASS

YDR342C_homolog 1653bp public: 1..1653 (SEQ ID NO 475)
 ATGTCATTAGATAATTCAACAGAAAACCGTGAATTTGGAAGAAAAGGAAGAAATTCCTCAAAGCAACCAACAT
 AACGAACAAGGCGAACAAACAGAGAACAAATGAGCATATACCTACTTTGCAAGATTAACCATTTGAAGGAA
 TATATATAGGATATTAGTATTTTGTGTTTCCCTTATTGCTTTTGGTGGTTCCTGTTTTCGGTTTCGATACCTGGT
 ACCATTCTCGTTTCATTACATGACTGACTTTTTCAGAAAGATTTGGTGGTACTAAAGCTGACGGTACT
 CTTTACTTTTTTCCAACGTTAGAACTGGTTTATTGATPAGTTTGTTCATGTTGGCTTGTCCCATTTGGTGCA
 TTATTCTTTGCTCAAAGTCCGCTGATATGATPAGTAAAGAGTTGATCATGACTGCTATGATCATTTAT
 ATTCTTGGCTATTATTGTTCAAATTGCTTCTCAACATGCTTGGTATCAAATCATGATTTGGTGAATTATC
 ACTGGTCTTTGCTGTTGGTATGTTATCAGTTTCTGTCCATTATTATCTCAGAGGTTTCTCCCAACAT
 TTAAGAGGTACATTAGTTTATTGTTTCCATTGATGATTACCTTGGGTATTTCTTGGGTTACTGTACC
 ACTTAACGCTACTAAGAAATATTCTGACTCCAGACAAATGGAGAAATCCATTGGGTTTATGCTTCTCTTGG
 GCCTTGTGTTTGGTTGGTGGTATGGTAAGAAATGCCAGAAATCTCCACGTTACCTTCTCCGTTAAAGATAGA
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 GAACTTCAAATTAATCCAAGCTGGTGTGTAAGAGAGAAAGATTGGCCGGTAAGGCATCTTGGGGTGCTTTA
 ATCACYGGTAAACCAAGAATCCCTTGAAGAGTTATTGTTTGGAGCTATGTTGCAATCATTGCAACAATTG
 ACTGGTGAATAACTATTCTTCTACTACAGTACCACCATTTCAGTCTGTGGTTTAAATCATTCCTTTC
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 TTGGGTAGAAGACTCTGTTTATTAACTGGTTCCGTTGCCATGTCCTATTCTTTCTEAAATTTACTCATTG
 ATTGGTACTCAACATCTTTTACATTTGATCAACUAGGTGGTCCAACCAAGAAACCAGATGGTAACGCTATG
 ATTTCATTACTGCATTTTATGTTTTCTTCTCGCTTCTACATGGGCTGGTGGTGTACTCCATTGTT
 TCTGAACTTTATCCATTAAAGTCAAGAGTAAGGCTATGCTTTTTCATTAATGCATGTAACCTGGTTGTCG
 GGTTCCTTCTTCTTCTTCACTTCATTATCACTGATGCTATCCACTCTATATATGGTCTTGTGTTT
 AIGGCTGTGTTAGTGTTTTCCATTTCCTTGTGTTTACCTTATGATTTACGAAACTAAAGGCTTACTTTA
 GAGGAAAATGATGAATTAATCTCTACCAAGGTTGTTCCATGGAATCAGCCGGTGGGTAACACCTTCT
 GACGAAGAAATGGTTTCTGTGCAAAAGGCTATACTGGTGATATCCACCTCAGATGAAGAGCAAGTTTAA

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YDR342C_homolog 550aa (SEQ ID NO 476)
 MSLDNSTENRDLBEKEEIPKXEHNEQGEQENNMNHIPTLEDKPLKEYIGISILCFLIAFGGFVFGFDTIG
 TISGFINMDFLRFRFGGTFKADGTLYFSNVRTGLLIGLFNVGCAIGALFLSKVGDVYGRRVGINTAMITY
 IVGIIVQIASQHWYQIMIGRIITGLAVGMLSVLCPLFISEVSPKHLRGLTLVYCFQLNITLGLFLGYC
 SYGTTKYSDSRQWRIFLGLCFAWALCLLGGVVRMPESPRLVVGKDRIDDAKISLAKTNKVSPEDPALYR
 ELQLIQAGVERERLAGKASWGALITGKPRILERVIVGGMLQSLQQLTGDNVFFYYSTTIFKSVGLNDSF
 ETSIILGVINIASTFVGIIYAIERLCRRLLTGSVAMSICPLIYSLIGTQHLIYDQPGGPTRKPDGNAM
 IFITALYVFFFASTWAGGVYSIVSELYPLKVRSKAMGFANACTNMLWGFLISFFTSFITDAIHFFYYGFVF
 MGCLVFSIFVYPMIYETKGLTLEEIDELYSTKVLVWKSAGWVPPSDEEMVRAGYTGDIHADDEEQV

YDR343C_homolog 1641bp public: 1..1641 (SEQ ID NO 477)
 ATGTCCTCAAGACAACGTCCTCATCAACATCTACAGCTGAGGCTGTAAATAATGAAATCAAAGTCAAACAT
 GAAATTCGACAAGAAGAACAAGCTCATACTAGTTTAGAAGATAAACCCTGTGAGTGCCATACATGGGTATC
 ATCATTAAGTGTTCCTTATTCGCTTGGTGGTTTCGTTTTCTCTTCGATACTGGTACTATTTCCGGT
 TTCAATTAATATGTCTGACTTTTAGAAAGATTGGTGGTACTAAAGCTGACGGTACTCTTTACTTTTCC
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 AAAGTCGGTGATATGTATGGTAGAAGAGTTGGTATCATGACTCCTATCATTTGTCTATATTGTTGGTAT
 ATTGTTCAAATTCCTTCTCAACATGCTTGGTATCAAGTCATGATTGGTAGAATTATCACTGGCTCTTGCC
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 TCCGTGTCTGTTTCCAAATGATGATTACCTTGGGTATCTTCTTGGGTATTGTACTACCTATGGTACT
 AAGAGTACTCAGACTCTAGACAATGGAGAAATCCATTAGGTTTATGTTTTGCTTGGCTTTATGTTTG
 GTTGGTGGTATGGTTAGAAATGCCAGAAATCTCCAGCTTACCTTGTCTGTAZACACAGAAATGAAGATGCT
 AAAATGTCATTGCTAAATACTAACAAAGTTTCCCCAGAGCACCACGCTTATACCGTGAACCTTCAATTA
 ATTCAAGCTGGTGTGAAAGAGAAAGATTAGCCGGTAAGGCATCTTGGGGTACTTTATTCAATGGTAA
 CCAAGAATCTTTGAAAGGGTTGTTGTTGGTGTCAATGTACAAAGCTTACAAACAATTGACTGGTGATAAC
 TATTTCTCTACTACAGTACCACATCTTCAAGTCCGTTGGTATGAATGATTCTTTCCAAACTTCTATC
 ATTATTGGTGTTAATAACTTTCGGTCCACTTTTGTGGTATTATGCTATTGAAACAATGGGTAGAAGA
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 CATCTTTATATTGACAAACCAGGTGGTGCTAGTAGAAACCAGATGGTGATGCCATGATCTTTATGACT
 TCACTTTATGTTGTTCTTCTTGTCTTCTACATGGCTGGTGGTGTCTTACTCCATATATTTCTGAACCTTAT
 CCATTGAAAGTTAGAAGTAAGGCTATGGGTTTAGCTAATGCTTCCAATTGGACCTGGGGTTTCTTAATT
 TCTTTCTTTACTTCTTTTACTGATGCTATCCACTTCTACTACGGTTTCGTCTTTATGGGATGTTTA
 GTTTTCTCCATTTTCTTTGTCTACTTTATGGTTTACGAAACTTAAAGGTCTTACCTTGGAGCAATTTGAT
 GAATTGTACTCCACCAAGTCCCTCCATGGAAATCAGCTGGTGGGTGCCACCTTCCCAAGAAGAAATG
 GCAACCTCTACGGGATATGCTGGTGAATGCCAAACCAGAAGAGGAACACGTTTAA

YDR343C_homolog 546aa (SEQ ID NO 478)
 MSQDNVSTSTAEAVNNEIKVKDEFQEEQAHSTLEDKPVSAIYIGLIIMCFLIAFGGFVFGFDTGTISG
 FIMMSDFLRFRFGGTFKADGTLYFSNVRTGLMIGLFNAGCAIGALFLSKVGDVYGRRVGINTAMIVYIVGI
 IVQIASQHWYQVMIGRIITGLAVGMLSVLCPLFISEVSPKHLRGLTLVCCFQLNITLGLFLGYCTTYGT
 KYSYDSRQWRIFLGLCFAWALCLVAGMVRMPESPRLVVGKDRIEDAKMSLAKTNKVSPEDPALYRELQL
 IQAGVERERLAGKASWGTLFNGKPRIFERVVVGVMQLQQLTGDNVFFYYSTTIFKSVGMNDSPQTSI
 TIGVINPASTFVGIIYAIERMGRRLCLLTSVAMSVCPLIYSLVGTQHLIYIDKPGGASRKPDGDAMIEMT
 SFVYVFFFASTWAGGVYSIISELYPLKVRSKAMCLANASNWTWGFELISFFTSFITDAIHFFYYGFVFMGCL
 VFSIFFVYFMVYETKGLTLEEIDELYSTKVLVWKSAGWVPPSEEMATSTGYAGDAKPEEEHV

YDR544C_homolog 1700bp (SEQ ID NO 479)
 CTAAAGTCCAAAGTTGGTTCAATTTTGGCAGAAAAAGAAAGGAAAMNTTCACTGGA
 CCTGATTCAATTTGCTGAAGATGAATCATTATCTGAGGTTTCTTTGCCACCTACAAGAACT
 AGGAATTCATCGGTGTTGTTCGCGAGTAACCTCAACTAGAAGATCTTTTATTGACCGCTTC
 CATAGAGATGAGTCTAGCACGTGGCAATAGCAGACAACATGAGCAGCACCACCACTCTTG
 AGTGATCCTTTGCCCTACCGCAGAGAAGCCCTCAACCCGAAATTTCCCAATCACCAGAAGCT
 CCACAGGCCCAATCACCTAGAGCCCTGATCAGAAAGTAATAAAGAACTGTTCCTACCTATG
 CAAACCGGGTCCGAAAGGAAAGGTGAAATCAGCAGTCGAGAGTTGATGTATCCTCTCAA
 AACTTGTACCCAGTTACTCCTACTCAGGATGGATTTCGTGGTTCTGTAAACCATTAACCA
 GAACCTGTTGATTTCTCCAAATGTGATTAAATACAAATGACTCGGAAGACTCTTTCTACASAA
 GAACCTAGAGCTCGTTACTTTGAAAAACACAATTTAGAAGTACAACCTGTATCTTCCCCA
 TTCCTACTCAACCCGCCAGCACCTGTGCCACAGAAATCCACATCTACACAAAGCAGTGA
 GGCATTTACTCGTTTGAAGCGGGTGATGATTCCAACTCAATCTCGGCTACTCCAAGATCC
 GAGCAAAATGTGTTTGGACAGATGCCAGACCTCAAAATTTGTCTCCTGAAAAGACTCTTGCT
 CCACCACCACCACCTTTCGAGAAATCTTTTGCACCATGAAGAACCACTGTAAGGGATTCA

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CCTCTTTTCCACAATTTACCTGCTGCCTCCCATTTCTGGAAGAGACTCGGTAATGGCTCCA
 TTAGCAAGTCAAGACAGGGGTCATTGCTTGTGAAAAATGATTTCAAACACGAAACTTGC
 GCATCCACCCCTCGGATTEAGCTCTTCTATTGCTGAAGTCATCAATGCCAGCTTTAAGGAT
 GGACAETTCATTAAATCACAAGTAGTTGGTCAAGTCCCTTCATTATAATGGTAATGCT
 TCCGATCCACTTGTGGTCACTATTCCCTAATAGTTTTCGATAAAGTACTCGTGAACAAGACT
 TTTATTGAGCATTTAGGTCAAAGCAAGTATAAACTGAACCCAACTTCAAATTACGCTCTAAA
 ACTCTTGGTGGGTTGAAATATCTTTTGAAACCAACACAGGTACCAGTGATAATTCAACAA
 ATATGGAAATTTGAACCTCATCAGTCAAGTTTGATGGTTAGCATTCGTTCAACTACAGCT
 TTGGTATTGGAAAAATTTTGTGTCTCTGTAGCTTTGAATCAAGACATTGAAGCAACATCT
 GCTTCTCTCAAAGCCTCAAGGTGCGTTTAATAAAGAGAAAAACAGAATAACATGGAGATAT
 CCACAGTCCCTCGCATTGAATGGTGTAGAGCGTTTGATAGCTAGATTTATGACTAATGGA
 TTGGTTCCTCCGAACATGAGTCTGGTGTGCAGATTAAATTTCAAGTTAAGGATCCACAGTC
 AACTACTGTACTATTTACAGTGAGAATGCCGAAGAGATTCTACGTTTAGAATTTGGTT
 AGCGTAGTTATAGTGGTATCTTTAAGTTATCTGTTTGGAGATTAGTCTCTTGTGGAAT
 TGAAAAAAGAAAAACGTGA

YDR544C_homolog 543aa (SEQ ID NO 480)

LKSKVCSIFGRKKKKEKFTCADSLAEDESLSEVSLPPTRTNRNSSLRSNSNSTRRSFIDRF
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 QNGSERKGENOOSRVDVSSOTLSPVTPTHDGGGSGVKPLPEPVDSPNVIKYNDSDOSSTE
 ERRGSLLEKHNLEVQPVSSPFTTQPPAPVPQESRSRQSSDGIYSFEAGDDSNPISATPRS
 EQNVFGQMFDPNLSPEKTLAPPPPSRKVLHHBEPTVRDSALFINLPAASIIHSGRDSVMAF
 LASQDRGMSLLKNDFKHENLASTLGLSSSIAEVINASFKDGLIKSQVVGZVAFNYNGNA
 SDPLVVTIPNSFDKVLVNKTFIEDLGQSKYKVNPTSTTSKTLGGLKYLKPTQVPVLIQQ
 IWKFEHQSSLMVSIRSTTPLVLENFVVSVALNQDI EATSASSKPOGAFNKEKNRITWRY
 PQSLALNGVERLIARFMTNGLGSEHESGVQIKFQVKDPQVKYCSZYSENGEBIPTFRNLV
 SGSYSGHL

YEL071W_homolog 1584bp public: 1..1584 (SEQ ID NO 481)

ATGCACAGCATTAGTACACACTGCTCCGTATTGATTAGACGAAACAACGTGGCATGTAGATTCACT
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 CAAAAAGTCCAACTGATGCAAAATCAAGCAACTTGAATCTCAAGACATCCAATACCTTAAAGTGTA
 TTACCTGAGAAATCCATTATTAAGTGAAGAGACTTATTGTTTTTCAACGAAGACTGGATGAGAAAG
 TATAGAGGTCAATCACAATTGGTTTTGAAACCGAAAACCAACGACAGTCCGTTCTATCTTAAAGTAT
 TGTAAATGATAACAGCTAGCTGTTGTACCACAGGGTGGGAATACGCGGTGGTAGGTGGATCTAAATCCA
 ATTTTGAAGTAAATCATCATTTCCCTGCTCGGCCATGAATAAAATCAGATCGTTTGAATCTTACAGCGT
 ATATTGAGATCGACGCTGGTGTATTTGGAACAGCTGTATCAGTATTTGCGCTACCCAGGCTACATT
 TTCCCGCTCGACTTGGGAGCTAAAGGGTCTGTGTCATGTTGGTGGCAATCTTGCATGTAAATGCTGGTGT
 TTGCTTTTGTACGATACGGTTCTTTGCATGGTCTGTTTTAGGTTTGAAGCTGTCTTGGCCGACGCT
 ACAGTTTATAAATCTATGCAATTCATTGCGTAAAGATAATACTGGTTATGATTTGAAGCAGTCTTTAT
 GGATCTGAAGGTACTTTGGGTATTATAACTGGTGTTCGATTCTATGTCCATCAAGACCACAAGCGCAA
 AATGTGGCATTTTTAGCTGTATCGAGTTATGAGGCCGTTCAAAGGTTTTTGTCCAGGCTAGAAAGGAC
 TTGCAAGAAATTTATCGGCTTTTGAATTCATGGACAACACCTCACAAAAGTTGACTGCTAAGCATTTA
 GGTTTGGAGCACCCCTATTGAAAGCGGTGACTTCCCATTCATATGTGTTAATTGAACCTCTGGCTCCAAC
 AAAGAGCACGACGACGAAAAATTGGAAACATTCCTTCCCGAATGCAATGGAAGAAGGTTTAGTCGACGAT
 GGGATTTATGCAAGATGAGGCTCAAATACAATCATTTATGGTCAITGGAGAGATCCATCCCTGAAGCA
 ACCACTTATGGAGGCGGTCTTTACAAGTATGACGTTTCTTATCCATTGGCAGATCTTTACGGGTGAGTT
 GACGACATCAATACCAGTTAAATGATGCTGGAATCGCCAGCTTGGACGATGAATCGAAACTTGTGCTT
 GCTGCATTTGGTTATGGTCACTTGCAGATGGGAATTTACACTTGAACGTTTTCTGTGACAAAGTATTCT
 CCTGAAATTGAAACTATCTTGGAGCCATTGTTCTATGAATGGATCGCAAAAAAATGGATTCATTTCC
 GCTGAACATGGCTTGGCATTCAAAAGAAAACTACATTGGGTATTCCAAGAATGAGATTGAGGTCAAA
 PTAATCAAMGAATCAAAACACATTACGATCCAAATGGAATCATCAACCCATATAAATACGTGTA

YEL071W_homolog 527aa (SEQ ID NO 482)

MQRRLVQTASYLIRRNNAVCRFSRYNGLPVASYSTKTVFFTADTYSQKVORDAKFKQLESQDIEYFKSV
 LPENSIITDEOLLFFNEDWMRKYRQSSQLVLKPKTTTEQVASILKYCNDNKLAVVPQCCNTYGLVGCNSP
 IPDEIIISLSAMNKIRSFDPVSGILKVDAGVILETADQYLAEQGYIFPLCLGAKGSCHVGGNVACNAGG
 LRLRLRYGSLHGSVLGLEAVLPDGTVYNMHSRLRKDNTCYDLKQIFIGSEGTGTTTGVSVILCPSRPQAG

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NVAFLAVSSYLAVQKVFVQARKELQEILSAFEFMDNTSQKLTAKHLGLEHPIESGTFPFYVLIETSGSN
KEHDEKLETF LGNAMEEGLVDDGIIAQDEAQIQLSWRESIPEATTIGCGVYKYDVSIPLADIVGLV
EDINTRINDBACTASLDDESKLVLAALGYGHIGIXNLHLNVSVRKYSPEIETILEPFVYEWIAKKNGSIS
AEHGLGFQKKNYIGYSKNELEVKLIKEIKQHYDPNGIMNPKYKVV

YER177W_homolog 795bp public: 1..795 (SEQ ID NO 483)
ATGCCAGCCTCCCGTGAAGATTCCGTTTACCTTGCTAAATTAGCCGAACAAGCAGAACGTTATGAAGAA
ATGGGTGAAAACATGAAGCCGTTCCTCTCGGCCAAGAATTGTCTGTTGAAGAACGTAATTTATTTA
TCTGTCTCTTACAAGAATCTCATTCGCTGCTGCTGCTTCTTGGAGAATTGTTTCATCAATTGAACAA
AAAGAACGAGCCAAAGCAAATGAGAGSCCAAGTTGCTTTGATCAGAGATTACCGTGCCAAGATTGAACCT
GAATTGTCTAAAATTTGTGAACATATTCTCTCTGTTGAGCGACCATTTAATTACATCTGCCCAAACCT
GGTGAATCAAAAGTATTTTACTACAAGATGAAGGTGATTACACACATACTTGCTGAATTTGCTATC
GCTGAAAAACGTAAGGAAGCTTCTGATTATCATTAGAGGCTTATAAAGCTGCTTCTGACGTTCTCTG
ACCGAGTTGCCACCAACCCATCCCAATCAGATTAGGTTTAGCAATTGAACCTTCTCTGTTTTCTACTATGAA
ATTTTGAACCTTCCAGATAGAGCTTGTCTATTAGCTAAACAAGCTTTTCGATGATGCTGTTGCTGATTTA
GAAACCTTATCTGAAGATTCATACAAGGATTCAACTTTGATTATGCAATTTATTGACACATAACTTGACT
TTATGGACCGATTATCTGAAGCCCTAGCTGCCACTGAAGAACAACAACATCUAGTCAAGCTCCAGCT
GCTCAACCAACAGAAAGGTAAGGCTGATCAAGAATAC

YER177W_homolog 264aa (SEQ ID NO 484)
MFASREDSVYLAKLADQAERYBPMVFNMKAVASSGQELSVEERNLLSVAYKMNIGARRASWRIVSSIEQ
KEEAKGNESQVALIRDYNAKIEAELSKICEDILSVLSDHLITSAQTGESKVFYKMKGDYHRYLAEFAT
AEKRKEAADLSLEAYKAASDVAVTELPPTHPIRLGLALNFSVFFYBILNSPDRACHLAKQAFDDAVALL
ETLSSEDSYKOSTLIMQLLRDNLTLWIDLSEAPAATEEQQSSQAPAAQPTGKATQE

YGR192C_homolog 1008bp public: 1..1008 (SEQ ID NO 485)
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AGAAAAGACATTGAAGTTTGTCCCGCTCAACGATCCATTTCCTCCAGACTATGCTGCTTACATGTTC
AAATACGATTCTACTCAGCGTAGATACAAGGGTGAAGTCACTGCTTCTGGTGACGACTTGCTCATTCAT
GGTCACAAGATTAAAGTTTTCCAAGAAACAGACCCAGCTAACATTCCATGGGGTAAATCTGGTGTTGAC
TACGTTATTTGAATCCACCGGTCTTTTCAACAACTCGAAGGTGCTCAAAAACACATTGATCTCTGGTSCC
AAAAGAGTTTATCATCTGCTCCATCTGCTGATGCCUUAATGTTTGTGTCGGTGTTAAGGAAGACAAA
TACACTCCAGACTTGAAGATTATCTCCAATGCTTCTTGTACCACCAACTGTTTGGCTCCATTAGCTAAA
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AAGACCGTTGACCGTCCATCCCAAGGACTGGAGAGGTGTTGAGAACTGCTTCTGGTAAACATTATCCCA
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TACGAAGAAATTTGCTCAAGCTATCAACAAAGCTTCTGAAGGTCCATTGAAAGGTGTTTTGGGCTACACT
GAAGATGCTGTGTTCTCCACCGATTCTTGGGTTCAAGCTACTCATCTATCTTTGATGAAAAGCCGGT
ATCTTGTGTTGCTCCCAACTTTCGTCAAATTGATTTCTCTGGTACGATAACGAATACGGTTACTCCACCAGA
CTTGTTCACTTCTTGAACAACGTTGCTAAAGCTTCTCTTGA

YGR192C_homolog 335 aa (SEQ ID NO 486)
MAIKIGINGFGRIGRLVLRVALGRKIEVVAVNDPFIAPDYAAVMFKYDSTHGTRYKGEVTA SGDDLVID
GHKIKVFERDPANIPWQKSGVDYVIESTQVPTKLEGAQKHIDAGAKKVIITAPSADAPMFVVGVNEDK
YTPDKIISNASCTTNCLAPLAKVNDTFGLREGLMTTVHSITATQKTVDGP SHKDWRGRTASGNIIIP
SSTGAAKAVGKVIPELNGKLTQMSLRVPTTDVSVVDLTVRLKKAASYEEIQAQIKKASEGPLKGVLCYT
EDAVVSTDFLGSSYSIFDEKAGILLSPTFVKLISWYDNEYGYSTRVVDLLEHVAKASA

YGR243W_homolog 399bp public: 1..399 (SEQ ID NO 487)
ATGGCTTCAACAGTTCAACACCGCATCCAAATTCACACGTTTTTTAAATTCAGAGACCGGTCCCTAGAACC
GTGCATTTTTTGGGCTCCAGTGTTCAAATGGGCCTTAGTTGCTGCTGGACTTAATGACATACAACGTCCT
GTTGAAAAAATTGAGCGGAAACCAACAGATAGCATTGTTTGCCACTGGTGCCATATGGACTAGATGGGCC
GGGTTTGTATTAAAACCAAGGAACATGCTTTTGCCATCAGTGAATTTCTTTTTGGGTTGGAGTTGCTGCT
TACCAATTTGTTAAGAATTGTCAACTACAGAAGAGATTGGGTGATTCCCAATCCAACTATTTAATTAT
ATCTTGAACGGTGATGCAGCTGCTGTAAAAGAAACAGAACCAGCCAAAGAATTAA

YGR243W_homolog 132aa (SEQ ID NO 488)
MASTVQHASKFQRFLNSETGPTVIFWAPVFKWALVAAGLNDIQRFVEKLSGTQQIALFATSAIWTRWA
GFVIKPRNMILASVNFPTGGVAGYQLRIVNYRRDLGDSFPMQVFNYILNGDAAAVKEPEPAKN

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YHL021C_homolog 1224bp public: 1..1224 (SEQ ID NO 489)

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 AGCCCAGACTCGGTAGACCCCATTCTAGCCAAAACCTATTCACTACAGCAGATGCAGCAACCGGCTTG
 CAAATTAACGCACCCCCAGTGGTAGAGGATTCCTCATTTGAAATCCAAATTAAGCAACAATGGCAAACCTC
 ACCAACTCAGTUTACUUCGTGTCTATTCTTAGAAAACCTCTCCACCAACAAACGACTCGGCCAAATCTTTT
 GACAAAGNTAGAACTTATCGGACAACAAGAACTCGAAAACAACCTTTGCCCTCCCTCAACATGGGACTAC
 GACGACATTTCTCACCACGACAACCTCTTTCTTCCAGACGTTGTACAACTTGAATACCTACGGGTAAACA
 TTTGTCAACAACATCCCCACCCACAAAATTTCTGACATGACAGAGGACAAACGCCAACGCAATGGUCAGTC
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 AAGAAGGAAAAAGCAACCAACAATTGCCATACCCAACACGTTTTTTCCATTTGCACATGGACTTGGCTCTAC
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 CAGACCCCAATCACCTTCCACTACGACAACAACAACGAGTACTACTACTACAAGCGGCGGTTAATCGAT
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 CCATTCGAGGTTGACCCCCACCCAGACTTTATCCGCGGAAATGCAATTTATTTGAAACCTTCATCAACGAC
 CCGGCAAAACCACTTTGAAATCAAAATGCCAGAGGCACTTGTCTCATTTTCCGAAACAGAGAAGAGCCCTT
 CACTCGAGAAACGCATTCTCCGACCTGAACAACGGCGACAGATGGTTAATGGGCCTTATGTTACACGGC
 GACAGTTTATAGATCAAAATTAAGTATAGGCTATAGAAAAGTACATACCTAA

YHL021C_homolog 407aa (SEQ ID NO 490)

MLRQPLRQIRFHSLALACYNSEKVTVTINGRTCTFNNVFLRDACQSPDSVDFISSQKLETTADAATGL
 QINAPFVVEDSSLKTQWSNNGKLTNSVYPVSFLFNYSTNKRIGKFFDKDRKLWDKQLEEDNFASLNMEDY
 DDILINDNSFFQTLYNLNRVGLTFVNNIPTPQLSDMTEDNATQWPVYKIAEKFGYIKKTFYGTLPDVKN
 KKEKATNIAYINTFLPLHMDLLYYESPGLQLLHAIQNSTLGGENIFCDSYLAAEHVRKTDPRAYTALT
 QTPITFHYDNNNFYYYYKRPFLIVEDPEVGDGFPKIASINYAPPFQGPFEVDPHIDFIRGMQLFETFINJ
 PANHFELKMPGTCVIFENRRALHSRNAPSDSNNGDRWLMGYVDGDSFRSKLRIGYRKVHT

YHR162W_homolog 354bp public: 1..354 (SEQ ID NO 491)

ATGTCATCATTTAAAAAATCACTGATTTTATTTTCAAAAACATCCCTTAGATATGTCTGTACAACCT
 CATTTTTCGGGTCAGTATCAAAATTTTGGGATTCCTATAGCTGCTATTTTAGATTTGAAAAAGATCCT
 GATTTAATTAGTGGACCAATGACTGGTTTCATTAATACCTTTATTCCTTTAGTGTTTATGAGGTAATCAATG
 GCAGTTACTCCTCAAAATCATTATTTATTTTGGGTGTCAATTTGTTAATGAATTGGCACAATTGAGTCAA
 GGATTTAGATGGGTTAAACATCACTATGATACTTCTTCAATGATGGTGAAGATACCAAAAAGATAACT
 CAAAATTTGA

YHR162W_homolog 117aa (SEQ ID NO 492)

MSSFKKFTDFLFSKQSLRYVCTTFHWGPVSNFGIPIAAILDLKDPDLISGPMTGSLILYSLVFMRYSM
 AVTPQNYLLFQCHFVNELAQLSQGFRWVKHHYDTSNDGEDTKKITQN

YLR109W_homolog 531bp public: 1..531 (SEQ ID NO 493)

ATGACTGACGGTAAATTTCCCACTAACATGAACCAAAATACATTCCTTATTCTAAAGATCATGCAAGT
 TTAACGTCTTGTCTAATCCAATACCATTTGGATTTAAATCTTTATTTCCAAATAATACCTGTTGATGTC
 ACTGCTGTGCCCGGTGCTTTTACCCCAACTTGTACTGAACAACATATCCCTCATTTATTTGAAACATTTG
 AAAGATTTCAAAGACAAGGGCGTCAAAAAAATCATTGTTTATCTCCCAATGATCCATTTGTAATGGCA
 GCTTGGGCTAAAGCTTTGGGTTATACTGATGAACAAAATTAATGTTATTTTGTCTACTGATCCTAATGCT
 TCTATTTCTAAAGAATTGGGTGATGGATTGTTGCTGATTGACTCTGGCAGGATGGGATTAACATTA
 CAAAGATATGCTAGTATTGTTGTTAATGGAGAANTCACTTATTTGGAAACTGAAGATAGTTTGGGATTC
 CTGGAATTTCTAGTGCTCAAAACATTTTAAAGAGAAATCCACAATTAA

YLR109W_homolog 176aa (SEQ ID NO 494)

MTDGKFPNTNRPKYIPYSKDHASLTACANPIPLDLKSLFPNNTVVVTAVIDGAFPTCTEQHIIPOYLKHL
 KDFKDKGVKKIIVLSANDPFVMAAWAKALGYTDEENYVIFATDPNASISKELGDCFVADITSAAGMGTRE
 QRYASIVNGEITYLETEDSLGFSEISSAETILKRIHN

YLR206W_homolog 879bp public: 1..879 (SEQ ID NO 495)

AAGAGAAAACAAAATAACAATTTATGGATTGGAATGATGAAACACCACCACAACAACCTCAATATATAT
 TTAGCAACCGGATTCTATCAACAACAACCACAATTTTATGUCUAGUAACUTCAATGGCAACAATTCCAA
 CAATATGATATGTTTCCCAACCAATACAGAATCCAATGGACACAGGATTATATANTCAACAGGCCTAT
 TATCAACAACCACAACAGCAGCAACAACAGTTTCAACCAACCAAGTTTACTGGTTTAACTATGGACAA
 CCACAACAACCACAAGCGCAACCAGAACCTTTACAACCAATGAAACAGGATCCATTAATCCATTTGCC
 ATGTCCTTCTGGGTCAAGACAATACCAACCAAGCCACCAACTCAATCCTTAAACAGTTTAGCTGAACAGCAA

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CAACAGCAACAGCAGCAGCAACCACAATTTTCTACTCAGCCAACTACTGCTCCACTCAAAACAACAAAAC
 ACATCATCATCAAGGTTTAAATGAAACTCATGAGTTGAATGATTTATTAAGTCAAGGAACTGGATTAGAT
 ATATTGGGTAACTGGAGATACTAGAATCCCACATCAACATACAAAGACACAAAATTTTATTAATTC
 AGTGGAACTGGATATAAACAACTGGTAATGAACCAATTAGATTAGTTCTTAATGCTACAGGTAATCCA
 TTTCTTAATACITGGTATTGGATATCAAGGTGCTACACACAGCAAGTGCCACAAACAGCAAGTGGCCACAA
 ATCAATCTGCTTATACTGGGTATGGATTTGGTAACGCTCAACCCTCAACAACACCAGCAATACCAACAA
 CAACAACAATCACGTAATGGTAATGATGGCCCAAGTTTAAATAGATATTTAA

YLR206W_homolog 292aa (SEQ ID NO 496)

MRKQNNLLDLNDETPPQQPQYVLAIFVYQQQPPQFYAQQPQSQQFQQYDMFGNPTQNPMDTGLYNQQAY
 YQSPQOQOQOQOFPNQFTGFNYGQPQOPOAQPEPLOPLKTGSSNNPFAMSSGSDNTNKPPTQSLNSLAEQQ
 QQQQQQQQFQFFFTQPTTAPLKQQNTSSSRFNETHELNDLLTQGTGLDTFGNTGDTRIPIQITKLTQNFINS
 SGTGYKQTCNPEIRLSSNATGNPFINTGTGYQCATQQQVPPQQQVPTNPAYTGYGFGNAQPPQQHQQYQQ
 QQQSRNGNDGPSLIDI

YMR043W_homolog 789bp public: 1..789 (SEQ ID NO 497)

ATGGCTATTAAAGAAGAAACAATGAATTTAGTCAAGGTAATGAGGGGAATTCCTCATTCACCAATAAC
 AACAAATAACAGCAACCAACAGCAACAGCAACAAATGCTGATGTTTCTGUACAGTAGATGATGACGAT
 GATGACGATGGTACTTCTCAAGGTAAAACTCAAAGGAAAGAAATGAGATCAAAATTCATTCAA
 GAAAATCAACAGCTCATATTACTTTTTCCGAAACAAAAGCTCGGATTATGAAGAAAGCTTATGAATTA
 TCAGTATTGACAGGTACTCAAGTGTTATTATTAAGTTGTTTCAGAACTGGTTTGGTTTATACTTTTACC
 ACTCCTAAATTACAACCTTTGGTCACTAAATCTGAAGGGAAGAACTTGATTCAGCATGTTTGAATGCT
 CCTGAAGAAGGATTTGGGTGATGATCAAGAGAATCAAAGTGATGGAAATCAAGGAGATTCACTGATCAA
 AGCCCTGCTCCAGCAACCAATCCAAATGTCAATGGGTGCTGCAGGTCATGCTCATCACATTCAACAACAA
 CAACAGCAACAACAACAAGCTCAACAGCAAGCTCAGCAACAATGCGACCAATGCTTCTCATGGTTTA
 CCTACACATTATTCCAATCCTCAAGGAGCTGCTAATCCTCCTCTACCTCCTCAACAACAAGGTCACAT
 CAACCTGGTATTCCATTACAAGGTGGTTATAGTGATCAATACCCTGTATTTTGCTAATATTCAAAATAAC
 AACATACCTAATCAACAGCAATATCAATGA

YMR043W_homolog 262aa (SEQ ID NO 498)

MAIKKEETNEFFSQNEGNSHSTNNNNNSNNNSNNNADVSAPVDDDDDDGGTSQGKTQKZRRKIEIKYIQ
 EKSRRHITFSKRKAGIMKKAYELSVLTGTQVLLLVSEIGLVYTFITPKLQPLVTKSECKNLIQACINA
 FEEGLGDDQENQSDGNTGDSFDQSPAPATNPVMEGAAGHAHHIQQQQQQQQQAQQQQAQQQMAPMPSHGL
 PTHYSNPQAGNPGVPPQQQCCQHPGPIPLGCCYSEQYSYFCNIQNMNIPNQQQYQ

YMR256C_homolog 330bp public: 1..330 (SEQ ID NO 499)

ATCACATGAAACAACCAGACGACCAAAAGTCTGAGAGAGAGAGAGAGAAAAAATATCGGCTCATTATT
 TTCAATTCACTTTTAACTCTAGTTAACTACTATTTACTTTCTTTCTTCTAATCTATCCATCCCACCATCCT
 ATCTATTTCAAATTATGAATCCACAAGAATTATTGAATTACAAAAACATTATCAAAATACTCCTAAACCA
 TTAATGGTTAAGAGGTAGACAATCCCACTTTTACTTTTNTCCATTTTATGCTTTATTTGCTGTTAGTACT
 GCCATCCCATTTATATTATAGTGTTAGAGCTGTTGCTGGTATAAAAGATGAATAA

YMR256C_homolog 109aa (SEQ ID NO 500)

MRMKQPDQKSEREREKKYRIITFNSLLIIVNTIYFLSSKVPSSHPIYSIMNPQRIIEQLQKHVQNTPKP
 LNLGRGRQSAFLVYFFYALFAVSTAIPLYYSVRAVAGIKDE

YOR267C_homolog 2091bp public: 1..2091 (SEQ ID NO 501)

ATCCAGATAAACATAAACTCAAACATATTCGAAAAAATAAACACGACAAAGATGACGAAATGTCTCTTG
 TCAACCTCAAACCATTTCTACGGAAGTACACGGAAGTTTCTTAGGATTTTCATATTGGAAGACATGAATCG
 GCGACTCGTTGACTTCTCCAGTTATGAGCAATTCATCCGAAAGTCATCATCACAGCCATCACCCCTCAT
 CAAGCCAAATCAAGTGCAAAACCATGTAACCCCTCTCCAGTTCAATCCCAATCTGGTACTGCCACTACC
 ATTCATCAATACAAATCACCAACCTCAAGCATCTGGATTACACCGCGGGGACTCCGATAAAAAATCA
 TCTGGGTCAAGTTGTTGATTTGAAAAAATCTCTCAAAACAAAGAAAACTTCAATCCAAAGAAAGCAACGA
 CATAGTATTTTGGGACAATATAGCAATCAGTTCATTTCAUACUACCAATGGCGCAGGTTCAATCGCCT
 GGTGCAGCGTGGGGGAACGGCAGTGCCTTGCAATCACGTGAACAATCATCTACGTCAATGAGCCACTTA
 ATCAATCAAAACATCTTCTCAACTTTTGTACAATGCTTCACATTTCTGTCAATAGCAATCGAGATCCCTTC
 ACGGACGACAACCTCCATTGGTGAAGAAGTATGCTAAGATCGGGAAAGAGTTGGCCAGTGGAGCCGGT
 GGTTCAGTCAAAATTANTCAACAGGCCAGTCACTGCAAGACCTTTGCTGTAAAGAAATTAGAGCGGAAA
 AGATCTACTCAATCATTCGAAGGATTACACTAGGAATGTACTGCTGAGTATTTGATTGGTTCTACTTTG
 AGGCACCCAAACATCATTAACCATCGATATCATCCATGAAACANTCGTTATTTTGAAATTTATGSA
 TATGACCATATAGATTTCTTTGCTGTTGTTATGAGTGGAGAGACGTCTCGAACGGAAATCAATTTGTT
 TTAAGCAATTTATCAAGCTGTGCCATATTTACACAAATTAGGGTTGGCCCATCGTGATTTGAACITG
 GATAATTGTTTATAACGAATGAAGGATTTTGAAGATATTCGATTTTGCTAGTCTGTCTCATTTTCAAG

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TATCCCTACGAACAGTTTGGTAACACCAATTCATTTCAGCCGTTTCATGGTATTGTTGGATCTGATCCT
 TACTTGGCCCCCGAGGTTTTGAAATCTCCTAATAGCTACAAACCCACACCTGTGGATTTTATGGTCTATT
 GCCATAATTTACTCTTGTATGACTTTGAAGAGATTTCCTTGGAAATACCTAGTCAAGAAAAGGATAAC
 AGTTTCCGACTTTATTGGCATGTATGATGATAAATTCATGATTATTATTATTGACTAACGAATGTCATAAA
 CTTTTGTTGCAACAGCGTAAACTAAAGAATACAAATGTTAGACTGAACAAAAGGAAAAAGCAGCTAGAA
 GAGGAAAAGGCGGACAAGCCTGAAGAAGACGAAGAAATGAAAGATGCCGATAGTGCACCACAGCAACAT
 CATCATTTCTCATGATGTAGAGCTGGGAAAACTGSTCGATCTACCGTTTGGCAAAGACAACTCAAATGAA
 GCTGTTACCGTTTTTAACAGATGAGCAAGCAGAAGAGATTATGCCACAATTAATGAGATTGATAGAAAA
 CTACAAGAGTTTGAAGATAAAAAGAATCAACTTAAAGAGAAATATGAGGCTTTGCCAGATGCTGATCCT
 AGATATCAAAAACAGTTGGCACAAATTCACGAAGAGGAAGAAAAGCAAAGACTAAAAGATGCCGAGCAC
 GGTGCCGATGAGAAAAGAAATCACATCATAAACAGATTTCATGCTCCGTATAGATTGATGAGATTCTTG
 CCACATTGCTGCTAGACCAGTCATATCAAGATTATTGGAGGTTGATCCAAAGAAAAGAGCAACTATGGAA
 GAAATTTCTAGAAGATGAATGGATTAAACAAATTCAATGCTGTACAGTTAAGCCACTTTCAAAATCAACA
 GATGCAACATTAGATTTTATTTGAGGATGAGGACGAAGATAATGGTGAAAGGAGTACCTCCACACGAGCAT
 ACAATTTGTCAAAGAAGGTTGA

YOR267C_homolog 696aa (SEQ ID NO 502)

NPDKHLKLFGRKNKHDKDELSISTSNHSHGSTRKFLGFHIGRHESGDSLTSPVMSNSESSESHHHSEHDF
 QANSSANHRNFSFVHSNTGTATTIPSIQSPQFQASGLHRGDSDEKSSGVSVDLKKFFKTKKTSNPRKEG
 HSILQYSNQLHSPPPMAQVHSPGAGSGNGSALQSRFQSSSTSLATLINQTSQLLYNASHSVNSNRDFF
 TDDNSPLVKYKGLCKEIGSGAGGSVKLITRPSDSKTFVKEFRAKRSTESLKDYTRKCTAEYCIGSTL
 RHPNIIKTIIDILHNNRYFBI MEYATIDFFAVVMSEGMSRTEINCCLKQIEGVAYLHLKGLAHRDLKY
 DNCVLTNEGILKTIIDFGSAVLFKYPYEQFGNNWSIQPCHGIVGSDPYLAPEVLKSPNSYNPQPVDLWSI
 ALIYCCMTLKRFPWKIPSQEKUNSFRLYCMYDDNFHDYLSNECHKLLQOKKLKNTIVRSNKRKKQLE
 EEKCKPPEEDEMCKDADSAPOQHHSDDVSGKGGSTVGKDKSNEAVTVLTDQAEELMAQLNEIDRK
 LQEFEDKKNQATKKYEAALRADAPRYQKQLAQIHBEFFKQRLKDAEHGADEKKKSHHKQIHGFPYRLMRL
 PHAARPVISRLLLEVDPKKRATMBEILEDEWIKELQCCTVKPVSKSTDATLDFI EDEDEVLVKGVPPHEI
 TTVKSG

YOR374W_homolog 1500bp public: 1..1500 (SEQ ID NO 503)

ATGTTTAAAAAGGCCTTACCATTAGTCAGCAAGCTCACAAACACCAAAAGGATACACTTATAACCAACCC
 CTTGGGTTATTTCATCAATAACGAATATGTTTCAACCCAAAGCAACAAAAGACATTTGAAGTTATTTCTCCA
 TCCACTGAAGAAAAAATAACTGATGTTTACGAAGCTTTAGAAGAAGATATTGATACTGCTGTTGAAGCC
 GCACAAGCCGCATACCACAATGGTTGGGCTCAAGGGCCACCAGAACAAGATCAAAAGTTTGTGTTCAA
 TTAGCCGACTTGATTGAAGAAAATGCCGAATTATTAGCTCAAATTGAAACITGGGACCAACGGTAAATCC
 TTACAAAATGCCAGACGTGATGTTGCCCTTGACAGTCTTACTTCAGATCCCTGCTGCTTGGCCGAC
 AAAATTTTGGGTTCCCAAAATCAATACTGGTAACACTCATTTCAACTACACTCAAAGAGTCCCATAGTTC
 TGTGGTCAAATTATTCCTTGAATTTCCCAATTATTGATGGCTTCTTGGAAATTGGGACCACTTCTTGGT
 ACTGGTTCTTACCCTGTTTTGAAGACTGCTGAATCCACCCCATTTATCTGCTTTATATCTTTTCCCAATTTG
 TTAGTCGAAGCCGGTATGCCAAAAGCTGTATCAACATTGTTTCTGGTTTTGTTGCTTACTGCTGGTGGT
 GCCATTGCTAAACATCCAAAGATTGAAAAAGTTGCTTTTCACTGGTTCTACTGCCACCCGGTAAATATATC
 ATGAATTTGGCTGCTGAATCAAACTTGAAAAAGTTACTTTGGAATTGGGTGGTAAATCTCCAAACATTT
 GTTTTCAACGATGCTGATTTGGACAAGACTATTCAAAACITGATTGTTTCTATCTTCTACAAATCTGGT
 GAAGTCTGTTGCTGCTGCTTCTGCTCTTTTGAATCAATCCGGTGTTTAUGACCAAGTGTTCAAAAATTC
 AAAGAAGCTGCTGAAAGTCTCAAGGTTGTTAACCCTATTGACGCAAGACACCTTTATGGGTGCCCAAGTT
 TCTGACGTCCCAATTGTCCAAAATTTTCAAAATACGTTGAATCTGGTAAATCTCAAGGTGCTACTGTTGTT
 ACCGGTGGTGGTACAGCTGATGGTAAAGGTTACTTTTGTCAAACCAACTATTTTCTGCTGATGTCAGAAA
 GATATGGATAATTGTGACAGAAGAGATCTTTGGTCCAGTTTGTCTCACTTTGATCAAATTTGATACTGTTGAC
 GAAGCCGTTGAATTGGCCAAATGATTCCGATTATGGTTTGGCTGCTGCTATTCACTCTGCTGACGTTAAC
 AATGTATTGATGTGGCCAAACAGAGTTAAAGCCGGTACTGTTTGGGTAAACACTTATAACGATTTCACAC
 CCAATGGTTCCATTCCGAGGATTCAGTCTTCAGGTATCCGGTACAGAAATGGGTGAAGAAGTTTTCAT
 CAATCACTCAAGTCAGAGCTGTGAGAATGAAAATCAACCCACCAAACTAA

YOR374W_homolog 499aa (SEQ ID NO 504)

MFKKALPLVSKLITPKGITYNQPLGLFINNFYVHPKQKQKFFEVISPSTEEKITEVVEALEEDIDTAVEA
 AQAAHYHNGWAQGPPEQRSKVLTKLADLIBENAEELLAQTFTWDNGKSLQNARGDVALTAAYFRSCGGWAD
 KILGSQINTGNTHFNVTQRPVTCGQIIPWNFPLLMASWKLCPVATGSTTVLKTAESTPLSALYLSQL
 LVFAGMPKGVLTNVSFGGATAGAAIAKHPEIKVAFTGSTATGKIIMKLAABSNLKKVITLELGCKSPNI
 VFNDADLCKTTONLIIVSIFVNSGEVCCAGSERLLIQSGVVDQVVEKPKFAAESVKVGNPFDEDTFMGAQV
 SDVQLSKLLXVVBSCSKSQGATVVTGGARADGKGYFVKPTIFADVKKMDIVREETFGPVVTLIKFDTV
 EAVHILANDSDYGLAAGIHSADVNNKIDVAFRVKACTVWNTYNDPHPMVFFGGFSASGLGREMGFEVLH
 EYTQVRAVRKKNPFI

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YPL089C_homolog 1836bp public: 1..1836 (SEQ ID NO 505)
 ATGGGCTAGAAGAAAGATTGAAATAGAACCATTCGACAGACGATAGAAATCGTACAGTGAAGTTTGTGAAG
 CGTAAGCCAGGGTTATTTAAAAAGCTCAGTAATTAGCTGTGCTCTGTCAAGTGGATTTAACGGTTATT
 ATCGTTGGCAATAATAATAAAGTATATGAATATTCTACTGTTGAGGCAAAATGAGATTTTAAATGCCTAT
 AATAAAACCATTTAAAGTCAGAAAAAAGTACATGAATCGAAGTCTCCAGAACATTATTTCGAACTTACA
 AAGAAACGACUATTTAAATGAACCACTTATGAATAAATCAGGGTCTGTAGTTGGCACTAATACUATTTG
 AACGATGAAGACTATGATCATAATGTTCAATGAAGCGGGGATGAGGATTCCGAATATGAAAGCGATGAT
 AATTCTCCACAACCTAAACGGCACAAAAGATCAGAGTCCGTTAAAAAAGAGCAAAACCCCAAGTGTTT
 AATAGTACCCAACTCCACCACCGCTCCACCACCTCATATATCTTTAAATTAATGTTCCAAACATTTACC
 AACCCCCAAATTTACAAAAACAGATTGATGAGACAAATAACACTTCGGCACCGCCCCOCTACTGGGACA
 AAAAATGAACCAACGATGCCAACGACCACTATTGAGGGTACAAATACCGAATGATGCCAAGAGCAATACG
 AATAATTCCCATAGTGGTGTTAATAATAGTGTGATGGCAAGGACACGGCGAGAACAGTGACGGCAGTCCGAC
 AATAAGTGCAAACCAACCAAAACCACTCAATTCGACCAATAACAAACATCAGGTACAGGGAAGTGTGATACCAAT
 TCATCGCAACTAAATTCAAATGGTAATAGTAATTTAGTGCCTCGGAATGTTCCAAATACCAAGATTTTCG
 GGATATTCAATCGTTTCGATCACCAGACTCAGCAAAACCAACATTACCGTTACCTTTGCAAAACCAATCA
 CAAACGTCAATCTCCAGCTAGTGTGTGATGACCAACAGGTTTTACCAATGACAGGAGGAAGCAATGCATATTTT
 GCAGGAATGCAACAATCAACCGTGGTGGTTCGTATGTCAATTTTCCAGCCCCAAGTATATCAGCAGTAT
 CAACAGTTCCAAATCAATCAACTACAAGAACCAACACCAACAGCAACAGCAACAGCAACCAACCAACCA
 CAATCTCAGCGCAGCCATCATCGCAACTGGTGTGGAAATCABAATGCACAATTTGGAATCAGCAGCAGCA
 TTCGGTTCCTGCTTTACCGACAGGGACACAAATTTAATAATGGTGAACAAACACCAATTTTCAAGATTGCCA
 TCAUGATAGCTTAATGATATGTTCCCTTCCTCATCTCCAACTTTCTTGCACCTCAAGATTGGCCA
 TCAGGTATAACACCAACTACTCATCTACCAAGATTTTGTGAATATGCCATTGAGTGGGAATTTGGACTG
 CAACAACCTCCAAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACA
 CAACA
 CAACAGCAACTGCAGTACCTGTTATCCCAATACAAACACAAACATCACAACAATGGCTTCAACTACC
 AATCACAATCAGCTAATCTAATACCAGGGTTTTTACAAAACCAACACAGCCACTGGAAATTCGGCA
 AATGCTTCCAAAGCTGAGTGATGCTGGTGATGGTACTAATCCAAACCACAGCAGGAAGTTCAAGTTCAGCA
 GATGTCAATAACACCAACAATGGACCTAATAAAAAATACATAA

YPL089C_homolog 611aa (SEQ ID NO 506)
 MGRRKIEIPLTDDNRITVTFVKRKAGLFKKAHLELAVLCQVDLTVLIIVGMNKNVYESTVLEANEIFNAY
 NKTIKVRKQVHESKSPYYSKFRKKRHLNEPLMNKSGSVVCTNTHLNDEDYDHRVHBEAGDEDSBYFSD
 NSPQPKRHKRSSESVKKEQNPKVFNSIQPPPPPPPHISLNNVPLSTNFPQNYKKQIDETNNTSAPPATGT
 KNEPTMQRPVLRVQIPNDAKSNTNNSHSGVNSDGDKTARTVTAVDNSATNQNTQSSNTTSGTGTADTN
 SSQIMSNNGNSNIYPGNVPMTHFSGYSSRSPDSRKPMPLPLQTKSQSSPASAVAPGLPLTGGSSNAYF
 AGMQQSPVGGSYVNYPAQVYQQYQGFQNLQLQEQQQQQKQQQQKQQQQPPSSQSVNQNAQLESAA
 FRSGIPTGTQFNNGEQTPLSGLPSRYVNDMFPFSPSPNFLAPQDWPSGITPTTHLPQYFVMMPLSGIGS
 QQSQQ
 NHKSANLIPGFLQNPQATGNSANASKSSDAGDGTNPTTAGSSSSADVMNTMNGPMNT

YAL003W_homolog 693bp public: 1..693 (SEQ ID NO 507)
 ATGAGTGAACAAAGAAGATTTAAATCTTATATCTGACAAATAATAGAGTTATTTCAATGAGACAATTGATT
 TTACAATTACTGACTACAGGAATAAACAAAAATATAACGATATACTAACATGTTTGATAGTACTACT
 GCTCACTCAAGCTGATGCTCACTGCTTACAAAGCTTTCCAAAACCAATTCACCAATTCACCAAGATGGTTC
 AACCACATTGCTTCATTCACTGAAGAATTCCGAAGACTTGCCAGCCGGTAAAGCCCCAGCCGCTTCCTGGT
 TCTGCTGCTGCCGCTGCTGAAGAAGAAGATGACGAAGATGTCGACTTGTTCGGTTCTGATGATGAAGTT
 GATGAAGAAGCTGAAAAATTGAAGCAACAAAGATTAGCTGAATACCGCTGCTAAGAAGGCTGCTAAAGGT
 CCAAAACCAAGCTGCCAAATCTATTGTCACTTTGGATGTCAAACCATGGGATGATGAACTGATTTGGAT
 GAATTATTGACCAACCTCAAAGCTATCGAAATGGAAGGTTTGAATTCGGGTGCTCAACCAATGGATGCCA
 GCTGGTTTCCCTATTAAAAAATTACAAATTAACTTGGTTGTTGAAGATGCTTTAGTCTCATTTGGATGAC
 TTACAAGCTGCTGTTGAAGAAGATGAAGACCAGTCCAATCTACTGATATGCTGCTATGCAAAATTC
 TAA

YAL003W_homolog 230aa (SEQ ID NO 508)
 MSDKFDLNLISDNRVSMRQLILQLSTGTINKKYKRYTNMFDSTPATQADVTVYKAPQKEFPQTRWF
 NHTASFTEEFEDI.PACKAPAAAGCAAAAAEPEDEDVDLPGSDDEVDREARKTKQQRILARYAAKKAAG
 PKPAAKSIVTLDVKPWEDETDLDELLTNVKAIEMEGLTWGAHQWIPVGFGIKKLQINLVVBDALVSLDD
 LQAAVEDEEDHVQSTDLAAMQKL

YAL060W_homolog 1185bp public: 1..1185 (SEQ ID NO 509)
 ATGAAGGCAATTGTACACCACGATAGAGGAGATATTAGATACGACCCCAATTTCCCTGATCCACAAATC
 ATTCGACTGGATGATGTCAAATCAAGTTTCAATTATGTGGGATTTCCGGTACTGATTTAAAPGAATAT
 ACTGATGGGCCGATTTTTTCCCAACCGAAAGCTCAATTGAATGAAATTTTCAATTCGAATCAATTCAA

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GTCATGGGTCATGAAATTAGTGGTGAAGTAATTGCTATTGGGGATGATGTAACCAATGTAAAGTGGGT
 GATAAAGTTGTTGTTGAACGTGACAGGAACCTTTAGATAGACATCGTACCAAGATCCTAAAAATGGC
 GATCTGCCCTAAACCAAAATGTCCTAAGTTGTTGTTTGGGTAACATAAATGGGTGATTAATCTTGCTTTA
 ATTGGTTGTGGATTGCTAATGGTGGATGTGCAGAAATTTAGTTGTTGCTAGTCTGAAAGTTATTGCA
 TTCGATCAGAAATAAATCCCTATGGATATGCGGCATTAATTCAACCAATAGCTGTAGTTGCCATGCT
 GTTAAAGTATCAAAATTTTAAACCCGGTCTTAATGCATTAATTTAGGTGGTGGCCCCATTGGATTAAACA
 ACAATTTTGGCTTGAAAGGTAATCAAGTCTCCCAAAATGTTTAAAGTGAACCAAGCATTAGCAAGAAGT
 CAATTGGCAGAGAAATTAGGAGTTATTACTTATGACCCCTACGGGTAAATCAATCGAACCAATGTGTTGAA
 GACTTAAAAAATTATCCCGGGAGGTTATGGTTATGAATATTTCATATGATTGTTCTCGAGTTAAGGCA
 ACTTTTGAACCTGGATTGAAACTTTGAAAATTCGTGGATCTGCAACAAATGTTGCCATTGGGCTCAT
 AAATCAATTCATATATCTATGGAATTTACCTTTTCAGAAAAAATGTTAACTGGATCAATTTGTTT
 GTTAAAAAGATTTTGAACCAATCAATTAAGCAATTGAAAATGGTTTAAATATCGATTTCATGAATTGAAA
 ATGTTGATTACCTGAAAATTCATTTACAAGATGGAATTGAAAAGGGTTTTCGAATTAAATTAATCAC
 AAGGAAAAACATATTAATATTGTTTCTCCGAAAAGTGAATATTTACTATGCAATGGAGTAAATGAT
 TCCAATAAATAA

YAL060W_homolog 394aa (SEQ ID NO 510)

MKAIVYHDRGDIRYDPNFFDPQLIRSDDVKIKVHYCCICGTDLKEYSLGPIFFPPKGELENEISQMESTQ
 VMGHEISGEVIAIGDDVTVNVKVGDKVYVVTGTCLDRHYQDPKNGDSPKPNCPSCVSGNYNACDYLAL
 (GCGFANGGCAEYLVVASSKVIAFDQNKIPMDIAALIQPIAVSWHAKVSNFKPGSNALTLOGGPGLT
 TIFALKGNQVSOIVLSEPALARRQLAEKLGVTYDPTGKSIEQCVEDLKLSPGGYGYEYSYDCSCVKA
 TFETGLKTLKLRGCATNVAIWAIKSIPLYPWEITLSEKMLTGSICFVKKDFEESIKATENGLISIDELK
 MLITSKIHLDGIEKGFLELINHKEKHILFSPKSKYLLCNGVNDNSK

YBL058W_homolog 1116bp public: 1..1116 (SEQ ID NO 511)

ATGTCTCAAAATACTCCAGATTCCCAATGATTCCTGAATTTGTATCTATAACAAATTCCTTCTACATAC
 CTTGCTGAACAGTATTTACTGAGAAACAGCAATGATTTAGTGGAGCCAGTTGAGGATTTCTATGCCAAC
 AATGAACCATCTCAAAAATCAGAAACCAAAAAATCTTCTTCTTCTAATGCTAAAGGCTCTGGTGGTTAAA
 ACATTTAGAGACTTGAACGATGAAGATGATGATGAAGAGGATACAAAGACCAATACCAATTTCTTTACT
 GGAGGAGAGAAATCAGGATTGCAAGTTCAAGATCCCAATAAAGATAACCATTAATGACAGATCAATAATT
 GATCAAAATTTTCCAAAAGCCAGAGAACAAATGCAACAAACAGATGATAGACCAAGTGCTTCTCAAGAT
 GATCAACCATCACCAATTAAATTTTTCAGGCAAGCGTTCAAAATTCCTTGAACGGAATGAACCAAGTCAA
 GTAGTGGAGGATCCTAATGCCAGTCTTAAAAAATTCAGACCTTAGTAAAGTGACTAGAGAAATTACATTT
 TCGAACCAAGGTTTCACAGTAGGTGATGGACCTTTGTCATAGATACCAATGATCCAAACAAACGCCAGTGT
 TTGCAAGAAATTGAACCAAGGAAGACTTCCAATGTCAATTTTAGATGTTGAATTTGGCCAACATGTTGA
 GTTTCTCTATACAGAAACCGACGAAGATTGCAACCTCCGAAAGAAATTTGGTGGTTATCACCGT
 GUAGGTCTATGACTAGGCTCACCCAGTACCTGGGGAAGTACTTGTAAATAATGAAGCATCATCTCAACCT
 GATATCAAAACCCAAACTGAAATTTCTAAACCAAAAGACGAAGGCGAAGCTGACTCCACACTTCAAAATA
 ACATTTGCCAATGGTAAAGAAACATCACACAAATTCATTTCTCGGATTTCTATTCTCAAGGTTTATCGAA
 TTTGTTAAAAATCATGAATATAATTTCTGAACCTACTAGACCATTCACTTTAAAGTCATCCATTCCCAGTC
 AAACCAATAGAACCAAGTAGTGACATTACAATTTCTGATGCTAAATTTGAAAATGCAAGTGAATTGTTCAA
 AGATGGAAATAG

YBL058W_homolog 371aa (SEQ ID NO 512)

MSINTFDSQLIAEFVSTNNSITYLAEQYLSRNSNDLVRAVEDFYANNEPSQKSETKSSSSNAKSGVVK
 TFRCLNEDDDDEEDUKTNINFTTGGEEKSLQVEDPNKDKDNORSIIDQIFQKAREQMQQFEDRPSASCC
 DOPSPIKFSGKQPKIGDGNFESQVVEDPNASAKKFRPSKVTREITFWKQGFVVGUGFLHRYDDPRNASV
 LQELNQCRVPMISILDVEFCQDQDVSVYKCTDEQWTPPKRKIGGYHAGHRLGSPVPGEVLVNNEASSQP
 DEKTEPEISKPKNEGGDSVQIRFANGKRTSHKFNSSDSILKVYEFVKHNEYNSEPTRPFTLSHAPPV
 KPIEESSDITISDAKLKNAVIVQRWK

YBR039W_homolog 804bp public: 1..804 (SEQ ID NO 513)

ATGGCTCTTAATCCATTAACAAACATTGAAAAATCACAAATACCATGAAGATTGTTGCCTCTACTAGA
 TTAGATTAAGCTCAAAAAGCCATGGCTTCATCTCGTGTCTTCAATGAAACTGATAAAGAAATCTTTGTTCT
 AATGCTGAACCAAAACCAATTCAGAAGAAAGCTTCTAATCTGATGACAAAACCTTATTGATTGTTGTT
 TCTTCCGATAAAGGTTTATGTGGTTCTATTCATTTCTCAAGTTTCCAAAGCTGAUAGAAAGAGAACTGAA
 GAATTAATCGTTAATGCGATATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT
 GCTGACAAAGTTAAATTCCTATTCATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT
 ATTGCTGATGAAATTCCTAAATTTAGGTAACCAAGAAACCAATTTCACTGAAGTTGCTTTA
 GGTGTTTTCATTGAACCATCTAAATTTTCCATTTATGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCT
 AGCAAAATATGAATCGAAAAATGAAGAAATCACTTCTGATGTTGCTCAATTCCTCTTATGCTAACAACCTG
 TTGACTGCTATGGCTGAAGGTTATCTATCTGAAGTTTCTGCTAGAGAAATGCTATGGACCAATGCCCTCC

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AAGAATGCTGGTGATATGATCAACAGTTACTCTATTTTGTATAACAGAACTAGACAAGCCGTCAT'TACC
AACGAATTGGTTGATATCATTACTGGTGCTTCCTCATTGGACTAG

YBR039W_homolog 267aa (SEQ ID NO 514)

MRLKSIKNIEKITNTMKIVASTRLSKAQKAMASSRVFNETDKELLSNAEPKPIEEEASKSDDKTLILIVV
SSDKGLCCSIHSQVSKAARKKTEELNGNVDIVCIGDKVKQILRTYADKVKLAFNGVVGKEEFPNTEVAL
IADEIAKLGNVENVEILYNKFVSGVSVFEPKFSIYAADAIANSPLSKYLENEEITSDVAQPSIANNL
LTAMAEGYASEVSARRNAMDNASKNAGDMINSYSILYNRTRQAVITNELVDIITGASSLD

YBR062C_homolog 450bp public: 1..450 (SEQ ID NO 515)

ATGTTATCTGCATCTAACGAAGAAGCCATAGCATCAGCATTGCGACAATTGAGTGAATCAGAAGGATCA
ACACTTGCCTCAATCACTCATGATCTGCTTGGTGAACAAAACATCGAAGGGGGTCACTGACGAATAC
TTGGATACPTTGGAAACGTATTCAGTAAACCAAATTTACTGATAAAGACGCATCTTGTCCAAATTTGTACA
AATCGATTCAAAGATGATAAGCATCCATTGATTGTTCAGATTTCCTTCTCGTCACTGAGTCAATCATATT
TTTGATTTCGAATGTGTTGGGCCGTGGTTGCAAAATGAATTCCTTGTCCAATGTGTGGAACCAATATC
TTAGAGGTCAGAAGCTAA'TAGAAGGAAAATTA'TAGATGAAGAAATAAAAAAGGCCUCAAAGAAAGATTC
GAGGAAGAAGAAGAAGGTTGGGATATATATGCAAT

YBR062C_homolog 149aa (SEQ ID NO 516)

MLSASNEEAIASALRQLSESECSLAQSLMDSLGEQKTSKGVTDYLDTLERIPVKQTDDKDA SCPIC'
NRFKDSKHEPLIVRLPCGHGVNHIFDLECVGPWLQMNSTCPMURTNILEVEANRRKIIDEELKKAQBEIS
EEEEEGWDIYG

YBR101C_homolog 855bp public: 1..855 (SEQ ID NO 517)

ATGGAAAATTTATTACATTTGGACATTTGCACAACTACAGGCGATAAAGCAGCTCTTGAAAAGATTGGA
GAACCCGATCAAAACCCACTTAATCAATTATTNKTTCCTCCCGATGAAGCCACTTTAATGAAGGAAAGT
ATAAAAGTGTGTGAATCAACCGATGTTCATTTAGAAGATAAAGAGATCGCCTTGGAAAATTTCCAAATG
TTGATTGAAAATTTAGATAATGCAATAATATTGGTAATTTGAAATTTATGGAATCCATTGATTGACATT
TTACCCMAAGAAGATACCCCTGTTGAATTTGAAAGTACTTATTTGTTGAATTAATTTGGAACCCGCTGTACAA
AACAAACCCCAAAATCTCAAGAAGATTTCAAATGAACTGAAGGATTGAGTGAATTTGATAGAAATAGCACA
CATCACAAAAATTTGAATTTCAACTGAAGGCATTGTTTGTCTATTTCTTTCATTTATCAGAAATTTTCAA
CCTGGATATGCAAGTTTGGAAATTGCAAGCTTTGAAACTCATTAATTTTGATAACAAGAACAACAAG
TATCAATTGAGAAATTTATCATTAATATCATCCATTTTGAAGTAATGGCTTGAAGCATAGCTTGAAGCCA
CAATTCANAGAACCAAAATTTACCTCACTATTTAGCCCTCGGTATTGAATGAGGATTCAAAACACTACTTGT
GTGGCAAAATCTTTAAACAATCTGTTTTCNCAATTTGAAATTAATTAACATATGAGTTTACCTTTACAAGAAAA
TATGAATAAATAGAGGAATCCAAGTGGTTGAAGAAATTGAGTGAGAAACTTAATATTGATGATCTCAAT
AATCCCAACACAGGCCACATCTCTTAG

YBR101C_homolog 284aa (SEQ ID NO 518)

MEKLLHWTLAQSGDKAALEKIGEPDQKALNQLFGQPDATLWKESTKVVESTQVSLDKBIALENFEM
LIENLDNANNIGNLKLWNLIDILAKEDTPVELKVLICGTTGTAVQNNPKSQEDPTNETGLSELIELAQ
DDKKFELQSKALPAISSPFINPUPGYAKPEKLQGLKLINFUNKKNKYQLRILSLISSILSNGLDDSIKA
QPKAKLPHYLASVLNEDSNTSIVDKSINIVSQINQLNYEFSLEEKYBINRGIQWVEGLSEKLNIDDLN
NAKQATSS

YBR139W_homolog 1653bp public: 1..1653 (SEQ ID NO 519)

ATGCAATTATCTACATTAGTCACTTGGTTGGCTGCTTTAACTGTGGTGCACAGGCAGTATCATTTCCXHC
AACAAATTTAAAGATCAGATATATATGGATTCTGAGGAAAGCTCCCCAGATTTATATTTGGAGTCAGCG
TTCAAAGACTTGGGTTCAATGGCCAGTTGATTTGATTACTGCTTGGGCAGAAATGCAATCTGAAATTAACA
CCTGAACAAATTTGCCAAATTAATCAATCAATATGAGTCTAAAAATGAAAAACCAAGAAAAATAAGCTT
AAATCCAAATGTGGAUATTTCTTCAUCAAAGTTCCAAGTTTGAAAAGCTTTCCAATGATATAATTTGCTGGT
TATTTCAATGCGTGTAAAAGAGAGTTTCCCAGAAATTTTGGGTCTTGATACAGGTGAACCAATACACTGGG
TATTTAGATATTTGACTCATTAGATAAACATCTTTTCTATTTGGTTTTTTGAAGCTACAAATGATCCAAAG
AATGATCCATATTAATTTATGCTTCAATGGGNGTCCAGGTTGCAGCTCTTCAACCGGATTAATTTTTTGAA
TTAGGACCATCTCGATCAACAAACCTTTACACCCAGTTTACAAACCATATTCCTTGGAAATCCAATGCG
TCGGTTATTTTCTTTAGATCAACCCGTTGGAGTTGCATATTCGATATACAGGAGGAGATGAAGTTAAGAA
ACTCTCAUTGCTGTCTAAAGACGTTTATGTGTTTTTGGAAATTTGTTTTCCTCAAAATTTCCACAAATTTCTG
ACTAATAAGTTTTCACATTTGCCGTTGAATCTACGCCGGTCAATTAATACAGCATTTGCTTCAGAAAC
ATTAAACATGCCGATAGGTCATTTGAGTTGGCATCTGTGTTGATTTGGTAAACGGTATCACCGATCCAACTG
ATTCAAGATGGTTTCTATAAAUCAAATGGGCTGTGGTGAACGTTCTTACAAACCTGTTTTGACAACTGAA
CAGTGTGATCAAATGGAAGGGATTATCCTAGATGTGCTAAATTAAGTAAATTAATTTACAGTTTCCAA
TCTCCCTTCACTTCTGTTCCAGCTCAATACTACTGTGATTCCCGTTTAAATTCACCCCTAAGCTCAAAACA
GGATTAATAATCTTATGATATCAGAAAGGATTGTGCTGAGCAAGCTGGTAAATTGTACTAGAAATGGAC

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TACTTGGATGAATACTTGAATCTCGATTATGTGAAAGAGAGCTGTTGGTGCTTCTAATATTGACATTTTT
ACITTCATGTGATGACACCGTGTGTTAGAACTTTATTTTATGATGGTGAATGAACCTTTCCAACAA
TATGTTGCTGAGTTATTGGACAAATAATGTACCTGATTTGATTTATGCTGGTGACAAAGATTATATTTGT
AATTGGTTGGGTAACTTGGCATGGGTAAACGAATTTGAATATTCAGATAGTGAACATTTTGCACCAAAA
CCATTACAATTATGGAAAACAAGATGGCAAGAAAGCTGCTGGCAAGTCAAGAATCACAAACATTTTACA
TTCTTGAGAATTTATGACGCTGGTCACATGGTTCCCTTTGATCAACCAGAAAATGCTCTTAGTATGGTT
AATACITGGGTACAGGGAGATTATTTCTTTGGTTTACAGGGGTAATAAATTATCTGAAGCTGATTAA

YBR139W_homolog 55caa (SEQ ID NO 520)

MQLSTLVTLAALTVGAQAVSFGNNLKDQIILLDEESSPDLYLESVFKDLGSLPVDLITAWAEMQSELS
PEQIAKLINQVRSKNEKPEKNKFNPMSTFSSPSSKFELSNDKFAGYSMRVKESFPBILGLDVTVKQYTG
YLDIDSLDKHLFYWFFBSNDPKNDPIILWLNGGPGCSSSTGLFFELGPSSINKLHPVYNPYSWNSNA
SVIFLDQPVGVGYSYTGGDEVKNLTLAARDVYVFLLEFFQKFPQFLTNKFHIAGESYAGHYIPAFASEI
INNADRSEFLASVLINGITDPLIQDGSYKPMGGGGGGYK/VLTTEQCDQMERDYPKAKLTKLCYSFQ
SALTCVPAQYYCDSRLFPYVAGTGLNPVDTRKDCAPQCGNOCYVEMDYIDEVYINLCYVVKAVGASNIDIF
TSCDDTVFERNFILDGDMKPFQYVAELLDNVPVLIYAGDKDYICNWLGNLAWVNELEYSDSEHPAPK
PLQLWKQDGGKAAGEVKNIKHFTFLRIYDAGHMVPPDQPENALSMVNTWVQGDYSFGLGUNKLSEAD

YCL052C_homolog 1446bp public: 1..1446 (SEQ ID NO 521)

ATGAGACAAAGAACCAACCATTTATAATCCTTATCTAGTCATGATGGAATCATAACTAATCTTAATCGA
ACAAATTTCCAAATTATCAAGCATACCTTAATCATTTATTCACAATTGAGAATAAATATACCATCACCACC
ACCACCACACAACCTTAACAAATCATCATTTATATCTGGCAATTAAAGAATTAAGAATTCAAAACGAAATTC
AATAATAATGAATCAGGTATACCAATTTTTTTCATTTTATTATGAACCAGGACTTAATATTTATGCTGTA
CCACAATCTAATGTCGACAAATTAGAATTTTGGCAACAAGTTGAACAATTGATAATGGAATTTATTAGGG
ATTAATAATATCTTCACAACAATGGATTTGCTAATGTTAATTTCTTTTTATTATCATGATATTCAACCTCAA
CCATTTATGAAATTTGAAGAAGGATGGAAATTCATTTACATCCTAAATCCAATTATGATTATATATATAT
AATCAAGATATAAATTTATTTATTCGGAATTTGTTAACAATGTGTGAGAAACAGAATTTAATCTTGAAGT
GGTATTTATAAGAAATTTGGTTTGTTTTTAATTGATGAAAAAATCTCAACTAATGATGATTTGAATTTA
AGTGGTATTTAGAGTGATATTAGATGAAGATAGTAATACTAATAACAAGAAGAATGATCATATAAGACA
ATGTTTTCATATATAAACCAACACATACGAGTTTTCATGATTCTACCACCAACACCACCACCAAGATCAT
CCACAACCATTTACATCCTATTTTGAAGTACTGAAGTTAACAACAACAATCTGTTATTCCAAGTATTTT
GATGTTGAGAAATTAATAATTTTACTATTTATTTTGAATTTAAATAAATCATTAATATTTGATCAATTTCAA
ACATTTCCCATAGGATCCCAATTAATTTATTAATAATGGGAATAAAAAATTTAGAATTACCAGAATATAAA
ATTAATCAATTCGGGTAAATGAAGTTTATTTGAATTTGAATTTGATAATGATAATCATATCCCTCATCAT
ATTAATTTAAGAGTTTCAATTCAGATATCAATTTACCTCAAAATAATCATTTCCCATTTCCAAATTAGTAAT
GTTTTAAATTCGTTACCAATAATTTTATAGGTTCTAATCTCAAACAAGGAAATTTATTAGATAAATCA
CCTTTTGTACTATAAAGAGATGTTAAATTTGGTGGTAATTTATGAAATTTATTTTACTGAAGATACAGTT
TTTTATCATTTACAGAAATTCGACAAATTCGCCAATTTCCCGTAGTTCAACACTATTAGAAATTAATATT
CCTCATGGGAAACTACATTTGATAGAGTCAATAATATAACTTCACTTGGTTTATTAATTCCTGTATTG
ATGATTTTATATAGCCATTTCAATAAGAGTTTTCATGAGTACCACCTTCAAAGACGAAAGGGATTAA

YCL052C_homolog 481aa (SEQ ID NO 522)

MRQRTTIYNPYSSHGIIITNLRNTNFQLSSIPNHLFTIENKYTITTTTTTQPNKSSLYSAIKELRIQTKF
NMNESGIPPIPSFIIEPGLNLXAVPQSNVOKLSTWQVVEQLIMELLGIKLSSQOWIANVNSFYVHDIQVQ
PLNLKECWKPKLHPRKSNYDYIYNQDKIITRELETVVSEETNLEGGIYKEIGLFLIDEKISTNDQNLN
SGIRVILDEUSKTNKKKKSCHKMFKHKPRHRSFDDSTTTTTTKLIPQGLHPILSTELNMTTIVIPDF
DVEECKFYVYLNLNKSLIFDQFPQNIPIGSQLIINNGNKNLELPEYKINQWCMELLFEFEFDNDNDIPHH
INLTVHSRYQLPQNNHSHSQISNVLNLSLPIFIGCNVKEGNLLDKSPFDTKRDVKIGGNYETVFTEDTV
FYHLQNSDNGSKSGSSTLLEINIPHGKTTFDKRVNMTSLGLLLGYLMILYAISIRVFMSTTSKTKRD

YCR009C_homolog 887bp public: 1..882 (SEQ ID NO 523)

ATGTGGAAAAAGAAAAAGAGGGGAATTTTTTTTGTGATTCATTTTITTTTTTCTTTATCTCGCACAT
TTCTTTCTTTCACTAGACATGCTTTGGGGAGGATTTAAGAAAGCAATCAATCGAGCTGGCGCATCTGTT
ATTGTCAGGGATGTTGACAAAGACTATCGATAAGGACTTTGATGTGGAGGAGAGAGGATACAAGACCTTA
AAGACTGACAGGGACGAATTTACAGAAAGCTGCCAAGGGGTATTTGGACAAACATCAACCCANTCACC
TCCCAAGTCACAAATTCGCCAGATTAATTTATTAATTTTGAAGAGGAGTGAAGCAGGACAAATCGCTCTAC
TCGAATGCTTGGGACTTATTACATGCGAGAGTGTCAAGAGATTTTGATGAGGAGAGCTGTGAACACAGATGAT
GGCCCGTATAGGGAGACTGTTTTGGATCCAATTTGAAAGTTTTTCCAAGTACTTTAGTGAGATTGAAGAA
GCAATCAAAAAGAGAGCACACAAGAAGATTGACTATGAGCAGTGCAAAAGCCAAAGTTAGACGGTTAGTC
CATTAACCTGCCAAAGATGCGGCCAAGTTCCACCGCGCCGAGAGGAATTTGTCGATGGCCAAAGAGATT
TACGAAGAGTTGAATGACCAAGCTCAAGGCCGAGTTGCCGAGTTGATTCATGAGGGGTCCCTTTCTAC
GATCCGTGCTTTGAGGGCTTGGTCAAGATCCAGTTTGAAGTTCTCTACTGAGGGGTACTCGAGATTGGCA

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CAGATCCAACAGTACTTGGACCCAGCGTCCAGAGACGAGTATGCCAATGGGTTCCTTGGACGGCAAGATT
GATGATATGTTGGCACAAATCCCAAGCTTTGAGCTATACTTCCTTTAGGAAAGTAG

YCR009C_homolog 293aa (SEQ ID NO 524)

MWKKKKREFFPCHSFFFTTYLAHFFLQLDMSWGGFKKAINRAGASVIVKDVKTMKDFDVEERRYKTL
KTAGTNLQKAAGYLDNIRAITNSQVTIAELIYNLYEESKQCGSLYSNVCTYYMQSVKEFDEETVKQID
GPYRETVLDPFGKFSNYFSEIDEAIKKRAHKKIDYEQCKAKVRRLLVDKPAKDAAKLPRAEKKLSMAKEI
YDELNDQLKAELPQLIALRVFPYDFSFELVKIQDRFCTEGYSRLAQIQQYVLPASRDEYANGLLDQKI
DDMLAQMQGLSICSLGK

YCR010C_homolog 858bp public: 1..858 (SEQ ID NO 525)

ATGTCAGCTGATTTAGAAAATCAACAACCACAAGATCATCATCTTATTATTGAAAACAAGGGTCATAAC
AGTAGCAACCACCACCACCACAACAACAATTCAACATCATCCTTATGATCCTCATCATCCTTACTAAA
ATTGAAACTGATGGAGATTTATGTTTACTTTTGGTAAATGAAAGATATTTTACGTTTGTGATTTTATGTTGAAGCA
TTTGGTGGTACTTTAAATCCAGGGTTAGCTCCACCACCCTAAAAATGATTTTGGCTAAATCCTGCTCCATTG
GGATTATCGGCATTTGCTTTTAAACAACATTTCTTTTAAAGTTTAAATTAATTGTTGAAGCTAGACGGCTTACT
ATTCTAAATATGTTGTTGGATTGGCAATTTTCTATGGTGGTGGCTGCCAATTAAGTTGCTGGTATGTTT
GAATTGGCCGTGGTAATACTTTTGGTGGTGGTGGCTTTGAGTTTATACGGAGGATTTTGGGGTGGTTGG
GCTGCTATTCAAGTTGATTCATTTGGTATTAAAGCTGGCTTTATGCTAAATAATACGAGAATTACATTAT
GCTCTGGCATATTTTAAATTCCTTGGTTTATTTTCACATTTTCTTGTATGCTTTTAAACGGTTAAATCT
ACTGTPGGCATTCTTTTAAATATTTTCTTTTAAAGTATTACATTTTATTATTGGCAATTTCTGATTTT
ACTGGTAAAGTGGCAATTAAAAAGCCGCTGGACTCTTTGGTTTAAATTAATCCTTTCTCTGCTTGGTAT
AATGCTTATGCTGGTATTTGCTAATCCCAAAATAGTTATATTAATCTGTTAAAGCTATTCATTAACAGAT
TTACAAGATCCAAACAGAAAAAATAATAA

YCR010C_homolog 285aa (SEQ ID NO 526)

MSADLENQPPQDIHILIIENKGDNSKNIHHNNNSTSPYDPIIHPIITKLETDGDYVTFGNERYLRSDLVLA
FGGTLNPLGLAPPPKNDPANPAIAGTSAPALITFVLSLINCEARGVTIPNIIVVGLAFPHYGGAAQLVAGMF
ELAVGNTFGGVALSSYGGFWGANAAIQVDSFGIKAAAYANNTEELHYAVGLIFLIQWFIETFFLMMLLTVKS
TVAFFLIFFFLSITFLLLAISDFTGKVAIKKAGGVFGLITAFVAMYNAYAGIANPQNSYITVKAILPLPD
LQDPTRKNK

YCR021C_homolog 1029bp public: 1..1029 (SEQ ID NO 527)

ATGTCCGCTGCTGTTTCAACTTTATCCGATATCATCAAACGTAATGATGCTGTTAACGTGAACCCACCA
AACCCAATTTATTGATTTACATATCACTGAACATGGTAGTGATTTGGCTTTGGGCTGTTTTTTCAGTTT
GCATTATGCAATTTGGCATTTGATTTCATTTACAGTTTTTACGAGTTAGAAAAATCTGGTTTGAAGAGA
GCTTTATTGACTATCCCATTTTAAATAGTGGCTGTTTTTGCCTTTGCTTACTATACTTATGCTTCTAAC
TTGGGCTATACTTGGATTTTGACAGAAATCAACCATGCTGGTACTGGTTTATAGACAAATCTTTTATGCA
AAATTTGTTGCTTGGCTTCTTGGGTTTGGCCATTAGTGGTTGCCATTTTCCAAATTAACCAATACCAAGC
TTTACTACTACTGAAGATGACTCTGATTGCTTAAAGAAATTCATTTCTTTGTTTGAAGCTTTGTTTACT
AGAGTTTGGCAATTTGAAGTTTTTGGTCTTTGGGTTTATTGATTGGTGGCTTTAAATTTGAATCTACTTACAA
TCCGCTTATTTCACTTTTGGCTCTTGTGTTCCAAATTCCTTGGCTATTTATTTAGTCATTAATGATGTGGTT
GTTTCATTTGGTTTCACTTCTCTCATTGAGTCTTTGGCAATGCTCTTATCCTTGGCTTTTGTATTGTTTGG
ATTTTGTACCCAGTTGCTTGGGTTTGGAGTGAAGGTGGTAAATGTTATTCAACCAGATTCAGAAAGCAGTC
TCTATGGTATTTTGGATTTGATCAGTTTGGGTGTTATTCCAAATTATCTTGAATTTGGATTTGCCATTAA
AACGTTGATGAAGAATCTTCCACCAAAATATGGCATTTCUATTTGAAACCAGAAAAATGAACATGCTTCA
ACTGCTACTGAAGATGTTGAAAAGCAGTTGGTGAAACCCCAAGACATTTCTGGTGATACTGCTGTTGCT
CCATCAGCTCTTCCAGACACTGCTCTTGGTCAAGCACAAACCCCAAGCTCAAGAACCTATTTAA

YCR021C_homolog 342aa (SEQ ID NO 528)

MSAAVSTLSDIKRNDAVNVPNPPIIDHTEHGSDDLWAVFSVTFALFAIVHGFYISFTDVRKSGLKR
ALLTIPLFNSAVFAPAYYTYASNLGYTWILTEFNHAGTGFRQIFYAKFVAVFLGWFLVLAIFQIITWTS
FTTTEDESDLLKPIISLFEALFTRVLALIEFVLGLLIGALIESTYKNGYFTFAVVFQLEFAIYLVINDV
VSFGSSSSHSVFGNALTAFVTVWILYPVAVGLSFGGNVTQPDSEAVFYGLIDLTTEGVTPTTETWTAIN
NVDEEFFTKIWHFHLKPENEHAPTATEDVEKAVGETPRHSGDTAVAPSGVPDGTGAQAQAEAEERI

YDR178W_homolog 510bp public: 1..510 (SEQ ID NO 529)

ATCATTTCAACTATTTCAGCTATTGCTTTAACCACTTTAACTAAATCATCATCATCATCATTTAACT
ACTACTGTTAGACCAATTATTATTGGCCAATTTTACTAGAGGAATTAAACTATTCTTCAACCACCAGCT
TATATTGTTGGTACAGTTAATGATGCTTATGTACCACCACCACCACATAAATTAGAAGGTTTCATTACAT
TCGACTAGTGAANGGATTTGTTGCTAATGGTATGTTACCATTAGTTTTTACCACCATTATTACTGGTGGT
GGTGGCTTCGACTTTAATTGATTCCACCATGTCAGCATTATTAATTATTTCAATTTGTCATACTGGTTTCCAA
AGTTTGTATTATAGATGATATTCCCTAAAAGAGTTTATGGATCTTATCATTAATTAAGCCATGTAATTTATTC

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ACTTTTGGTACTGGTATTGCTGGTTATGGTATTTATC AAAATTGAAACTAAAGAAAGGTGGTGGTTTCCAAT
ATTATTTCAAACTTTGGAAAGCTTAA

YDR178W_homolog 169aa (SEQ ID NO 530)

MISTYSRIGLTTTLTKSSSSSSSLTTFVRPLILANFTRGIKTIPTQPPGYIVGTVNDAYVFTPPHKLEGLIH
WTSERIVAIGMLPLVLAPFITGGGASTLIDSTMSALLLFHCINTGFQSCIIDDIPKRVYGSYHMYAMYLC
TFGTGIAGYGIYQIETKEGCVSNIIISKLMKA

YDR202C_homolog 387bp CDS: 1..387 public: 1..387 (SEQ ID NO 531)

ATGACAGCAAATATCTTGAATAATAAAACATTTCATAGATACTGTATTATCAATACAACTCAAAAT
GATAAAGAAATTACATTGGTATATATAAATATAATTTTACCCCGATTACCTCAAAATCATAGAGACTTTA
CAGATTTGTTCAAATTTGTTGAAGTACAATTCACCACAAGAACCTGATTCCAAACAAATGTATTGAAAAA
GGTCCATCTATCAAGCTACCTTTGTCTTTAACCAATCAACAAGATTCTGTCAATGGCATAATAACCCGA
GATGGACCATATATCACAGATCTTAATTTGACGGTTAAGAAATCATTATTTCAACAAGCATTTCCATAAG
TTGCGCTTAATAAAGCCAATGGTTTATAGAACAACCTGTTAAT

YDR202C_homolog 129aa (SEQ ID NO 532)

MTANILNMKTFIDTVLSIQSTQNDKELHWYIINIILPDL PQI IETLQICSNLMLYNSPQRPDSKQCIEK
GPSIKLPLSLTNQQDSVNGIITREGPYITDLNLTVKNHYFNKHPHKLRLIKPMVLEQIWN

YDR256C_homolog 1458bp public: 1..1458 (SEQ ID NO 533)

ATGGCTCCAACATTTACGAATTCFAACGGTCAACCAATTCACAGAACCAATTTGCCACTCAAAAGACTTGGT
CAACACGGTCCATTGTTGTTACAAGATTTCAACTTGATTGATTCAATGGGCCATTTCCGATAGAGAAAGA
ATCCCAGAAAGAGTTGTCCACGCTAAAGGTTCCGGTGGCTTATGGTGTPTTTGGAAGTCACGTGACGATATC
ACTGATATTTGTCTGCCAAATTCCTTCCACACTCTTGGTAAGAAAACTAGAAATCTTCCACCAGATTTCTCT
ACTGTTGGTGGTGAATTAGGTTCTGCTGATACTGCTAGAGATCCAAGAGGTTTTGCTACCAAATTTTAC
ACTGAAGAAGGTAACTTGGATTTGGTTTACAACAACACTCCAGTGTTTTTCATTAGAGACCCATCTAAA
TTCCACATTTTCATCCACACCCAAAAGAGAAACCCAGAAACTCACTTGAAGGATGCTAACATGTTTGGG
GATTACTTGACTAGCAATGAAGAATCCATTCAAGTTATGGTTTTATTTCTCCGACAGACCTACTCCA
GCTTCTTTACAGAGAAATGAATGGTTACTCTGGTTCACACTTATAAATGGTCCAAACAAAAGGTGAATGG
TTTTACGTTCAAGTTCAATTCATCAGTGACCAAGGTATTAAGACTTTGACCAACCAAGAGCTGGTGCT
TTAGCTGGATCTAACCCAGATTACGCCCAAGAAGATTTGTTCAAGAACATTGCTGCTGGTAACTACCCA
TCATGGACTGCTTACATTCAAACCATGACTGAAGCCGAAGCTAAAGAAAGCTGAATTTTCTGTGTTTTGAT
TTGACCAAACTTTGCCCACACAAGAAATACCCATTGAGAAGATTTGGTAAGTTCACTTTGAATSAALAC
CCAAAGAACTACTTTGCTGAAGTTGAACAAGCTGCTTTTCTCTUCAGCCCACTGTTCTCTTACATGCSAA
CCATCTGCTGATCCAGTCTTGCAATCAAGATTGTTCTCTCTATGCTGATACCTCACAGACACAGATTTGGGT
ACCACTATATCTCAAATCCAGTGAAGTGTCTGTCTACCCGTTGCTGTTTTCAACCCACATATGAGAGAT
GGTGCTATGACTGTTAATGGTAACTTGGGTAGCCATCCAAACTACTTGGCCAGTGATTAAGCCAGTTGAA
TTCAAACAATTTTCTCTTCAAGAAGACCAAGAAGTTTGGAAATGGTGGCTGCCACTCCATCCACTGGAA
GCCACCCCAAGCTGAATTTCAAACAAGCTCAAGAATTTGGGAAAGTGTGTAAGAGATATCCAAACCAACAA
GAACATTTGGCCCAACAACATTTGCTGTACATCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT
GCATACTTTGGTAAAGTCTCTCAAGACTTGGCTGATGCTATCAAAAAGGAAGTTTGGAAATTAATCTCCA
AGAAATAA

YDR256C_homolog 485aa (SEQ ID NO 534)

MAPTFTNSNGQPIPEPFATQRVGQHGPLLLQDFNLIDSLAHFDRERIPERVVAHAKGSGAYGVFEVTD
DDIIMICAAKFLDTYGGKTRIFTRFSTVGGELGSAVTAREPRGFATKFTYEEGNLIDLVIKNTPVFFI
RDPKFPFHFIHTQKRNPEPHLKDANNFWDYLTSSNEESIHQVMVLFSDRGTPASYREMNCYSCHITYKWSNKKGEW
FYVQVHFISDQGIKTLTNEEAGALAGSNPDYAQEDLFKNIAAGNYPSWTAVIQTMTRFAAKEAEFSVFD
LTKVWPHKKYPLRRFGKFTLNENPKNYFAEVEQAAPSPAHTVPYMEPSADPVLQSRIFSADTHRHRLG
INYTQIPVNCPVGTGAVFNPHMRDGMVNGNLGSHPNYLASIKPVEFKQFSLQEDQEVNMGAAATPFHKK
ATPADFKQAQELMKVTKRYPNQRELAHNIIVHAAGADAATQDRVFAYFGKVSQDLADAIKKEVLELSP
RK

YER103W_homolog 1971bp public: 1..1971 (SEQ ID NO 535)

ATGTCTAAAGCTGTTGGTATTGATTTAGGTACAACCTATCTTGTGTTGCTCATTTTGCCANTGATAGA
CTTGAAATATTGCTAAATGATCAAGGTAATAGAATACCCCTTCATTGTTGCTTCACTGATACTGAA
AGATTGACTCGTGATGCTGCCAAGAATCAAGCTGCTATGAACCCAGCAAACACTGTTTTCGATGCTTAA
CGTTTTAATTGGGAGAAAAATTTGATGATCCAGAAGTTATAAATGATGCTAAACATTTCCCATTTTAAAGTC
ATTGATAAAGCAGGTAACCCACTGATTCAACTTCAATATAAAGGTGAAACTAAAACATTTTCAACAGAA
GAAATTTCTTCAATGGTTTAAACAAAATGAAGAATTTGCTGAAGGTTATTTGGGTTCTACTGTTAAA
CATGCCGTTGTTACCGTTCCAGCTTATTTCAATCATTECTCAACACAAGCCACCAAGATGCTGGTACT

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ATTGCTCGTTTGAATGTTTTTAAGAACTATTAATGAACCTACTGCTGCTGCTTATGCTTTAGAT
 AAAAAAGGTTCAGAGGTGAACATAAGTTTTTAATTTTCGATTTGGGTGGTGGTACTTTTGATGTTTCA
 TTATTAGCCATTGATGAAGGTATTTTCGAAGTTAAGCCACTGCTGGTGATACTCATTGGGTGGTGAA
 GATTTTGATAACAGATTAGTCAACTTCTTTATTCAAGAATTCAGAGAAAGAACAAAGATAATTCC
 ACCAACCAAGAGCTTTAAGAAGATTAACTGCTTGTGAAACAGCCAGAGAACTTTGTCTTCTTCT
 GCTCAAACCTCAATTGAAATTGATTCCTTATATGAAGTATTGACTTCTACACTTCAAACACCCAGAGCC
 AGATTTGAAGAATTGTGTGCTGACTTGTTCAGATCCACTTTAGATCCAGTTGGTAAAGTTTTTAGCTGAT
 GCCAAGATTGATAAATCTCAAGTTGAAGAAATTCTCTTGGTTGCTGGCTCCACCAGAAATCCAAAGATT
 CAAAAATTGGTTTTCTGATTTCTTTAATGGTAAAGAATTGAATAAAATCTATCAACCTGATGAAGCTGTT
 GCTTATGGTGTGCTGCTGTTCAAGCTCCCATTTTAACTGGTGATACCTCTTCCAGACTCAAGATAATTG
 TTATTGCGATGTTGCTCCATTGTCACTAGGTATTGAAACTGCTGCTGCTATCATGACCAAAATTGATTTCCA
 AGAAATCTACTATTCCAACCTAAGAAATCAGAACTTTCTCCACTATGCGGATAACCAACCAGGTGTT
 TTGATTCAAGTGTTTGAAGGTGAAGAGCTTAAACTTAAAGATAACCAACTTGTGGGTAAATTTGAATTA
 TCTGGTATTCCACCAGCTCCAAGAGGCGTCCCTCAAATTGAAGTTACTTTTCGATATTGATGCTAATGGT
 ATCTTGAATGTTTTCTGCTTTAGAAAAAGGTACTGGTAAAACTCAAAGATTACTATCACCACCGATAAA
 GGTAGATTATCCAAAGAAAGAAATTGATAAAATGGTTAGTGAAGCTGAAAAATTCAAAGAAGAAGATGAA
 AAGGAAGCTGCTAGAGTCCAAGCCAAGAATCAATTGGAATCTTATGCTTATTTCATTGAAAAACACAATC
 AATGATGGTGAATGAAGATAAGACTTGGTGCAGATGATAAGAAAAATTAACTAAAGCCATTGATGAA
 ACTATTCTTTGGTTAGATGCTATCTCAAGCTGCTTCTACTGAAGAATACGAAGATAAACCTAAGAAATTA
 GAATCAGTTGCTAATCCAATCATTAGTGGTGTCTTATGGTGTCTGCCGTTGGCGCTCCAGGTGATGACGGC
 GCAATCCCAAGTGTGCTGGTGGCTTCCCAAGTGGTGGCCAGGTGCCGTTGGTCCAGTGGTGTACTGGT
 GGTGAATCAAGTGGACCAACTGTTGAAGAAGTTGATTAA

YER103W_homolog 556aa (SEQ ID NO 536)

MSKAVGIDLGTYSVAFHAKDRVEILANDQGNRTTPSFVAFTDTERLIGDAAKNQAAMNPANTVFDK
 RLIGRKDDPEVLNDAKHFPFKVIDKAGKPVIOVEYKGETKTFSPPEISSMVLTKMKEIAEGYLGSTVK
 DAVVTVPAYFNDSSQRQATKDAGTIACLNVLRIINEPTAAAIAYGLDKKGSRCHEHNLITFDLGGGTDFDVS
 LLALDEGLFEVKATAGCTHLGGEDFDNRNLVNFIIQEFKRNKKDIDSTNQALRLRLTACERAKRTLSSS
 AQTSEIDSLYEGIDFYTSITRARFEELCADLFRSTLDFVGKVLADAKIDKSQVEIVLVGGSTRIPKI
 QKLVSDFFNGKEINRSINPDRAVAVGAAVQAATITGDTSSKTQDTITFDVAPISTGTEATAGGIMTKLIP
 RNSTIPKKSETFSTYADNQPGVLIQVFEGERAATKDNLLGKFEISGIPPAPRGVPOIEVTFDIDANG
 TILVSALEKGTGKTQKITITNDKGRLSKEEIDKMSAEKEEEDKEAARVQAKNQLESYAYSLKNTI
 NDGEMKDKIGADDKEKLTKAIDETISWLDASQAASTEYEDKRKELESVANPIISCAYGAAGGAPGGAG
 GFFPGAGGFPGCAPGACGPGGATGGESSGPTVEEVD

YGR086C_homolog 954bp public: 1..954 (SEQ ID NO 537)

ATGCATAGAAGTTATTCTTTAAGATCCACTAGAGCTTCAACTGCAATCTCAATTTACAAGCTCCACCTCCA
 CCACCATCATCTACCAAAATCCAAATTTTTTTGGTAAAGGTTGATTAGTCATACTTTCCGTAAACAAGCT
 GCTGGTGTCTTAGGTCCAGAATTGTGAGAGAAATTGGCCATTTTAATTAAATGGAAAAAATTTAAATC
 AGATCAATTGAATCACTTCTGTTGAAGAGAAAGATGTTGCTAAACAAATTATCTTTATGGGTTGAAGCT
 AATGAAGATCATATTACTCATATCACTCATAAATTGGCGCTTTAATCTATGAAGTTGGTGAATTGGAA
 GATCAATTTATTGATAGATATGATCAATATAGAATCACTTTGAAATCTATTAGAGATATTGAAGGTTCA
 GTTCAACCAAGTAGAGAAAGAAAAACAAAAAATTACTGATCAATTTGCTTATTTGAAATATAAGATCCT
 CAATCACCAAAATTAATGTTTTAGAACAAAGAAATTGGTTAGAGCTGAAGCTGAATCTTTAGTTGCTGAA
 GCTCAATTGAGTAATATTACTAGAGAAAAATTGAAAACCTGCTTTTAATTTATCAATTTGATTCATTTAGA
 CAACACGCTGAAAAAATTCTTITAATTGCTGGTTATGCTAAAGCTTTAATAGAAATTATAGATGAAGT
 CCACTCACTCAAGTTGAACCTAGACCAGCTTATGACGGTTATGAAGCTTCTAAACAAATTTATTATTGA
 GCTGAAAAAGCTTTAGCTTCTTGGACTTTTGATTCTGCCGTTGTTGCTCCAACCTTTATCATTAGCTGCT
 CATGATGAAGAAGCGAAGAAGATTATGAAGGTTGTTTATGAAGATGATGAATTGGCTAATGAAGCTGAA
 AATTTAAGAATTGCTGAAAAAGATTTTGATGAAGTTGAAGCTAAAATTTGCTGCTTAA

YGR086C_homolog 317aa (SEQ ID NO 538)

MHRTYSLRSTRAPTASQLQADPPPPSSTKSRFFGKGSISHTFRKQAAGALGPPELSRKLAILIKMEKNLM
 RSTELTSRERKDVAKQLSLNGEANEDDISDITDKLGLVLIYEVGELEDQFIDRYDQYRITLKSIRDIFGS
 VQPSRERKQKIIDQIAYLYKDFQSPKINVLEQELVRAEAESLVAEAQLSNITREKLKTAFFNYQFDSIR
 EHARKTAITAGYVKALLELLDESPTVPTGETRPAYDGYEASKQIILDAENALASWTFDSAVVRPTLSLAA
 HDEEABEDLEGAYEDELANEENLRIAEKDFDEVEAKIAA

YGI197C_homolog 1536bp public: 1..1536 (SEQ ID NO 539)

ATGTCTCATGATGATTCAAATCTGAATTCAAACCCAGCTCAAATCCAACCTCCAATCCTGTGTCAAAG
 CCGTCTGATATGGGTCAGATCAAGCAACGACAGTGGCTCCGAACCATCAATACAACATTTTACGTTAGCC
 CCACTCGAACCAAGGCGATGAAGAGGATATGGAATGGGTGAGCCAATATCACGACAATCAACCTTT
 CTTGACACATACAAATCTCGATATTCTTTTCCACGAGAAATTTGCGAGCTCAAAGAAAGGAATTGTCC

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ACGAAATATCTTAAAAATTTATCTAGTCATGCCCATTTGGTTGCTTAGGAGTGTTFCTATATATTGCGGT
 TCAATGTATCAGAGGAAACCCGAATTAAAAACTTGAAATGTTGGTAGITTTAGAGATGAAGAAATTT
 AATGGCAICCCCTCCACTTTTTTGGCAATCAGCTTCGTGATTTATTGGCCACCCCAACGGCTAGAACACTC
 GCGGATTGGAAATATATAACACTAGCGAATTTGAAACTATTGCATCAAAACACAAACACAAATAAAT
 GAAGAGCTCATTGCTCAAAATTCATCATCAAAATTTATGCGGCTCGACATATGTCAAGCAAAATTCATCT
 TATAACATATACAATGCATTAGCCAAATGGCAATCAGTACAATGTCAGTGACATCTGTGATTGTTACTAT
 CAAACAGGAAGACACCTAACTAGTGTGGGCCATATGTGGTGGCATCTATAGATGCCATTCAAACATATG
 TGGTTGGATCAAAACCTGGTGATGAGGGACATTTGTGAGAATTGCTAATATAACTCTTGACAATGCAAAAC
 TCGGTTCGTGTCGCCACTACCGCCCTTGGCAATCCAAATAAATTGATATGAGACCATCTACTAGTGGAGTT
 TTAGTTGCAGCTTTACAAATTTGGTCTTCTTTATCTTGTTCATTGTTAGCTTTTTTCAGTTTCAATTTTTTT
 GTUGATATACACCGATCAGTGGCATTAATGGTGAAGCAAAAGAACTTTTACTTTTATCCAGTTTTTTGA
 TCAATCATATCGTATTTTGTATCAGTTTAATGTTTGGTTTGGTTACTTTAGCGTTTCAAGTTGATTTT
 GCTGTTACATTTGCTAAATCTGGCTTCTTACTTTTACTGGATGGTAACATTTTAAACAATGTGGAGTGT
 GGATTGGCTAACGAATTCGCCGCTATGCTCATACTTACTATCTATCCACCAATGTTTGGGTTTTGGTTG
 ATCTTCTGGGTAATTTATAAATATCACACCCACATTCACACCAATTTGCTTGTACCTCAATTTTATCGG
 TATGGTTACGCTATGCCAATGCATAATGCTTTTGAATTTTATTCTGTTACTTTTTTCAACACGTATAAG
 GGATTAATAGGAAGAGCATTTGGAATCATAATTCATGGGTGGTATTTTAACATTAATGGCACCAATA
 GTGGTGGTTTTACTTTGGTAGCACTATGAGTAAAAAGCTGCTGCTCCCGCTGCTGCTGCAAAAAAGGAA
 AAGGAAAAGTCAAAGTAA

YGR197C_homolog 511aa (SEQ ID NO 540)

KSHDDSNNSNPNPSNPPTSNPVSKPSDMGRSSNDSSGSEPSIQHFTLAPLEPQGDDEEDMEMGEPISRQSTF
 LERVQSRVSPFHENIRAQRKELSMKYKTYVVMATGCIQVFSTYWGSMYQRFETRIKNLKNMLVVLEDEEL
 NGIPPLFGNQLRDLLEPTARTLGLWKIYNTSEFETIASKHNNTLINEEVLRIHQHNYAAATTVYKQNS
 YNLYNALANGNCTNVSDSVYCYEYETGRHLTSVGPYVVASIDAIQTMWLDQNSVMRDIVRIGNITLNDAN
 EVAVATTALAFQIIDMRPSTSGVLVAALQIGLLYLIVISFFSFNPFVDIHRSVALMVKQRNELLRYVFA
 SIISYFVILSMFGLVTLAPQVDFAVTFCKSGFLVYVMVTFLTMMNSVGLANELAAMLILTIVPPMVGFWL
 IFWVLIINTFPTFTPIALLPEFYRYGYAMPLHNAFELYSVLFFNTYKGLIGRSIGIIIAWVVFELTLMAPI
 VVVYFGSTMSKKAAAPAAAAKXEXKXK

YGR250C_homolog 1890bp public: 1..1890 (SEQ ID NO 541)

ATGTCCTGCTGCTGAAACTAATCAACTTCAAGAATCTATGGAAAAGTTGAACATTGGTTCAACTACTGAA
 GAACAATCAGCTGCTGCTGCTACTTACCAGCTGCTGATCAATCAGCTGAAGAACAAGCAGAAATCATCTGGT
 GTTGGCCGAGANTTCTGCCCTCCTTGTACGTTGCTGCAATTTGAACCCATCTGTTAAATGAAGCTACCTTGTTC
 GAAATCTTTTCTCCAAATCGGTCAAGTTTCCCTCTATCAGACTTTTCTCCTGATGCTGCTCTAATAAATCT
 TTAGGTTATGCTTACGTCAACTTACCACAAGTACCAAGATGCTGAAAAGCCTATTCAAGAATTTGAACCTAC
 AACCCGATCGAAGGTGCTCCATGTCGTATCATGTCCTCTCAAGAGACCCATCTGCTAGAAGATCTGGT
 CATGCTAATTTTTCATCAAGAATTTGCATCCAGCCATCGATAACAAAGCTTTGCATGACACCTCTTCT
 GCTTTTGGTAAATTTTGTCTTGTAAAGTTTCCCAACCGATGAATTTGGTCAATCAAGTGTTTTGGTMTT
 GTCCACTATGAACTGCTGAAGCTGCTGAAGCTGCCATTGAAATGTCAATGGATGTTATTTGAACGAT
 CCTGAACCTTTTCTGCTAAGCACATTTCTAAAAAACACCCCTGAATCTAAGTTTGAAGAAATGAAAGCC
 AACTTCACCTAACATTTATGTTAAAAACATTGACTTGAACCTATTCAAGAAGAAAGCTTTGAAAAATTTCTTT
 TCTCCATTGGTTAAGATTTACTTTCCATTTACTTTGAAAAAGACCAAGATGGGAAATCTAAAGGTTTGGT
 TTTGTTAATTTTGAAGATCATGAATCTGCTGTTAAGGCTGTTGAAGAATTGAACGATAAAGAAATCAAC
 GGTCAAAAGATCTACGTTGTTAGAGCACAAAAGAAAAGAGAAAGATTGGAGAATTGAAGAAAACAATAC
 GAAGCTGTTAGATTAGAAAATTTGCCAAATACCAAGGTGTCACCTCTTTCTTGAAGAAATTTGGATGAC
 ACTATTGATTCTGAAAAATTAGAACAAAGATTCMAACCATTTGGTACCATTACATCTGCCAAGGTTATG
 GTTGATGAAGCTGGTAAATCAAAAGGTTTTTGGTTTTGTTTTGCTTCAACACCCAGAGAAGGCCACCAAG
 GCTATCAGTGAATGAACACCAGAAATGATTACGGCAACCCATTTGATGTTGCTTTGGCTCAACGTAAG
 GATGTTAGACGCTCTCAATTAGAACAAACAATTCAGGCCAGAAACCAATGAGAATGCAAAATGCTGCT
 CCTGGTGGTTTTACCTGGTCAATTCATTCCACCAATGTTCTACGCTCAACAAGGTTTTTTCCACCAAT
 GGCAGAGGTAACGCTCCATACCCAGGCTCTAATCCACAAAATGATGATGAGAGGTTAGAGGTCAACCATTC
 CCAGAACATTCGCCAAGACCGCTCCAAATGGCCAACCAAGTTCTGTTACGGTATTCCACCTCAATTT
 CAACAAGACTTTAACGGTCAAAACATCAGACCTCAGCAACAACAACAACAACAACAACAACCAACCTGGATAC
 TATCCAAACCGTAACCAACCAAGCAAGAGAGACTTGGCTGCTATCATTTCTAGGTTCCACAAGATCAA
 CAAAGAGAAATTTGGGTGAAGAAATTTGATCCAAAGATTTGCTACCGGTAAGGCTCAAGAAACCAAG
 CCTGCTGGTAAATCACTGGTATGATCTTAGGTTTGAATAACCAAGAAATTTTGGATTTGTTAGATGAT
 GATGAATGTTTCAATAACCATTTGAGATGCTTTGACTGCTTTTGAAGAGTACAAGAAGCTCTGAACCT
 CCGGTAATGCTGAAGAGCAAGCTTAA

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YGR250C_homolog 629aa (SEQ ID NO 542)
 MSAETNQLQESKEKLNIGSTTEEQSAAATTTADQSAEESQGESGVAENSASLYVGEINP?SVNEATLF
 ETFSPIGQVSSIRVCRDAVSEKSLGYAYVNYHKEYECEKAIEELNVMPIEGRPRCRIMWSQRDPSARRSG
 DGNIFIKNLHPAIDNKALHDTFSAFGKILSCKVATDEFGQSKCFGFVHYETAEAEAAIENVNGMLLND
 REVVFVGKHISKKDRKSKFEEMKANFTNIYVKNI DLNYSSEESFEKLFSPFGKITSYLEKDQDGKSKGFG
 FVNFEDHESAVKAVEELNDKEINGQKIYVGRQKKRERLEELKKQYEA VRLEKLAKYQGVNLPVKNLDD
 TIDSEKLEEEFKPFGTITSAKVMVDEAGKSKGFGFVCFVCTTPEEATKAITEMNTRMTNGKPLYVALAQRK
 DVRRSQLEQQIQARNQMRMQNAAAGGLPGQFIPPMFYGQQGFFPPNGRGNAPYPGNPQMMRGRGQPF
 PEQWPRPGPNGQFVYVYGI PPQFQDFNGQNMRRPCCQCCQPPRGYYFNRNQT SKRDLAALI SSVPQDQ
 QKRILGEELYPKIVATCKAQEPEAAGKITGMMLCLENQFI LDLLDDDELNNHPEALTA FEYKKSBA
 AGNAEEQA

YKL117W_homolog 666bp public: 1..666 (SEQ ID NO 543)
 ATGTCCTCGACAACCACTCAAACCTCCAACCTGTATTATGGGCTCAACGTTCACTCTGAAGATGACCGCTCCC
 AAAAATATCATTTATTTAACCATTCAAATATCTGATCCAAATGATTTAAAAATAGATTTAAAAAGTGAT
 CATTTAATTATTGATTCTAAATCTAATGATTCAGTTTATTCATCAATTCGATTATCATTTTACAAATTGAT
 TTTTTCAAAAGAAATAGATCCTGATCAATCAAAAATTAATACTGAAAATGGTTACATATTTTATATGATT
 CTTTCGTAAAAAGATCAACAAGAAGATATTTGGCCACGTTTAACTAAAGAAAATTTGAAATATCATTTAT
 ATTAAAACTGATTTTGATAAATGGGTGGATGAGGATGAACAAGATGAAGTTAAAGATGATCCAAATGAT
 TTTGGTGGACCTGGTGGACCTGGTGGAGCTATGGATTTCTCACAAATGTTGAGCCCATCGCCCGGTTTA
 GGTGGCACTGGTGGAAAGTGGCGGTCTCGGTGGCTCGATCTTACTCCATTCGCTTCCTCAATTGGGTCAA
 GCTGGT
 AAAGCGCAAGAAGAAATCAAATGCCACTGCTACTGAAAAAGAAATA

YKL117W_homolog 221aa (SEQ ID NO 544)
 MSSTTTQTPTVLNAQRSSIEDDAAKNI FYLTIQISDFIDLKIDLKSDHLIIDS KNSDSVYSSIDYHLQID
 FFKEIDPDQSKINTENGSHIFMILRKKDQOEYWFRLTKEKLKYHYIKTDFDKWVDEDEQDEVKDDPND
 PGGPGGPGGAMDFSQMLSGMGGLGGTGGSGGPGGVDLSALASQLGQAGGAGGAAGLDGEEGEEGDEEAK
 KAQREESNATATEKE

YKR075C_homolog 3042bp public: 1..3042 (SEQ ID NO 545)
 ATGTCGTTATCAGGAGAAGTGTTTTCAGGAGGAGCAACCACTTCTCAACATATCGAGGCGACAAGATGAT
 GACCATTTTGAAAATACAACCTTTAATTGAAAAGAACTAGATCCATGGGTTTATTAGATCAATTTATC
 CTTGATAAACTAAAAGAACAAGATGGTAATAATTGAGAAGCAATTCATCAACACAGCTGCAATCAACA
 ACCAGCTCAAGAACTTGGCAGCTATGGCAGCTATAGCATCACAAACAATTCGTCATNCTTAACGAA
 ACTCCAAGCAGTCAACATCATGAACTATAGAATCCATATCTAATAACTCCGATGGCGATGTAAUCCAT
 TCATCAGATGTAGCGCCATCATCTACATCACCTGTCAATTCACCTTCACCAACTTCCCTCACCAGCATTA
 GATTTAAAATCTCCAGAACTGTTCGCTCATGATCATACAGATTTAGCTGTTGAACTTCACGTCATGTT
 CATATTATTCACCAATGCGGACGTTTCTGATATTTGGAAGTCTTGGGATACGTTATTTCCAAAAGAA
 AAGATGTTGCTAATGCTGCAAGATTTGGAATATGCTTCATCCGAGAACTTCCGCTCAAGACGCTCTAAT
 UTCAGACTATAAGTCCAGAACTGCTGAAATTTGGTCCGAAAGATAGTGATGTTACTTGGCTTTATGGAACA
 ATATTAAAAGATGATGACCATGTGAATAATGAAAATCACGACTCTGATGCTATTTGAACTACTGCTACT
 AGTTCTGTGTCGCGGGATATATCTATTCACAAAAATGTTCCAGTAAGAAATGGACCTAAACCAATATG
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 ATACATCAAAAACAAAAGAGAGAACAAAAATTTGAACACAAAGAAATTTGAAAAGACACATCAAAATGAAT
 CATCCCGATGAATATTTTGATCCCGAAGCCCTTCTGAACAAATTAACAGTCAATATAAGAAATACAGCT
 CCTACTCATAACACTAGTGTGGCCAAATTACAAGCTTGTGTGAAACTTCCCAATTTCTTCACTCTTCTGCT
 AGTTTGAAAGATTTGATGAAAGATGAAGCCGTTGTTGTGCTTCTTTCAGAACAAATCAGTCAAGATCAA
 AACCAAGAAGATGTAATGTTTCTCGGCGCGTTCAATCCAAAGTGAAGACACATACATTTTAATGAC
 GAGTGTATGCAATGTATTGCCATTGATGTGATTTCAGATGATGAGCAACGATATATTTCTGATGAAGAA
 GATTATGATTCTGATGATGACGATGATGATTATTTATGATCAATATGAACCACTTAATGACAGCTCTAGCT
 CAAAGTCACCTATATGAAGGAGACGATGAATCCATTTAGGCAAGCCGATCAACAGGTAGAGGATGATGAA
 GATGGATCTGAAGATGAAGAAGACGATGAAGGGGGATTCTTTTTAAATGTAAGATCCAAATTTCAATGCC
 CCAATAATTTTGGGCCAGCATTCAAGTGCATCAACTTCTACTCCAGTGGCAGCATCTTTAAGTCGTAC
 ACAGATATTACTCATGATACAGCATCAATATCTACCAACCAACAGTAATCTTATATAACCAATTCAAATTA
 TTACCTTCAACATCTATTAATTTATGGTTCTGATGAATCTAGTGATGAGGCAACCCCTTATACGTCGAGT
 CTTTCTCATAATGTCAATAATGATATTAAGTAGAGGTTATGATTATTATTATGATTACACACTGTATAC
 ACAATGTAATCCAAACAATTCAGTGTATGCATCTTATCAAGTCCAGATGTTGATGATTTCCAGAAAACT
 CTTGATATGGGATCCAAATTTTGATTATGAATTTATTCMAATAACGATAGTATCCCTGTAGTAGATACA
 ACATTTGAGAATAATAGTACCATTARTAAATATGCCAATTCCTGATAGTCTGCGTCACTCACTTTTATCA
 GTTGCTACTTTCCGCTGGAGGTAAATTTCTGGTGTCACTGTAAATTTCCCUAAAATTTCCCATAGCTTAAT
 GTCAATCTTAACUCCACAACAACAACAATTCACAAGCMAAACCAAGCCAAAGACAAAGGCATCTCTCT

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TTCCANTTGAGTQANTCAGAACATCACTCAAAATAGTGATTCCGATGATGATGGTATTTACAGGAATTATCA
 ATAGGTACAAGAAGATCTAGTCAAGCTTTAGCTCAACTCGGTATTTCAATCATCATTTGACAAGTTCTACA
 CAAGAAACAGCACCACAACATTTCCCCGATGCTAAAGAGATTGAACCGGTTGCTGAACATGTTTGGAGT
 ATTAACCCACCATATTTCTCGACTTCGATTTCTAAGCAACCTACAAGTTCAAGTTCACTTTACACAACCTG
 TTTTTCGGAGGTGCTGGTGGGTTAAGTAGTACTGATAAAGAGTTCTCGAAACCTGTTTTAGGAGGATCA
 ACGTCAGCATCAACATCAACATCGCATGATGAGAAGACTACTACTATTGATTCTTCAAGTACTCOGTTT
 TTCCAAGTACCAAATAGAGATTATACTCCTTCTCCAGATAATAATACTTTGACTCGTACATTATCTAAT
 ACATCCAAGAAATCTTCAACCATTAACACCACAACAACCTTCAGAGAATGCATTTCAGAGGTTGATGGACAA
 CAATCACRAATCACAATCACAATCACAATCACAGTTGCCACTCCAAACAACAACCTGCAACCACGACGGGGA
 TTATTATTTTGATGAAGAAGATTCTGAAGATCTTGAAGATGAAGGAATGGTTATTGGTGGTAAAAGAGAA
 GAAAGAAATACATCCACAAGCATATAATGCATTAAAGTCAAGTTGCAGGTAGAAATGGTATCCATAGT
 CCAAGTCCACAATTTGGTAAATGCTAGTGCACATCTCAACATCAAGATCAAGGTCAAGATGAAGATGAACAT
 GAACATGAACATGAAGAAATCATAAGAATCTTGTGGTCAAGCTAGAGGTTTAGTTAAACACTTTCTT
 GGATAA

YKR075C_homolog 1013aa (SEQ ID NO 546)

MSLSGEVTFSGGATTSQHIEAQDDHIFENTTFXLRKTRSMGLLEDFIPDKLKEQDGNNSSEANSSTTAAST
 TSSRNLAAMAAIASQTINSSVNETPSSQHHTIESLSNNEDGVDTHSSDVAPSSSTSPVNSPSPSTSSPAL
 DLKSPPELLPHDUTDLAVEFSRHVDYLSHQWDVSDIKSWRYVISKRKDVANAARLENA,SWRTWAQRRSN
 LKTIISPEVVMWSKDSOVTVLYGPILKDDHVMNENEDSDAIEITATSSVAGIIISIAKKCSSKNGPKPII,
 KKRTMRFQSMISHSNLLKLQLATQIHQKKREQKLKQCEELKRQHQLNHPDEYFDPEALSNKLNSQYKNTA
 PTHNTSIAKLQSLKTFNSSSSASLKLMLKDEAVVVPSSSEQISHDQNQFDGNVSGDVESKGERHIFND
 EVMQCEAIDVYSDDEQRYSNDEEDYDSDDDDDYDQYEPNSDSLAQSHLYEGDDDESIEEADDEVEDDE
 DQSEDEEDDEGGFFLNVKSKSNAPETLGHSSASTSTPVPAPLSLRITDITDDTASISTTNSKSYRTIQI
 LPSISINYGSDSSDEANFYITSSLSHVMNDISRGYDYDYDYNTVYTCNPNNSVYASVQSPDVPDVPEN
 LDMCSNFDYEFIEENDSIPVVDTTFENNSTINMFIYSSEPSPLSVALSGGKNSGVTVNSPNFPPIVN
 VNSNPQQQQSQAKPKPKTKASPFQLSDSEDDENEDSDDFGISGLSIGTRRSSQALAESVFOSSLTSSST
 QETAPQHFFPDAKBIEPVAEHSVSSINPRYSSTSIKQPTSSSSLSQSFQAGGLSSTDKELSKSFLGSS
 TSASTSTSHDEKTTTLSSSTGFFQVFNRDYTFPLNNITLRTLNTSKSSPLPQTTSENAPRGDQ
 QSQSQSQSLSQLPSQQSQPRRGLLFDEEDSEDSSEDEGMVIGKREEKKLHGQGNALSQVAGRNGIHS
 PSPQFGNASAHLDQDQCHENEHEHEHEENHNKLVGQARGLAKHFFG

YLR216C_homolog 1221bp public: 1..1221 (SEQ ID NO 547)

ATGCTGTAAGTGGTGAGTGTGTTGAGAACATTCCACCAGTATTTTTCCAAATTTATATAAAATGAG
 ATAAAAATTTTGGTTTCTGGTATTTTCTTTTCCACCAACTCATGACTGCCACACCTGTTTATTMTGAT
 ATTTTCATGCAACGGCAAAACCAAGGGCCGTGTTCTTTTCAAACCTCTACGATGATGTTGTTCTTAAACA
 GAGCTAATTTCCGTTCTTATGTACTGGTGACAAAGCTATATCACCAAATCTGGTAAACCACTTTCC
 TATAAAGACTCAATTTTCCACAGACTGATCAAGACATTTATGTGCCAAGGTGGTGACTTTACCGCTCCT
 TCCGACCATTTGGGAAGTGGTGGTGAGTCCATTTACCGAGAAAGTTTCAAGATGAAAACCTTTAAGTTG
 AACCATAAACCAATTTTGTGTCAATGGCTAACTTCGGACCAACACCAACTGGCTCAATTTTCT
 ATTCACAACAGTTTCCACACACCACTTGGACGGTAAACACCTGTGTGTTTGGAGAAGTCAATTGAAGGGA
 TCAATTGTACGTCAATTAGAGAGAGCGGAAAACCTGCCAATCACAGACCAGTAGAAGATTGGAAAAAT
 GCTGATTGTGGTGAGCTTCCAGCCAACATAGAGCCGTTGCACCTGGGTGCCCATGATCCAACTGGTAT
 ACGTACGAAGAGATTTTAACCGACAACGAUATATCGACATCAACAACCCGCAATCTGTTTTCCGGCT
 GTEACCAAAATCAACCATATTGGTACCAAACTTTTGAAGAAGGGAATTAGAAAAATCATACGAAAG
 TATACCAAGGCCAATAGCTACTTGAAGATTACTTTCCCGAAGGTTTGTCTCCAGAAGACTTATCAACA
 TTGCATGGCTCAATTTATCGTGTACTTTGAACGCTGCGTTAGTGGCAATTGAAATGAAACACGGCAAA
 CATGCAATTGCTGCTGCAACAATGCATTAGAAGTAGAGCAATCGACGACAAATCCAAAACCAAGCA
 TTATACAGAAAAGGTATGGGCTATATCTAGTCAAGAGACGAGAACAGGCTCAAAACATTTCTGAAGAA
 GCTCTCGAANTAGAACCTAACGATGCTGCTATCAAAAAGGATTACAAGAAGCTAAACACAACATCAAG
 TTGGCTGCTCAACAAACAAAGAAGGCAATGGCCAAGTTCTTCTCATAA

YLR216C_homolog 406aa (SEQ ID NO 548)

MCKVVSVFENIPVFFPNLYKNEIKFSFVFPPPHQIMTATPVYFDISCMGKPKGRVVPKLYDDVVPKT
 AANFRSLCTGDKGISPKSGKPLSYKDSIFHRVIKDFMCQCGDFTAPSDHLCTGGESTYGRKFFDENFKL
 HNKKPFLLSMANSQPMNGSQFFITTVPTPHLDXKHVVFGEVIEGKSTVRQLERSEKANDRPVEDWKI
 ADCGELPANYEPVASSAGTGTGDTYFETITDNDTIDNNPQSVTAAVSKIKDITGKLLKEGKLEKSYEK
 YTKANSYLNHYFPEGLSPEDLSTLHGLKLSCYLNALVALKLKHGKDATAAANNALVEQIDDKSKKA
 LYRKGMGYITVVDDECAOKILEEALILEPNDAAIQKGLQBAKHNIKLRREKQKKAMAKFFS

YMR009W_homolog 537bp public: 1..537 (SEQ ID NO 549)

ATGCTCGAATTTATTTTCATGATAACAAACATACACTTCAAAATTTTACTGAAGATCACAATTCAAGGA
 GAACCAGTTAGTTTGTATCAACTAGCTGAAATTTGGTGTATTTACAAGTACATTACTACCCAGGAAGAA

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TTAGACGCATTTGGCTACTGAAAGAGAATACAAGAATAGAGATGTTGTTACTTTAAACTTACCAGCCTTC
 AATAATGATATTCGATTCCTTATANTCCCAATCCAACTTTTACRAAGAACATTATCATGAAGATGAG
 GAAATTAGATATATTGCTGAAGGTTGAAGGTTATTTTGATGTTAGAGATAAACAAGATCGTTGGATTAGA
 GCTAAATTTATCCCTTACGATTTGTTGATTTTACCAGCAGGAATTTATCATCGTTTTACATTGACTAAT
 GCTGCAAAACAGCTCAAGGCAGTTAGATTATTTAAACATGAACCTAAATGGGAAGCTATCAATAGAGAC
 ACAGGAATAAATACCGAAGCTCGTGAACTCTATGCTAAGACTATTGCAGTATAG

YMR009W_homolog 178aa (SEQ ID NO 550)

MVBPYTHDNKDTLENFTEDHNSCEPVSEFDQLAEIGVYKYICTQEELDALATEREYKVRDVVTLNLPAP
 NNDIDAYNAKMQQFYKEHYHDEEIRYIABEGYFYDVRDKQDRWIRAKLSFYDLLILPAGIYHRTIATN
 AAKFVKAVRFLKDEPKWEAINRDTGKNTREARELYAKTIAV

YMR11W_homolog 1641bp public: 1..1641 (SEQ ID NO 551)

ATGCTTCAAGACAACGTCATCAACATCTACAGCTGAGGCTGTAAATAATGAPATCAAAGTCAAAGAT
 GAATTTCCACAAGAAGAACAAAGCTCATACTAGTTTAGAAGATAAACTGTGAGTGCATACATTGGTATC
 ATTCAATTATGTTGTTCTTATTGCTTTTGGTGGTTTTCGTTTTCGGTTTCGATACTGCTACTATTTCCGGT
 TTCATTAATATGTTGACTTTTTAGAAAGATTCCGTTGCTACTAAAGCTGACGGTACTCTTTACTTTTCC
 AATGTCACAACCTCGTTTAAATGAATGGTTTGGTCAACGCTGGTTGTGCCATTGGTGCATTATTTCTGTCT
 AAAATCGGTTGATATGTATGGTAGAAGAGTTGGTATCATGACTGCTATGATTGTCTATATTGTTGGTATT
 ATTGTTCAAATTGCTTCTCAACATGCTTGGTATCAAGTCACTGATTGGTAGAATTAATCACTGGTCTTCCC
 GTTGGTATGTTATCAGTTTATGTCCTTTGTTTCATTTCCGAGGTTTCTCCAAAACATTTGAGAGGTACT
 TTGGTGTGCTGTTTCCAATTGATGATTACCTTGGGTATCTCTTGGGTTATTGTACTACCTATGCTACT
 AAGAGTTCATCAGACTCTTACAAATGGAGAATCCATTAGGTTTATGTTTTGCTTGGGCTTTATGTTTG
 GTTGTGCTATGTTTGAATGCCAGAATCTCCACGTTACCTTGTGCGTAAAGACAGAAATTCAGATGCT
 AAAATGTCATTTGCTAAAACTAACAAAGTTTCCCCAGAGGACCCAGCCTTATACCGTGAACCTTCAATTA
 ATTCAAGCTGGTGTGAAAGAGAAAGATTAGCCGGTAAGGCATCTTCCGGTACTTTATTCATGGTAA
 CCAAGAAATTTTGAAGGGTTGTTGTTGGTGTCTATGTTACAAGCCTTACAACAATTGACTGGTGATAAC
 TATTTCTTCTACTACAGTACCCTATTTTCAACTCCCTTGGTATGAATGATTCTTTCCAACTTCTATC
 ATTATTGGTGTATTAACTTTGCTGCCACTTTTGGTGGTACTTATGCTATTGAAGAATGGTAGAAGA
 CTCTGTTTGTAACTCCTTCCCTTCCCATGTCTGTCTGTTTCTTAATCTATTCTCTGGTTGGTACTCAA
 CATCTTTATATTGACAAACCAGGTGGTGGTCTAGTAGAAAACCAGATGGTGTATGCCATGATCTTTATGACT
 TCACCTTTATGTTTCTTTCTTTGCTTTCTACATGGGCTGGTGGTGGTTTACTCCATTATTTCTGAACCTTAT
 CCATTCAGAACTPAGAAGTAAGGCTATGGGTTTAGCTAATGCTTCCRAATTGGACCTGGGGTTTCTTAATT
 TCTTTCTTTACTTCAATTTATTACTGATGCTATCCACTTCTACTACGGTTTCGTTCTTTATGGGATCTTTA
 GTTTCTTCCATTTCTTTGCTTACTTTTATGGTTTACGAAACTTAAAGGTCTTACCTTGGAAAGAAATTGAT
 GAATTGTACTCCACCAAGTCTTCCATGCAAAATCAGCTGGTTGGGTGCCACCTTCCGAAGAAGAAATG
 GCAACCTCTACGGGATATGCTGGTGTATGCCAAACCAGAAGAGGAACACGTTTAA

YMR11W_homolog 546aa (SEQ ID NO 552)

MSQUNVSETSPALAVNNEIKVKDEFQRQEEQAHTSLEDKPVSAIYIGIIMCFLIAFGGFVFGFDGTISG
 FINMSDFLERFPGGKADGTHVFSNVRTGLMIGLIFNAGCAIGALFLSKVQDMYGRVRVGIMTAMIVYIVGI
 IVQIASQNAWYQVMIGRIITGLAVGMLSVLCPLFISEVSPKHLRGTHVCCFQIMTTIGIFLGYCTTYGT
 KSYSESRQWRIPLGLCFAWALCLVAGMVRMPESPRLVVGKDRIEDAKMSLAKTNKVSPEDPALYRELQI
 IQAGVERERLAGKASWGLFNQKPRIFERVVVGVMQLALQDLTGDMYFFYYSTTIKFSVGMNDSFQTSI
 IICVINFASTFVCIYAIERMGRRLCLLTGSVAMSVCFLLIYSLVGTQHLYIDKPGGASRKPDGDAMIFMT
 SLYVFFFASTWAGGVYSIISELYPLKVRSKAMGLANASNWTWGFELISFFTSEITDAIHFYVGFVFMCCLL
 VFSIFVYVFMVYFKGLTLEEIDELYSTKVLFPKWSAGWVPPSEEMATSTGYAGDAKPEBEHV

YMR110C_homolog 1986bp public: 1..1986 (SEQ ID NO 553)

ATGAGTAAACCATCTTCCATCAAAAACCTCAAGGCATCTGCTATTAAACCCCTCGGCTAATTCAAAATCA
 AAAACCCCAAAAATTGAGACCCCAAAAATGCAACCAAGTTGAAACACGATTAGAAGCCGAAGTTCCAACA
 ACTAAAAGTTTCAATTAAGAGAAACAGTATTACTACTGAATCTCTTAAGGCTTCAGAAGATAAGTCTACT
 CCACAAAAGCACTAACACCCCTGCTGCTGTAGCAAAAGTCTAATCCAAATACCAATGAGAGCCAGCT
 AAAATTCCAAACGAAAACTCTTAAAAACACAATCAACCACTGAGTCAAAAACAAAACGGTGCAACAACA
 ACAAAAGGAAAAATCTGATGTTCTGTTGGAGACAAAATCGACCTCATCACTACTGTCAGCAACAATAAC
 TCGGTCTTACAATAACUGAGTTGTGGAGATTCCTATTGGTCTTGAAGAATTTACTAAGGCCTTCCAT
 ACTGCCAAAACACACTCTTTACAGTTTATGATTGAACCAATTACGAAACTTGTACTTTACATGAAGAC
 AACCAGGAAGCTTTGTGTGACGCTTTTGAAMAGCACTTTTCAACGCTCTTCTTCCGAAACAPAGAACTAT
 GAATTTGCCACTGGATTGAATGAGCTAGTGTATTATATGTACAGCTCCACAAATGGAGCAAMCCATCA
 CCTGTTGACAGGTTGCCATTCAATTTCTTTTGAATCCAGTTTACATTGAGAGAAATTCCTTGGGAACA
 ATTTTAGTCATTGCTGCTTTCAATTAACGTTTTTGTCTCCATCTCACCAATAGTTGGTGTCAATATCA
 AGTGGCAACACAGTTCACCTCAAGCCTCTGAGTTAACACCCCGTTTTTCCAAGCTTTTTACTGACTTG
 TTGTCAAAAAGCATTGGACCCAGAGATATTTTGTGTGTCAATGGGCGCATTCCTGAAACACATGCTTIG

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TTGGAACAAAAATTTGACAAAAATGTTTATACCTGGTAGCGGTTTGGTAGGTACAAATAATTTGCGAAAAAG
 GCTGCGGGAACCTTGACACCCAGGTATTTTGGAGTTGGGAGGAAAGTCACTGCTTTTGTPTTGGATGAC
 ATTTCTGACAACGACTTCCCACTGTTCTCCGAAGAATTCCTTGGGCTAGATTTGTAAATGCTGGTCAA
 ACATGTATCGGTGTTGACATATGTTTGGTGGCAAAGTCCAAAGCACGACAAATTTATCCTGGCCTTGCAA
 GAGGTAAATGAAAAAGATTTTTCAGACGTTGACAAGACGAGAAACTTTACCCATATGATCCATGAC
 CGGGCATTTTGAGAAAAATGGAGAGTATACTCAACACTACTTCTGGTAATGTGATAATTTGGAGGCAAGCTT
 GATCATGGCACAAACATATGTTGGGACCTACCGTGATTGATAACCTAACCTGGACAGATTCTCTATGAAA
 GACGAGATTTCGGTCCAATTTTACCAATTTTAACTACACTGATCTTGAAAAATCCTGTCGTGAAATTT
 ATTGCTAACCCACGATACTCCCTTGGCACAATATATCTTTACAAGTGGACCTACATCTAGACAGTATAAT
 TCCCAAAATTAACACTACTACCACTTTGCTTAGATCTCGCGCATTCCTTATCAATGACCTTTTGATGCAAT
 ATTGCTTTGACAAATGCTCCGTTTGGTGGTGTGGAACTTCGGGAAAACGGTGGCTATCATGGACAGTTTC
 TCATACAGAGCTTTTACACATGAGAGGACCGTCTTCAACAAACATTTGTGGAATGATTGGGTACTCAA
 TCAAGATATCCCCCATATGCCAATAAAAAAGACAAATTTGATCCCGACCTCCCAACAAAAGTACGGTGGT
 AGAGTTTCTTCAATACACAAGGGAATCTGAGAATTCGAGGTCCACCCCTCTTGTTTTCTGCTTGGAAAC
 AATGCTCTTGGGGTAGCTGAATTAGTACGTGATTTTATTGGAGCTGGTTTGTGA

YMR110C_homolog 661aa (SEQ ID NO 554)

MSKPSSIKKSKASAIKPSANSKSKTPKIFTPKIQVETRLGEGVPTTKVSIKRNSTTTESVKASEDKST
 PQSTNTPAAAVAKSNPNTNAEPKIPNEKSLKTESPSSQKONGATTTKESDVSLETKSTSSITVSMNN
 SVLQYTELSEIPIGVERITKAPHSGKTHISLQPRKQLRNLVFTMKONQZALCDALQKDPHRLPSETRNY
 EFATCLNELVFIMSQLHKWSKPPVDELPLNLSLNPVYTERIPLGTTIIVTAAFNYPFFVSTSPITVGAIA
 SGNITVALKPSSELTPRFSKLFTDLLSKALDPEIFPVVNGAIPETTCLEQKFDKIVYTGSGLVGTIIAKK
 AAETLTPVILELGCKSPAFVLDDISDKDLATVARRLAWGRFVNAGQTCLOVDYVLVAKSKHDKFISALQ
 EVIEKEFFQDVKTRNFTMHITHDRAFERMESILNITSGNVIIGGKLDHGTRYVGTVIDNVTWTDSSMK
 DELFGPILFILTYTDLEKSCRELANEDTPLAQYIFTSGPTSRQYNSQINTITTLVRSCGLVINDVMMH
 LALHNAPFGGVGTSGNGAYHGBFSYRAPTHERTVLEQHLWNDWVLKSRYPYANKKDKLIASSQPKYGG
 RVWFNREGNVRIGGPPLLFSAWNNALGVAELVRDPFAGL

YNL031C_homolog 411bp public: 1..411 (SEQ ID NO 555)

ATGGCTAGAACAAAACAAACAGCAAGAAAATCTACTGGTGGTAAAGCCCCAAGAAAACAATTAGCTTCC
 AAAGCTGCTAGAAAATCTGCTCCATCTACTGGTGGTGTCAAGAAACCCACACAGATATAAGCCAGGTACT
 GTTGCTTTGAGAGAAATCAGAAGATTCAAAAATCTACTGAATTAATTGATTAGAAAATTTACCAATCCAA
 AGATTAGTCAGAGAAATTCGTCAGATTTCAAAACCTGATTTAAGATTCCAATCTTCTGCTATTGCTGCT
 TTACAAGAAGCGTTGAAGCTTACTTGGTTGGTTTATTTCGAAGATACTAACTTGTGTGCTATCCATGCT
 AAGAGAGTTACCATTCAAAAGAAAGATATGCAATTAGCTAGAAAGATTGAGAGCTGAAAAGATCTTAG

YNL031C_homolog 136aa (SEQ ID NO 556)

MERTKQTARKSTGGKAPRKQLASKAARKSAPSTGGVKKPHRYKPGTVALREIRRFOKSTELLIRKLRFQ
 RIIVREIAQDFKTDURFQSSATGALQEAVENYLVGLFEDTNLCIHAKRVTIQKXNQQLRRRLRGERS

YNL134C_homolog 1086bp public: 1..1086 (SEQ ID NO 557)

ATCAAAGCAGCTATCATTTCTGCATCTTTCGAACCTTATCAATTAGCGGAAATTAAGATATTCCTCAA
 CAAAAATAAAAGAAAATGAAATATTAATCAAAGCAGTAGCTTTTGCATATAAACCCCACTGATTGGAAG
 CACATTGTTTATCAATGGGCAGCCAGGTGATGTTGTTGGTTGCGATGTTAGTGGGATCATTCAGAA
 GTGGGTTCTCAAGTAACCTGGGTTTGCAAAAGGTGACACTGTAAGTCTTTTATAACTGCTAATAGATCA
 CCTCCACCTGGAGCTTTTGCAGAAATATGTAGCTGTTGATCCTGCTACTTCGATAAAGTACAATAAGAAT
 TTTGAACAATCTGACTAATTTACAAGTATCTGAAATCCACTCATTTGAAGGGCCAGCAAGTATTAATTTA
 GGTITGGTTACCGTTGGGCTTTTCAATTTCTCATTTACTTACGAATTSACAACAAAAGCAACCTGGGGAT
 AGTAITTTGACTTGGGGAGGAGCAACTGCAACTGGAGTTCTAGCCATTTCAGGTTGCCAACTACTGTAT
 AATCTCAAAGTAATCACCACAGCATCACCCAAAAACCACACCCCTCTTGAACCAATTAGGGGCGAGATTAT
 CTTTTCGATATCCAGACCGCTGATCTTGTCAATTAANTTAAGAAATATCCCAAAATTAATTTTGGCTCTP
 GATAUGATTGCAACACCAGAAACCTTTCAAAAAGTTTACGACTCAACAGAGGGGTCTCAAGAAATATTT
 ATTGATTCTTAGCAGGTTTAGACTATTCGATCAATTCCTGCCAATGATGUCAGAGGAGATCAAGTACAT
 TGGGGGCACACCATTCCTTGTTTTGGCATCTTTAAAAGAGAAAACCTGTGTTTAAATGAAAATTAATGTTCAA
 ACACCTGAATGTTAGATGATTTTACTCAGTGGTGGCAAAAGGTGGTCCCTCAAAATTAATGATCCTATT
 AAACATACAAAATTTAAAGTTATTAAAGAGGATTAGACTCCGTAAAGTGAAGGTTAGAAATGTCTAGA
 AATAATAAACCTCTGCTGAAAAGGTTGTATTTAGAGTTCTGGATCTGTA

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YNL134C_homolog 361aa(SEQ ID NO 558)
 MKAATISGSPFYQIARTKDIQQKIKENEILAKAVAFAINPTDVKHIVYQLGSPGDDVVGCDVSGIIEE
 VGSQVTGFAKGDVSAFITGNRSPTGAFABEYVAVDPATSIKYNKNFEHLTNLQVSEIHSFEGAASTKL
 GLWTVGLSPSHYLRIDNKKQPGDSILLWGGATATGVLAIQVAKLVYNLKVITTAPEKNHTLLKQLGADY
 VPDYGDADVYVVKIKNIGQIKFALDTIATPETFQKVYDSTEGSQEVFIDSLAGLDYRSIAANDARGDQVH
 WGHITACLASLKEKTVFNENYVQTPPELLDDFTQWVQKVVPQIIDRIKHTNLKLLNEGLDSVSWGLELSE
 NNKLSAEKVVPFRVSDS

YNR002C_homolog 798bp public: 1..798(SEQ ID NO 559)
 ATGACGCTTCATCTTCTCAAAAATCTGTTGGATCTTCAATCATAGATGCAAACCAAGGACCAATATAAA
 AAAGTTCGAAATTCGTCGAGAGGGTGGTGAATTTGTTATTATCAATCGTCACAGTACTACAGACATGAC
 TTGATGGCTGCCCTTCGGGGGTACTTTAAACCCAGGTGCTTCTCCTTGCCCAAAGATCAATATCAACCT
 GCTCCCTCGGGTTATGTGGGTTTGCCATGACCACTTTCTCTTATGCTTTTACAATGCCCCAAGCTATG
 GGTATCAAAGTTCCAAATGTGGTAGTTTTCATTGCATGTTTCTACGGTGGTGCAGCTCAATTTTTTGCT
 GGACGTTTGTAGTTTGTGACTGGAAATACATTTGGTATGACTGCATTGACATCTTACGGTGCCTTCTGG
 TTCAGTTATTTCAGCAATCTTGGTTCATAGTTTGGTATCGCTECAGCTACGAAGCTTCTGAAGAAACA
 GCTTCACAGTTACCAANTGCCATTGCCATTTTCTTACTTCTTGGGGTATCTTACATTTATGTTGTGC
 TTGAACACTTTAAAATCTACAGTTACTTTCAGTTCTTGTCTTCTTATTGTTTGTAAACATTCCTTTTG
 TTACCTGCTGGTCAATTTAGTGGAAAGAGTCGGTGTCTACTAGAGCTGGTGGTGTCTTTTGGTGTATACA
 GCCATTGTTGCTTGGTGAATGCCTTAGCCGCTACTGCTACTCCAACCAACTCTTACTTCCAACCTETT
 TCTATTCCATTGCCAGGTAACGTTGTTTTCAAGAAATAG

YNR002C_homolog 265aa(SEQ ID NO 560)
 MTSSSSQKSVCSILLIDANQGFLKKVELAGEGGGFVILNRKKYYRHDLMAAFGGTLNPGASFPYKININP
 APLGTCGFAMTTFVLSINNAQAMGKVNIVVVSIACFYGGAAQFFAGCFEEVNTGNTFGMTALTSYGAFW
 LSYSAILLVDSFGIAAAYASSEETASQLENAIGFFLLAWGIFTFMLWLNLTILKSTVIFSSLPFLLFVTFLL
 LAQGHFSGRGVTFRAGGVFGVLTATVAVWMDALAGTATPTNSYFQPVSIPLPGNVVFKK

YOL139C_homolog 630bp public: 1..630(SEQ ID NO 561)
 ATGTCTGAAGAATTAGCTCAAAAAACTGAAGAATTGTCATATAGATTCCAAGACTGTCTTTTGATTCCAAA
 GAAGAATTTANTGCATACCATTCATTGAACAGTAGATGGACATTTATGGTACACTAAACCACAAACCAAC
 AAGAGTCAAAAACTGCCATGATTTATTTAAAGCCAGTTATAACTTCTCATCTGTTGAAGAATTTTGGGGA
 ATTTACAACTCGATTCCACCAGCAAAATCAATTACCTTTGAAATCAGATTATCATTGTGTCAAAGAAGGA
 ATTAGACCGGAATGGGAAGATGAGGCTAACTCAAAAGGTGGTAAATGCCAATTTCTCCTTCAACAAAAAA
 CTGGAAAGTCAATCCAATCATAAATGATTTGTGGTTAAGAGGTTCTGTTGGCAGTTATTGGTGAACCTATT
 GAGGATGAAGAAACGAAGTCAATGGGATTGTGTGAATATCAAAAGCAAGCTTACAGAGTCGGTATT
 TGGACCAAGAGATTGTGATGAATCCAANTTAAGACTGTCGGTGCAGAGATTCAAGAAAGTCTTGCAATTA
 AACGATGAACAAAAAGTTGAATTCATGTCGCATGATGCTTCCAACACTAGAGGGCGCTGAACCTCAANTT
 GTTTTCTAA

YOL139C_homolog 209aa(SEQ ID NO 562)
 MSFELAQFTEETSLDSKTVFDKSEEFNAKHPLNSRWTLWYTKPQTNKSENWHDLLKPVITTFSSVEEFPW
 IYKSIIPANQLPLKSDYHLFKGIRPEWEDEANSKCKWQFSENKKSEVNPTIINDLWIRGLLAVIGETL
 EDBENEVNGIIVLNIRKQAYRVGTWTKDCDESKLKTVGERLKKVLQLNDBQKVEFMSHDASNTRCAEPQI
 VL

YOR120W_homolog 888bp public: 1..888(SEQ ID NO 563)
 ATGCCAGCTCAATTGCAAGTTAACACTGATTATTTTCACTTTAAACAAATCGAAACAAAATCCUAGCTGTT
 GGATTAGGTACTTGCCAACCAACCAATTAAGACCAAGCTTACAGAGCUGTCTTAGCAGCTCTTAAGAAC
 GGATACAGCACATTGATACCGCTGCAATTTATGGAAATGAAGAACAAGTCGGTAAAGCCATCAACCPAC
 TCTGGAGTTCCAAGAGAAGAATTGTTTGTACTACCAAAATTCGGAATGCTGACCATAAAAATATTGAA
 GAACCTTTACAGACTTCATTGAAAAAATTTGGTCTTAACTATGTTGACTTGTACTTGATCCATTGGCCA
 GCCTCAATTCAGCAAGTCAACTAATAAACCATATACTGATTTTGATTATGTTGATACTTATAGACGTTTA
 CAAAAAGTTTATAAGAACAGCAAGAAAAATCAGAGCAATTCGATGTTTCTAAATTTCAUAAAAAGAAATTG
 CAAGAGTTATCTCTTCGGAAACCTGTCCATGTTCTTCTGCTGTCAACCAAAATTGAAGCTCACCATTG
 TTCACTCAGCCTGAATTTGATGATTATTTGAAGAAAAAGGTATCGTTTTGCAAGCTTATTCACCATTG
 GCTTCTACAAACTCTCCATTATTCAGAAACGAAACUATCGTTAAATCGCTGAAAAGAAATGGTGTGAA
 CCAGCTCAAGTTTGTGATCTTGGGCAATTCAGAAAGACTGTGGTTTTGGCTAAATCCGTCACCGAA
 TCAAGAGTTATTTCTAACTTGAAACATTCACTTTTACCTTCAGAAAGATTTCCAAACATTCAGCAAAATG
 TCTGAAAAAGATGGTCTTGTGAGAACTTGTAACCCAGCTTTTCAACAACTTTTGATGATTAA

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YOR120W_homolog 295aa (SEQ ID NO 564)

MPAQLQVNTDYFTLNNCNKIPAVGLCTWQATNEDBAYRAVLAAALKNGYKHTDTAATYGNEEQVGKAIKD
SGVPREELFVTTKLWNADHKNIIEEALETSLKKLGLNYVDLYLIHWPASIDKSTNKPYTDFDYVDTRYGI
QKVYKNSKKTIAICVSNFTKKKLERLLSSEGVDVVPVAVNQIEAHPLLCPPELYDYLKEKGLVLEAYSPL
GSTNSPLFKNETIVKIAEKNGVEPAQVLVSWAIQRKTVVLPKSVTESRVISNKTFTPLPSEDPETLNKL
SEKDGVVVRTCNPAFNNFDD

YOR122C_homolog 381bp public: 1..381 (SEQ ID NO 565)

ATGCTTTGGCAAGCCTACACTGATAACTTAATTGCTAACGGTAAAGTCGATAAAGCAGCCTTATATTCA
AGA3CCGCTGACGCATTATGGGCCCCAATCGGGATCATTCGAATTACAACAACCAGAAATCACTGAAATT
GCCAAAGSTTTCCGATAGTGGCTGAAGGTTTGCACACCAGCGGTTTACACGTTTCAAGGCCAAAGTACTTT
TTGTTAAGAGCTGACGACAGATCAATTTATGGTAAACACCAAGCCGAGGGTGTATTTGTGTTAGAACCT
AAACAAACTATTTTGTATCGCCCATCTATCCAAGTGGTGTTCACACCAGGTGAAGCTACCACTCTTTGTTGAA
AAATTAGCCGATTACTTGATCAATGTCCGTTATTAG

YOR122C_homolog 126aa (SEQ ID NO 566)

MSWQAYTDNLIANGKVDKAALYSRAGDALWAQSGSELCQFEITEIAKGFDSAEGLQTSGLHVQGGQKYF
LLRADDRSIYKGHEAEGVICVHFKQTILIAHYPSGVQPGEAATTLVBKLADYLINVGY

YOR261C_homolog 993bp public: 1..993 (SEQ ID NO 567)

ATGTCAACAACCTGCAACTAGCACAAATGAATTGGCCCTTTCTGGATAAGTCAGTAGTAGTTCTCCCTTG
GTTTTACTATCTGTGGTGGACCATTATAATAGAGTTGCCAAAGATTCTAAGAAGAGAGTTGTTGGGGTA
ATATTAGGATAAATCTACTGACACAATCAAGTTACAACTCGTACGCAATTCCTTTTGAAGAAGAC
GAGAAGAACCCTGGAGTATGGTTTTTGGACCACAATTTTATAGATTCAATGGGAGAAATGTTTAAAAAA
ATTAATGCCAAAGAGAAATTGATTGGCTGGTACCATTCCAGGACCTTAAATTGAAACCATCAGATTTGAAA
ATTAATGAGGTTTTTCAGAAGATACACCGACAACCCATTGTTCGTTAATTGTTGACGTTCAACCAAGAGAA
GTTGGTATTTCCAACAGATGCATATTTTGGCCGTTGATGATATTAACCAACGATGGCTGCTGCTGCTGAAAAG
ACATTTATTCATGTCCCTTCCTCGATTGAAGCAGAAGAAGCTGAAGAAATTGGAGTTGAACATTTGTTA
AGACACATCAGAGACCAAGCTGCTGGTAACTTGTCCCTTAAGACTTTCTCAAAACATCAATCATTTATTG
GCTTTACATCAGAAGCTTGGAGAAATTGCAATTTATTGGATAAGGTTTACCAAAAGAAATTAACCTATG
AATCATACTATTTTGGGGAAATTACAGAATGTTTTTAATTTCTTGCCAACTTCATGCAACCAACTGGGG
AGTGATCTCGATGGTGGTTTCAGACTCGTCTCATGCAATTAGCCACTGCATTTACTGTCAGACAAATGAC
CAATTCATCATCATATACATTAGTACATTAGTTCCGAGCTATTATTGCATTCCTATGATTTGATCGAAAAAC
AAGTTAGAAAAATAAAAGTTGAACGAAAAATAAGCACAAAGCTTCCGTGGCTGAACCTGTCATTTAAATAGC
GAAAAGAAAGATTCTATAGAAGATTAA

YOR261C_homolog 330aa (SEQ ID NO 568)

MTTATSTINELALLDKSVVVSPLVLLSVVDHYNRVAKDSKKRVVGVILGDNSTDTIRVTNSYAI PFEEED
EKNPGVWFLDHNFIIDSMGEMFKKINAKEKSLICVYHSCPKLPKPSDLKINPVFRRYTONPILLIVDVQPRE
VGLPTUAYFAVDDIKNDGSAAEKTFIHVPSGLIEAEAEFIVEHILRDRDQAAGNLSRVSETHQSLL
GLHQKLGFTANYLDKVVYQKKLPMNHITLQKLQNVNLLPNLMKXQSGSDLDGSSDSSHALATAPTVRKND
ELMIIYISTLVRALLAFHDLIENKLENKKLNPKAKASVAESSLNSEKKDSIED

YPR035W_homolog 1122bp public: 1..1122 (SEQ ID NO 569)

ATGACTACTTCCCTTACACAACAACTGCTATTTTGGCCAAATATTTGGAATTGTCTCAAAATGGTAAA
ATCTTAGCTGAATACGTTCTGGATGATGCTGAAGGTAACACTAGATCCAAATGTAGAACTTTATCCAAA
AAACCAACTAGTGTGATGATTTACCTGAAAGGAATTTATGAAGGTTCACTACTGGTCAAGCTCCAGGC
CATGATTCTGATGIGTATTTAAGACCAGTTGCTTTTATCCTGATCCATTTAGAAAAGGTGACAAATATC
ATTGTTTTTAATGAATGTTGGAACAATGATGGTACITCCAAACAAATTTAATCATCCTCAAGAAATGTGCT
AATTGATGAAGGCTCATGCTAGTGAAGAAGTTTGGTTTGGTTTGAACAAGAATATACTTTATTTGAT
CAATATCATTATCCTTATGGTTGGCCAAAAGGTGCAATCCAGCTCCTCAAGGTCCTATCTACTGTGGG
GTTGGTACTGGTAAAGTTGTTGCTAGAGATGTCAITGAAGCTCATTTATCGTGCTTGTCTTTATGCTGGT
ATCAACATTTCTGGTATTAATGCCGAAGTTATGCCATCTCAATGGGAATTCCAAGTTGGTTCATGTGAA
GGTATTGAAATCGGTCATCAATCATGGATTGCTCGTTATTTATTACAAAGAGTTGCTGAAGAAATTTGCC
GTCAAGATTTCCCTCCATCCAAAACCTTTGAAGGGTGATTCGAATCGTGTGGTGTCTACTAATGCTT
TCTACCAAAATCTATGAGAGTTGCTTGGTGGTATGAAGTTATTGAATCTGCTTTGAGTAAATTCGCCAAA
AGACACNAGGAACATATGTTATGTTATGGTGCCGATAATGATCAAAAGATTAACTGGTGGTCAAGAACT
GGTCAATATGGATACTTTTTCATCAGGTGTTGCTAACAGAGGTGCATCTATCAGAATTCAGACAAAGCT
GCTAAGAAAGGAIATGGTTATTCGAAGATAGAAGACCAGCTTCTAACATTTCATCCATACTTGGTCACCT
CGTATCATGCTGACACAATCTCTGGTTCTATTCAGATGCTGATATGGCTAAAGAAATCCTTTAGAGAA
AGCAGTGATGATAACTAA

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YPR035W_homolog 373aa (SEQ ID NO 570)

MTTSLTEQTAILAKY₁ELSQNGKILAEVWIDAECHTRSKCR₁₁LSKKP₂₁TSVDDLPEWNYDGSSTGQAPG
 HDSDVYLR₃₁PVAFY₄₁PD₅₁FRKGDNI₆₁JVLNECHWINDGTFN₇₁KFNHRECA₈₁KLMKAHASEEVW₉₁FGLEQ₁₀₁EX₁₁₁LF₁₂₁D
 QYDYPY₁₃₁GWPKGGF₁₄₁PAPQ₁₅₁CFYCGVGTGKVVARDVIEAHYRACLYAGINISGINAEV₁₆₁MPSQWR₁₇₁PQVGPCE
 GIEMGDQL₁₈₁WIARY₁₉₁LLQ₂₀₁RVAE₂₁₁EPVKIS₂₂₁FHPKPLKGDWNGASCHTNVSTK₂₃₁SMRV₂₄₁PGGMKV₂₅₁ISALS₂₆₁KLAK
 RHKEHMLLYGADNDQRL₂₇₁GRHET₂₈₁GHMDTFSSGVANRGASIRI₂₉₁PRQVAKBGVGYFEDRR₃₀₁PASNID₃₁₁PYLVT
 GIMVETICGSI₃₂₁PDADMAKEFLRESSDDN

YMR099C_homolog 900bp public: 1.900 (SEQ ID NO 571)

ATGCCAGTTGAAGAGCTTGAAGACCGTGTATCATCTACTGATCCAAATGACTCAACTAACAGAGCCACC
 ATTTTC₁₀CAAAATTTGGTGC₂₀TACTGTACTTTCTTGG₃₀CAAAAACAAATAATCAAGAAAAATTTGGT₄₀TATCAGAA
 GGTGC₅₀TCAATTTAGATGGAAGTAAAGCCGTTAGAGGTGGTATCCCATTTAGTTT₆₀TCCAGTTTTCGGTAA
 CAAAAAGATTCAAATCA₇₀CCAACTTTCAAATTAACCTCAACATGGATT₈₀TGCTCGTAATTCAACTTGGGAA
 TTCTTGGGACAAACTCAAGAAAGTCC₉₀TATTACGGTTC₁₀₀AATTTGGATTAGGTCCAGAAAAATGTTGATCCA
 GAAACTTTGAAATTATGGAATTATGATTTCACTTTCAATTTAACTGTTAGTTT₁₁₀GACTAAAGATAAAAT₁₂₀TG
 GTTACTTTCAATTGACGTGGAAAAACAC₁₃₀TGGTAAAGAAAGCATTTGAATTTAATTGGTTTGTTC₁₄₀CATACATAT
 TATAGAATCCATGACATCAACCGATACACTAGTTTACCAATTTAATTGACCAACAATGTTACGATCAAT₁₅₀TG
 ATTGGTGAATCATATATCGAAAGGCCACCGTTATCAGTTTTCATGAACAATTTGATAGAAATTTATTTCA
 AAAGTCAGTTTTCGAAAAATCCATTCAAGTCGTTGATAAAGGTC₁₆₀CAAGTTCTTTCAATCTTCAATACAAAA
 AACTTGCCTGATTCGGTGTGATGGAATCCATGGACTAAGAAAGCTGAAGGTATGGCTGATTTCCAAACCA
 AATTCAGGGTTTCATCAAAATGGTCTGTGTTGAGCCAGGTCA₁₇₀TGTTAACTCAATGCTCTCTTTACCAGCT
 GGTGGGAAATGGTCAGGTGGTCAAGAAATCACTATTGGCGGTGAGATTAAAGTTCAAGCTAA₁₈₀TATTTAT
 TAG

YMR099C_homolog 299aa (SEQ ID NO 572)

MPVEELED₁RVIIITDPNDSTNRATILKFGATVVSWEQNNQEK₁₁LWLS₂₁EGAHLDGSKAVRGGI₃₁PLVFPVFGK
 QKDSNHPT₄₁FKLPQHCFARNSTWEFLGQIQ₅₁ESPITVQFGLGPPENVDP₆₁ETLKLWNYDFTLIL₇₁TVSLTKDKL
 VTSIDVENTGKEAFEFNWLPH₈₁TYYRIHDITDTLVN₉₁LLIDQCYDQLIGESYIEKAPVISPHBEFDRIYS
 KVSLEKSIQVVDKGQVLFN₁₀₁LHRKNLPDSVVWNPW₁₁₁WKAEGMADFOPKSGPHOMVCVEPHIVNSMVS₁₂₁LPA
 GGWKSGGQ₁₃₁EITIGGEIKVQANIY

YR085W_homolog 3519bp public: 1.3519 (SEQ ID NO 573)

ATGGATGGTGGCGATAC₁TATATATGTATAAAACAATTTAATGCCAGATTAGGCCGATGAATTGACTCTT
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 AACTTCTTCACTGGAGAAGCAGGCTTATATCCAAAAACATTTACTCAATTAATAACCAACCAATGATAGT
 AAAACACTTCTTAGATCGAGGTCAAGAAGAATGATGGCACTTAAAGTTCCGACCAAGAAACACACCA
 AAGCACACCACTACTCCCGTGGTGTGAGTAATCTCAATCCCAACACTCCTCCAAATTAACCTCCAAACA
 TTGTCTACTTCAACAGAACCTTCCCATTTAGCTGAACCAATGTCTCACTTAAATTTAAATTAAGAAITCT
 CAATCTTCTCAATATACTGGGTCTCATTGGAACGCCAAATTTGATAGAGCAATTACAAGAACTTCAAGGG
 TCTAATGCCGACTTGAACCAATTTGGCAATAGTTTAAATGAGCACAGAAACCAACCACTACAAATACCAAC
 ACTAATATAATAATAATAATAATAATAATAATGCTGCTACTAGTAATAATTACAACCAACCAACAGTTAAATG
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 TTGAGTGGAGATAAAATCTGACAAATCTTAACTGAAGATTTTGGACCCCTTTGAAAGCAAAATACTTTGGACA
 CCAAGCAAGTTTCTTCTTATTTTGCCTTGGTGTTAGGGTTTGTATATGGATGTGGCTGGGAATTTGCT
 CAACACAAAATCACTGGAGAAATCTTGGTTTGAATTTGAATTTAAATCTTTTGAAGAAGATGGATATTGAT
 TCATTTGGTACCAGATTCAAATTAATAATAAGAAATTTGGGAAATTAAGGAATTTGAATACTGAAGGAGTT
 AAAGATAAACAATTTGAGAACAGATTCTCTGTGACTGGATCAACTGGTAAAAATGACACTACCTCATCA
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 TACAAATAATAATAGTCAACAACAAGTGGTTCTCAACATCATCAGAGGAAAGGTCAC₁₁₁TGTGGGTGGAT
 GTTGGCCCCACAACAATACTTGGCTCTGATTTCTACATTTATCTCGCTAGAGAAGGCTCTCTCAACCCACA
 TCTGGTGGAGAGCCCAATTTGATACAAGTTATAAATTTGGTGTGGAGCGAATACGATAGACCCCTTCA
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 AACTCAGGACAGCTTCAATTAATGATCTGTTTTCCAATCATAATAGAAATGGATCAATCAACTTCA
 AAACAACCAACAAGAGAAATTCATCAGTAACCAACATAACAATAACAATAACCGGTAACAGCAACCCAC
 AAGCATCATCAGACAGCTCAATTCCTGGTATTTCTCATCTTCTGCTCTGCTGATGATGATGATGATGATGAT
 CCAACACCAAAATTTATTCAGTAGTAAGTTCCAAAGTAACAATTTGTACAGCGGTGGTATGATGATGATGAT
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 AGAGAAACCACTAGTGGTCAATCGTCTCTTCATGAATCAGGATCCAAATCGAAAGGAAATCAACAAATTT
 TTTGATTTATCCAATTCACCAAGTTGATATTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
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 ACAGGATTTAGTCAATCAAAACCTAATAATTCATCAAGACTTAAAGGCATTCCTGCCACGTCACATCAAA

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AGTTTCCGAAGTTTAAACAGGGTUGAAGAACTGAAAACATCAGUATTTCAAGAAGGTATACGTGAGATT
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 AAGGAAAAAGGTTTTGATTGATATTACTGCTCATAAAGTGATACCTATTGATAGTGTAGTGATGATACCT
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 GTTCCACCGGCTCCAGGGTTTAAAAAGGGGTTAACGTTTACGCAACCGAAAACCTCATTATTTTGGCTGT
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 GTTCCTGTTGTGAGTAGTTGTTCTACCCCAACTGTCAGTTTGAATAAAGCTCAAGAATTGTTAGCTAAA
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 GGAACATTGGGAACAACGGGGACAATAGGTACTCCAGGAACAACAGGTGGTACGGTAUCCAACAACACCA
 CAAATACCAAGATCATCAAGTCAAAGTGGTGGTTTGGCTTACCTTATTATTAGCTTCTGGGTTATTA
 TCACCCAAATCAGGAGGTGGTGCCGGTCCAGGAGGAATTGTATCATCGTCTTCTCCAAATTAATGAAAAT
 GGACUTTTAAGAAATTCAACTTCAAATTGAGAATATTTTGGTGATATTACTTATAAAAGTTTAAAACCA
 CCATCTCGACAAAATTCCCAATATGCAAGTATCACTAGTGGTGGTGGUAGTAATTGGGTTTGGGATATGGT
 TCCACAACTAGTGGCCTAGGTGGACAGCAACAGCAATTGGAGGAGGAGGAGGAGGAGTATTATCATCA
 TCCATCCATATTCTACTGGTTCTGGATCAACAGCAAGTTCAATGAATTATAAATATATAACAACAAC
 AACACACAACAACAATTCTGTTAATAGTCCGATTAATGAATTTAGATCTTCAAGGGGATTGAAATCATCA
 TCGTCACCAACGACAACAACAGGTACATCTTCAACATCAGGGGAAAAAACCCCAATCAGGTAGAACATCA
 GATAAANTGTTGGGATTTTCAAGTGATGCTTCAGGTAGTCACTACTTTTGTATTAAACCGAAAAAAATAA

Y9L085W_homolog 1172aa (SEQ ID NO 574)

MEGGDTYICLIKQFNARLGDLSLKIGDKIQVLADREYNDGWYMGKNLLTGEGLYPKTFTQLITNDNS
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 QSSQYTGSHLNSQIDRALQELQGSNADLTNSGNSPNEHRNHHYNNNTNNNNNNNNNAATSNYKQPQLM
 SKKSNDELSSQYQYQSQSQQPKHLSGDKSRQSLTEDLLDFLKANTWTPKQVSSYFALVLGFMDVAGKFA
 QHKITGEILLFELDLNLLKELDIDSPGTRFKLYKEIGKLKELNTEGVKDKQLRTDSSSTGSGTKNDTSS
 ALNSPPTASTTLHDAVPHIDNNMLNNTGKQQTQLMPSAVLTNTSDYNNNSQQQSGSQIHQRKRSSSDV
 VAPQQYLASDSEFMSPRRAPQPPSGESPLDTSYKFGAGSEYDRPPSHYGMXTRTNWASSHALGSSSPCI
 NSRPASSIYDSFSNHNRRNGSSSTSKQHHRNRSVTVNNNNNNNGNENHKKHHRRHSSVPSYLSGNDDSAK
 PTPKLLSSKFQSNMLYKGGDDGHGDFTTSSNNNNNSKLVSPAQIKRETTSGQSSLHESGSKSKGKSQI
 FDLNSPVDIDDAKFSFKKSNVSVRTKSMDAIGENGDDRRVASDSTGLSQSKFNSSRLKGIKIRATSTQ
 SPSISLGSKKSKTSFAQEGIREITPDEAIKTASHGCGYMSKRNNNLAWRTTRYFTLHGTRLSYTQSLKDK
 KEKGLIDITAHKVLIPIDSADDTDKADRYAAMYASITPAGNYCFKLVPPAPGFKGLTETQPKTHYFAV
 ETEEHRAWVKALMQATIDDDSVFVVSSCSPTVSLNKAQELLAKAREETKLKRBQLKANGYIRSID
 INDTSFSASLDYPMGSDIGFGSTSPVAATSAFKLTLDTNFRKSSGTMGTGTGTGTGTGTGTGTGTGTGT
 QIPRSSSQSGGFASPYLLASGLLSFKSGGGAGGPGGIVSSSSPINENGPLRNSTSNSEYFGCTTYKSLKP
 PSRQNSQYASTDSGGGSIQFGYGSNNSCLGGPATAIGGGGGVLSSSTPYSTGSGSTASSMNYNNNNNN
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YBR019C_homolog 2028bp public: 1..2028 (SEQ ID NO 575)

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 ATTGAATTCATTGTCAAACAACATGTTCCATTCTATGATGTTGATATCAGAAATATGAGCAATTGAAAT
 AAAGTTTCCAAGATTATAAGATCTCTGGACTCATTCATTTGCTGCTTTTGAAGCTGTTCGTGAAACA
 ACAAAATCCCTTAGCATATATGATAATAATGTAACAGGTACTGTCAACTTATTGGAACATATGTAA
 GCCAATGATGTAAGACAATCTTTTTCAGTTCTTCAGCTACTGTCTATGGTGATGTTACTTAGATTGCT
 GATAATTCAATGATTCCTATCCCTGAACAATGTCCAATGGATCCAAACAATCCATATGGAAGAACAAAA
 TTCATTATTGAGTCGATTTTAAAAGATATTTATAATAGTGATGATGCTTGGAAAGTAGCAATTTTGAGA
 TATTTCAACCCAATTGGTGGCTCATCATCTGTTTATTAGGTGAAGATCCATTTGGGATCCCAATAAC
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 GGATCCACTCTCTTTTGAAGTTTATCATGCATTTAGTAAAGTTGTTGGTAGAGAAATGCCCAATGAAGTT
 GTTGAAGACGGTGTGGGGATGCTTGGATTGACTGCTAAGCCAGACAGAGCAACAAGGAATTGCAA
 TGGAAAACTGAACCTTACCAATTGATGATGCTTGTAAAGATTATGGGAATGGACTACTGAGAACCCTTTT
 GGATTCACACTTGAAGAATTATTTGGGAAGAAATTTGATGGGTTCAATAACCGTTTGCACAGTTTGTGT
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 GTTGGTAGAATATGCCAATAGAAATTTCAATGGAGAATTTAAATTGAATGGAAAAATGTACAAAATTAAC
 AAAATGAAGGACCAACACTTGCATGGTGGTCCAAATGGATTGGATAAACAAAGATTTCTTTGGTTC
 GTTGTGAAAAATCTGTGATGGAAGTTTCTGTTGATTTCTTCTTGGTTGATAAAGATGCTAATGATGGG

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TTUCCAGGTGAGCTTGAAGCTATCGTACATTACACAAATTGATGACTCCTCAGTGGAAATTGAATATGAA
TGTCAATTATTATCTGGTGAAGCAACAATTGTCAATATGACTAACCATAGTTATTTCAATGTTTCCAAC
TCAGACACTATTGAAGGAACCGAGGTAAATTTGATTACTGATAAAATGTTAGAAGTGGATTCCACAATTA
TTACCAACTGGTAAATTTATTGAAAATGAAAAAGCTGCTACCCCAATTGTGTTAAATGAGAATGACGTA
TTTGAUAAATTGTTTATTGTTGATGAAGAATGTGGTATAGATACTCGTGATAAACCTTTGAAAACAAGTC
TTTGAAGCAACTAGTTTTGTCCACAAACAACAATTGAAGATATCCACCCTGAACCAGCTTTTCCAATTT
TACACTGCTGACGCTGTTAATACATAAGGTTTTTGGGAAAAGATGTGGTTTCTGCGTGGAAACCAAGTAGA
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AGTAAATTAATATGAATTTCAATAG

YBR019C_homolog 675aa (SEQ ID NO 576)

MSNEYILVTGGAGYIGSHTVIELISNGYKVIVVDNLNSSSYDAVARIEFIVKQHVFFYDVBIRNVEQLN
KVFQDYKISGVIHFAALKAUGESTKIPLAYYDNNVSGTVNLEVCANDVKTIIVPSSSATVYGDVTHRG
DNSMIPPEHCPEMDPTNPYGRTKFIIIESILKDIYNSDDAWKVAILRYFNPICAHPSGILGRDPLGITPN
LLPYLAQVAIGRREKLSIFGNDYNSRDGTPIRDYIHVVDLAKGHIAALAYLKNLQSKGLYREWNLTGCK
GSTVFEVYHAFSKVVGRELPHEVVGRRAGDVLDLTAKPKRANKELQWKTELTLDACKDLWKWTTEHPF
GFNIENYSWKEFDGFFNNRLHSFVAGDLKVNLANRCALIQAITLKDSNMVKAYNNAEDFKSE7NPFPGTT
VGRYANRISNGEFLNGKVYKLTKEGANNLHCGANGFDKQDFPGPVVKSRDGKFFVDFLIJVDKDGNDG
FPGLEALVHYTFIDSSVEIEYECCQLLSGEATFVNMTHSYFNVSNSDTLEGTEVKLITENKMLEVDSQL
LPTGKFLIENKAASPIVLNENDVFDNCFIVDEECGIDTRDKPLKQVFEATSEVTMNLKLISTTEPAQPF
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YCR005C_homolog 1194bp public: 1..1194 (SEQ ID NO 577)

ATGAGAGGTATCAAAGGTTTAGTTTGGGAAGGTTCTGTTTGGACCCAATTGAAGGTATCCGTTTTCAGA
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GCTCTTTTCTGGTTGTTGTTGACTGGTGAAGTTCCAACCTGACGCCCAACTAAGGCTTTATCCGAAGAA
TTTGCTGCTAGATCAGCATTACCAAAGCACGTTGAACAATTGATCGACAGATCTCCATCTCACTTCCAC
CCAATGGCTCAATTTCCATTGCGGTTACTGCTTTTGAATCTGAATCCCAATTTGCCCAAGCTTTAIGCT
AAAGGTGCCAACAAATCCGAATACTGGAAATACACTTACGAAGATTCCATCGATTGTTAGCTAAATTG
CCAACCATTGCTGCTAAGATTTACAGAAAAGGTTTTCCACGATGGTAAATTTGCCAGCTGCCATTGACTCC
AAATTGGATTACGGTGGCTAACTTGGCCAGTTTGTTAGGTTTTGGTGAACAACAAGGAATTTGTTGAATTA
ATGAGATTGTACCTTACCATCCACTCTGACCACGAAGGTGGTAACGTCTCTGCACACACCACCCACTTGG
GTTGGTTCCGCTTTTATCTTCCCAATTCTTGTCAATTAGCTGCTGGTTTGAATGGTTTAGCTGGTCCATT
CACGGTAGAGCTAACCAAGAAGTTTTGGAAATGGTTGTTCAAATTAAGACAAGANTTAACCGGTGACTAC
TCCAAGGAAGCCATTGAAAATACTTGTCCGAACCTTGAACCTCCGCTAGACTGTGCCAGGTTAGCGT
CACGCTGTCTTGAAGAAAGACCGATCCAAGATACACTGCTCAAAGAGAAATTTGCTCTTAAACATATGCCA
GACTACGAATTTGTTCAAATTTGGTTTCAAACATTTACGAAGTCCGCTCCAGGTGTTTGAACCAACACGGT
AAGACCAAGAACCCATGGCCAAATGTGCACCTCCCACTCTGCTCTCTTCTTACAACTACTACGTTTGGCT
GAACAATCTTTCTACACTGCTCTTGTTCGGTGTPTCCAGAGCCTTTGGTGTCTTGCACAAATTGATCTTG
GACCGTGGTATCGGTATGCCAATTGAAGACCAAAATCTTTCTCCACTGAAAAATACATTGAATTTGGTTC
AAAAACATCAACAAAGCTTAA

YCR005C_homolog 397aa (SEQ ID NO 578)

MRGIKGLVWEGSVLDPIEGIRFRGRTIPDIQKELPKAPGGEEPLPEALFWLLLTGEVPTDAQTALSEE
FAARSALPKHVEELIDRSPSHLHPMAQFSIAVTALESESQFAQAYAKGANKSEYWKYTYEDSIDLLAKL
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VGSALSSPFLSLAAGLNLGAGPLHGRANQEVLEWLFKLREELNCDYSKEAIEKYLNETLNSGRVVPVYG
HAVLRKTDPRYTAQREFALKHMPDYELFKLVSNIEVAPGVLTKEHSTKNPWPNPVDSIISGVLLQYYGLT
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YCR345C_homolog 1653bp public: 1..1653 (SEQ ID NO 579)

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TATATTGGTATTAGTATTTTGTGTTTCTTATTGCCCTTTGGTGGTTTGGTTTTCGGTTTTCGATACTGGT
ACCATTTCTGGTTTCATTAACATGACTGACTTTTTAGAAAGATTGTTGGTGGTACTAAAGCTGACGGTACT
CTTTACTTTTTCCAACGTTAGAACTGGTTTATTGATTGGTTTGTTCATGTGTCGGTGTGCCATTGGTGCA
TTATTCTTGTCTAAAGTCGGTGATATGTATGGTAGAAGAGTTGGTATCATGACTGCTAIGATCATTTAT
ATTGTTGGTATTATTGTTCAAATTTGCTTCAACATGCTTGGTATCAAATCATGATTGGTAGAATTTATC
ACTGGTCTTGTGCTGGTATGTTATCAGTTTGTGTTGCTCATTTATTTATCTTCAAGAGTTTCTCCCAACAT
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AGTTACGGTACTAAGAAATACTCTGACTCCAGACAATGGAGAAATCCATTGSGTTTATGCTTTGCTTGG
GCCTTGTGTTTGTCTTGGTGGTATGGTAAGAATGCCAGAACTCCACGTTACCTTTGTCGGTAAAGATAGA
ACTGACGATGCTAAGATTTCACTTCCCAAACTAACAAGGTTTCTCCAGAGGACCCGCAATTATACCGT

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GAACCTTCAATTAATCCAAGCTGGTGTGAAAGAGAAAAGATTGGCCCGTAAGGCCATCTTGGGGTGTCTTTA
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GAGGAAATTGATGAATTATCTCTACCAAGGTGTTCATCGAAATCAGGCGGTTGGGTTCCACCTTCT
GACCAAGAAATCGCTTCGTGCAAAAGGCTATCTCGTGATATCCACGAGATGAAGAGCAAGTTTAA

YDR345C_homolog 550aa (SEQ ID NO 580)

MSIHNSTNNRDLERKEEIPKNEHNFQGFQNNENNEHIPTELEDKPLKEYIGISILCFLLIAPGGFVFGFDTG
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IVGIIVQLASQHAWYQIMIGRIITGLAVGMLSVLCPLFISEVSPKHLRGTLVYCFQLMITLGIFLGYCT
SYGTKKYSISRSQWRIPGLGCFAMALCLLGGMVMPESPRLVGVKDRIDDAKISLAKTNKVSPEDPALYR
ELQLIQAGVERERLAGKASWGALITGKPRILERVIVCCMLQSLQQLTGDNVFFVYSTTIFKSVGLNDSF
ETSIILGVINFASTFVGIIAIERLGRRLCLLTGVSAMSICFLIYSLIGTQHLIYIDQPGCPTRKPDGNAM
IFITALYVFFFASTWAGGVYSIVSELYPLKVRSKAMGFANACNWLWGLISEFTSEITDAIHFYVGFVF
MGCLVFSIFFVYFMIYETKGLTLEEIDELYSTKVVPWKSAGWVPPSDEEMVRAXGYTGDIHADEEQV

YDR545W_homolog 1194bp public: 1..1194 (SEQ ID NO 581)

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TCCGCTATTTCAACAAAGAGCCATCTTCGCCAATCACTGAAGGTAGAGATGTTTTGGCTCAAGCTCAATCC
GGTACTGGTAAAACCGCTACCTTTTACCATTCTCGCATTTACAAAGAATCAATGAAATGAAAAAGCCACT
CAAGCTTTAACTCTTGGCCCCCAACCAGAGAAATTCGCTTTTGCAAAATCAAGAAATGTTATCACTGCTATTGGT
TTGTACTTCAAGCTTACTGTCCATGCTTCTATTTGGTGGTTACCTCAATGAAGTGACGAAATTTGAAGCTTTT
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AAAACCGATAAAGTCAAGATGTTCAATTTTGGATGAAGCTGATGAAATCTTATCAAGTCGATTTTAAAGAA
CAAATTTACAACATTTTCAGATTATTACCAGAAACCACCCAAATTTCTCTTATTATCTGCCACCATGCCA
CAAAAGCTTTTGGAAAGTCACCACCAAAATTCATGAACAACCCAGTCAGAAATCTTACTCAAAAAGATGAA
TTGACTTTTGGAAAGGTATCAAAACAATTCATATTAAATGTTGAATTAGAAGATTACAAATTCGAATTCGTTT
TGTGATTTGTACCAATTCATTTCTGTCAACCAAGCCGTCATTTTCTGTAACTACATCCAAAGGTTGAA
TTTTTAACCAACAAATTGAGAGAACAAACATTTTACTGTCTCTGCCATCCACGCTGATTTGCCACAAGCC
GAAACAGACACCATTAAGAAAGAAATTCAGATCTGTTCTTCAAGAAATCTTGATCTCTACTGATTTGTTA
GCTAGAGGTATTGATGTCCACAAAGTTTCTTTAGTTATTAACATACGATTTGCCAGCCAAACAAGGAAAC
TACATTCATAGAATTGGTAGAGGTGGTCTGTTTCGGTAGAAAGGGGGTTGCCATCACTTTCTCACTGAC
AGAGATGTTGGTATGATGAGAGAAATGAAAAATCTACTCTACTCAAATCGAAGAAATGCCAGCTGAT
ATTGGTGTCTTATTTGCCTAG

YDR545W_homolog 397aa (SEQ ID NO 582)

MASECITEIDSGLIETNYENWVYKFDIINLKNIVRGIFGYGYETPSAIQQRALIPITEGRDVLAQAQS
GTGKTATFTSALQRINFNEKATQALILAPTRELALQIKNVITAIGLVLKVTVHASICCTSMSDDIEAF
RSGVQIVVGTGPRVLDMEERRYFKTDKVKMFIIDEADEMLSSGFKEQIYNIFRLLPETTQIVVLSATMP
QDVLEVTTKFMNPNVRILVXKDELTLLEGIKQFYINVELEDYKFDCLCDLYDSISVTQAVIPCNVRSKVE
FLTNKLRQHFVTSALHADLPQAERDTIMKEFRSGSSRILISTDLLARGIDVQQVSLVINYDLFANKEN
YIIRICRCGRFCRAGVALNFVTD RDVGMMRELEKFYSTQIEEMPADIGALFA

YIL057C_homolog 606bp public: 1..606 (SEQ ID NO 583)

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GTTCTGTGAAGAACTTXXGATAATGATTTTGATTATTTUCATGGTAGATTACATTTATATCCACCAATTT
GTTATCAAGAGTTGTCAAAATAATCTTGAAAAAATCAAGCCTACCATGAAATGAAAACTCCAAGAAATTT
AGACCTGALTTACAACATCATATTCAAAAACNTTTAATTAAGATTTTGAATAATGTTGTGTTTACGAG
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TGTACAAATGAATCAGCTATGGTTGATGTTGAATATAAATCCATTCCAATTTAA

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YLL057C_homolog 201aa (SEQ ID NO 584)

MAGKKKSKSEALFLDLNFKPMOHLQVPKTRSSSITEIESADFTGTNRQVLI/PPTIKPDELEQPFPSF
VRDETWDNDFDYFHGRLHYYPFFVMKSCQNNLEKIKFTMNKNSKKPRDLQHHIQKHLIKULEKCCGYE
LNFSGKEVVETDNKVTWKFKDET DHGFSKEEEDMYDRHWRLDLVSCTNESAMVDVEYKSI PM

YKR097W_homolog 1662bp public: 1..1662 (SEQ ID NO 585)

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TGCTGGGGTCCAGTGAATAAACAAGTTGACGAATTAACCTTGAAGATTCTTAGATCAAGAGCTTTGGAT
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GCATGTTTGGGTCAACCATTTCTGGTGTGTCACCCCAATGAATATGCTCAACAATTTGTTGACAAGATT
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AAGAGATGTCATTGAAATACACCAGAGCTATCTGGATGCTATCCACTCTGGTGAATTGTCTAAAGTC
GAATACGAAAAAGTTCCAGTTTTCAACUTTAATGTTCCAACTTCTTGTCTCGTGTCCAAAGTGAATTT
TTGAACCCCACTAAAGCTTGGACCCCAAGGTACTGATTCAATCAACAAGGAATCAATCTCTTGGCTACC
AAGTTTGTGAAAACCTCAAGACATACGCTGATCAAGCTACTGTTGAAGTTAAAGCTGCTGGTCCAGAA
GCATAA

YKR097W_homolog 553aa (SEQ ID NO 586)

MAPPTAVESSINFCCHPTIKSTODPLVQKLSLNTDVERHNAPPPTLYEDCLLEKGTITISSTCALMAYS
GNKTRGRSPDKRIVDESTSSHNWCPVKNQVDEIWKTSRSLADYLRTRREKLFVVDDAYAGWDPRYRI
KVRTTCARAYHALFMTNMLIRPTEEELENFGEPDFTIYNAGQFFANLHTKGMTSATSVIEINFKDMEMVI
LGTEYAGEMKKSIPTVMFYLMPIKHKVLTLLHSSCNQGVKEGDDVTLFFGLSGTGKTTLSADPQRKLTGED
EHCWSDNGVFNIEGGCYAKCLDLSAEKEPELFNSIKFGAILENVVYDFITKVVDYEDSSITENTRCAYP
IDFIPSAKIPCLADTHPTNIIILLTCDASGVLPFVSKLTNAQVMYHIFISGYTSKMAGTLEGVTEPQATFS
ACFGQPFYLVLPKMYAQQLSDKISEHNANAWLLNTGFWGSSVAQCGKRCPLKYTRAILDAIHSCELSKV
EYKVPVFENLVPTSCPGVPSEILNPTKAWTQGTDSFNKRIKSLATKFAENFKTYADQATAEVAAGGEE
A

YOL126C_homolog 1014bp public: 1..1014 (SEQ ID NO 587)

ATGCTCAAAGTCCCTATTTTATAGAGCTGCTGGTGGTGGTCAACCATATCTTTATTGACCAAATTA
AACCCAAATGTTGATCAATTGGCATTATTTGATGTCGTCAATGTTCCAGCAGTTGGTGCTGATTATCT
CATATCAATTTCTGATTTCTCAAACTCAATCTATTATACCAAAAGATAAAGAAGATAAAACTGCATTAGCT
CCTGCATTAAAGGTTCTGATTAGTCAATATCCAGCTGGTGTCCAAAGAAAACAGGTAATGACUAGA
GATGATTTATCAATATTAATGCAATCAATCGGTCAAGGTTTATGCTGAAGGTATTGCTGCCAATTCTCCA
AAAGCTTTTGCTTGGTGATTTCTAATCCAGTCAATTTCTACTCTACCAATTCTTGCCGAACTTTACAA
GCTAAAGGTGTTTATGATCCACCTAGATTTTGGTGTACTACTTTGCATATTGTTAGAGCCCAATACT
TTTATTTCTCAATTAATTCCTAGATCAAACTAAACCATCTGATTTCAATATTAATGTTGTTGGTGCCCAT
TCTGGTGAAACCATTTGTCATTATATTCAATTAGGTAACCTCTAAACANTATTATGATATATTATCTCAA
GAACAAAACAAGGAATTAATCAAAAGAGTTCAATTTGGTGGCGATGAAGTTGTTCAAGUUAAGAATGGT
GCTGGTTCGCCCACCTTATCCATCGCTTATGCCGGTATAGATTAAGCCGAATCAATTTTAGCTGCTGT
AATGGTAAACCTGATATTTGTAATGTACTTTCTTGAACCTGGATTCTTCAATTAAGGTYCTTCTGAA
GCTAGAAAATTTGGTAAACATTTAGATTTCTTTTCAATACCAGTTCAATTAGGTAATAACCGGTATTACT
CAAGTAAATATGATATCTTAAATCAAAATTTCTGATGATCAAAAGAAATTTGTAGAGTTGGCATTTGAA
CAATTACAAAAGAAATATTGAAAAAGATGTTTCAATTTGCTAAGAAATAA

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YOL126C_homolog 337aa (SEQ ID NO 588)
 MVKVAI LG AAGGIGQPLSLLTKLNPVDELALFDVNVPGVADLSHINSDSKTQSYLPKDKEDKTALA
 AALKGS D LV IIPAGVPRKPGMTRDDLFNINASTVQCLAEGIAANS PKAFVLVISNPNVNSTVPIVAETLQ
 AKGVYDPA R LFGVTTLDI VRANTFI SQLFLDQTKPSDFNINNVGCHSGETIVFLYSLGNSKQYYDILSE
 EQKKELIKRVQFGDEVVQAKNGAGSATLSMAYAGYRLAESILA AVNGKTDI VECTFLNLDSSIKGASE
 ARKLVKDLDFPSLPVQLGKNGITEVKYDILNQISDDEKKLLEVAIEQLQKNIEKGVSTFAK

YBL072C_homolog 621bp public: 1..621 (SEQ ID NO 589)
 ATGGGTATTTCTAGAGATTCACGTCACAAAAGATCCGCCACTGGTGCCAAAAGAGGCCCAATTCAGAAAG
 AACAGAAAGCTTTGAATTACGTAGACAACACAGCCAACACCAAGATTCCTCCAAAAGAATTCACCTCTGTC
 AGAACCCAGAGGIRKGTAAACCAAAAATTCAGAGCTTTGAGAGTTGAAACCGGTAACCTTCTTTEGGCTTCC
 GAAAGGTGTTTCCAGAAAAACCAGAATTGCTGCTGCTGTTTACCATCCATCTAATAACGAATTGGTTAGA
 ACCAACACCTTGGACCAAAATCTGCTGTTGTTCAAATCGATGCTACTCCATTCAGACAATGGTACGAAAAAC
 CACTACGGTGCTACTTTAGGTAAAAAGAAACCGTGCTGCTCATCTCTCAGCGCTGCTGAAGTTGCCGAT
 GCCAAGAGATCAAGAAAAGTCGAAAGAAAATTGGCTGCTAGATCTGGTGCTGCTGCCATTGAATCCGCT
 GTTCACTCTCAATTCGGTTCCTGGTAGATTATACGCTGTCATTTCTTCAAGACCAGGTCAATCTGGTAGA
 TGTCATGCTTACATCTTCCAAGCTGAACAATTAGCCTTCTACTTCAGAAGCTTAACCTGCTAAGAAATAA

YBL072C_homolog 206aa (SEQ ID NO 590)
 MGI SRDSRHKRSATGAKRAQFRKKRKFELGRQPANTKIGPKRIHSVTRGGNQKFRALRVETGNFSWGS
 EGVSRKTR IAGV VYHP SNNBLVRTNTLTSAVVQIDATPFROWYENHYGATLGKKKGGAHAHAHA AEVAD
 AKRSRKVERKLAARSGAAATESAVDSQFGSGRLYAVISSRPGQSGRCDCYILEGEELAFYLRRLTAKK

YBR009C_homolog 318bp public: 1..318 (SEQ ID NO 591)
 ATGTCAGCTACCGGTAGAGGAAAAGGTGGTAAAGCTTAGGAAAAGGTGGTGCTAAACGTCACAGAAAA
 ATTTTAAGAGATAACATTCAGGTATTACAAAACAGCTATCAGAAGATTGGCCAGAAGAGGTGGTGTT
 AAACGTATTTCTGCTTTGATTTATGAAGAASTCAGAGTTGTCTTGAAACAATTTTCCAAAACCTTATC
 AGAGATGCTGTTACTTACACTGAACATGCTAAAAGAAAACCGTCACTTCATTGGATGTTGTTTACGCT
 TTGAAGAGACAAGGTAGAACCTTGTATGGTTTCGGTGGTTAA

YBR009C_homolog 105aa (SEQ ID NO 592)
 MSCTGRGKGKGLGKGGAKRHRKILRDNIQGITEPAIRRLARRGGVKRTSALIYEEVRVVLKQFLENVI
 RIDAVIYFEMAKRKTVTSLDVVYALKRQGRITLYGFGG

YBR189W_homolog 489bp public: 1..489 (SEQ ID NO 593)
 ATGCCCGGTGAATACCGGTTTAAAAACAAGGGGGGAATCTACAGAATTGGGGTTCCAAATGCTCCTAAA
 ATCAGAAGAGCTGCTCGTGAAATTGTAAACAGAGGTGAAAAGGGCCCCAAAAGATTATTCGGAAGGTA
 ATGCCTTTGATCAGAACATTAATCAGATTCCCTTTCTTGCTCTGAGCACAAAATGAAATTGGATTATGTC
 TTGGCTTGGAAACCCAGAAATTTCTTGAACAGAAGATTCCAACCCCAAGTTTTTCAAATTAGGTTTAGCT
 AGATCTATCCCCACGCCAGAGTTTTSATCACCCAAAGCCACATTGCTGTTGGTAAACAAATTGTTAAC
 ATCCCATCATTTACTGTCAGATTGGACTCTCAAAAACACATTGACTTTCCCCACAACTCTCCATACGGT
 GGTGGTATAGAGCCCGTATAGATTAAAGAGAAAAGAACAGGTAAAGGTGGTGAAGAAGGTGCCGAAGAAGAA
 GATATA

YBR189W_homolog 162aa (SEQ ID NO 594)
 MAGEYRFYKQGQGNLQNWGSKCPKIRRAAREFVTRGEKGPKKIRKVMALIRLRVRFGLSEDKMKLDYV
 LAWKPEVFLNRRFQPOVFKLGLARSIPHARVLTTOSHIAVGKQIVTIPSFTVRLLSQKHIDFAHNSPYG
 GGRAGHVKKKNQKGKGEGEAESEE

YBR191W_homolog 330bp public: 1..330 (SEQ ID NO 595)
 ATGCCACACAAATACTACCACGTAAGACTGGTATTGTTTACAACGTTACCAAATCCTCCGTTGCTGTT
 ATCATTAACAAAGTTGTTGGAAACAGATACATTGAAAAGAGAGTTAACTTGAGAGTTGAACATGTTAAA
 CACTCTGCTTGTGCTCAAGCAATCTTGAACACAGTTAANTCTAACCTGCTAAAGAAGAGAGAAGCTAAA
 GCTAACCGGTGAAACUGTTTACTTGAAGACACAAGCTGCCAAGCCAAGAGGTTCAAGAATTATCTCCACT
 GAGGTAACATTCTCAAACTTTGGCTCCAGTCGCTTACGAAACTTTTCAATTAA

YBR191W_homolog 109aa (SEQ ID NO 596)
 MPRKZYIIGKIGLVYVNVFKSSVGVLINKVVGNNRYLEKRVMLRVEHVKHSACRQEFLNRVKSNAAKKREAK
 ANGETVYIKRQAAKPRGSRIISTEGNIPQTLAPVAYETFI

YCL035C_homolog 384bp public: 1..384 (SEQ ID NO 597)
 ATGATAGACAAAATGCTGCTGATTCTTGCTGGGGATTCAATTTGTGGTATCAACCACCTCCACCTACT
 GCACAAACTGAGAAAGAAATCGAACACACTATTAACCTCTCACAAGATTGTTATTATTCCTAAACCTTAT

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TGTCCATTTTGTGACCAAACCAACATCTATTAAATGAACAATATCCACAAGAATCGTACGAAGTCATA
AACTTGAATATTCTCGATGACGGATTGACTATTGCAATCAATTGATGCTAATCTGGTCAATATATG
GTGCCCATATCTTCATAAACGGACAACACGTTGGAGGAAATTCAGAAGTTCAGCAATTGCACACCAAT
GGGAAATTGCAAGAATTATTGAATCCTCAGAAATATTGA

YCL035C_homolog 127aa (SEQ ID NO 598)

MIDKMSSILANGFNLWYQPPPTAQTEKBIHTINSHKIVLVSKTYCPFDQTKHLINLQYYPQESYEVI
NLNILDGLTIQNQLYANTGQYMPVPIIFINGQHVGCNSEVQQLHTNGKLQELLNPQKY

YDL004W_homolog 486bp public: 1..486 (SEQ ID NO 599)

ATGTTTCAGACAAGTTTTCGGTCAAGTTACCAAAACATCAATCACTGGGGTTAAGAGAACCTTATGCCACC
GAGGCCGCGGTGTCTACAGATGCTTTGAAATTATUCTTGGCAATTGCCACACCAACCTTATACACGAC
TCCGAAGTCCCAACAAGTAAACTTGCCATCTGTCAACGGTGATTGGGTATTTTGGCCCAACCACATTCGA
ATTGTGCAACAATTGACACCAGGATTGTTAGAAATCATTTCCAAAAACGGAGACTCTGACCAATACTTT
GTCAGCGGCGGTATCGCCATGGTCCAACCAGGAACAAGTGTACTATTTCCGCCATCGAAGCATTCAAC
ACCGAUCAAATTGATCTTCTGCGGTCAAAAACCTTGATTGCCGATGCCUAAAAGAGAGCTGAATCTAGT
GATGAAAAGGTGCTGCTGAAGCCAACATCGAATTGGAAGTGTAGATGCTTTACAACATTTTACTAAG
TAA

YDL004W_homolog 161aa (SEQ ID NO 600)

MFRQVFRQVTKQSFTGVKRTYATEAAVSTDALKLSLALPHQTLYNDSEVQQVNLPVNGDLGILANHIF
IVEQLRPULLEIISKNGDSUQYFVSGGLANVQPGNKLTISALEAPKTDQILD SAYKNLIADAQKRAESS
DEKVAAEANTELEVLDAIQHFTK

YDR099W_homolog 795bp public: 1..795 (SEQ ID NO 601)

ATGCCAGCCTCCCGTGAAGATTCCGTTTACCTTGCTAAATTAGCCGAACAAGCAGAACGTTATGAAGAA
ATGGTTGAAACATGAAAGCCGTTTGCCTCTGGCCACCAATTGTCTCTTGAAGAACCTAATTTATTA
CTGTGTTGCTTACAAGAAATGTCAATGGTGCTGCTCGTCTCTCTGAGAAATTGTTTCAATCAATTGAACAA
AAAGAAGAAGCCAAAGGAAATGAGAGCCAGTTGCTTTGATCAGAGATTACCGTGCCAAGATTGAAGCT
GAATTGCTTAAAATTTGTGAAGATATTCTCTCTGTGTTGAGCGACCAATTTAATTACATTTGCCCCAACT
GGTGAATCAAAAATATTTTACTACAGATGAAGGTTGATTACCAUAGATACTTGGCTGAATTTGCTATC
GCTGAAAAACGTAAGGAAGCTGCTGATTTATCATTAGAGGCTTATAAAGCTGCTTCTGACGTTGCTGAG
ACCGAGTTGGCCACCAACCCATCCAATCAGATTAGGTTTAGCATTGAACCTCTCTGTTTTCTACTATGAA
ATTTTGAACCTCCCCAGATAGAGCTTGTCATTTAGCTAAACAAGCTTTCGATGATGCTGTTGCTGATTA
GAAACCTTATCTGAAGATTCTATACAAGCATTCMACTTTGATTATGCCAATTATTGACAGATAACTTGACT
TTATGGAACGATTTATCTGAAGCCCCAGCTGCCACTGAAGAACACAACANTCCAGTCAAGCTCCAGCT
GCTCAACCAACAGAAGGTAAGGCTGATCAAGAATAG

YDR099W_homolog 264aa (SEQ ID NO 602)

MPASREDSVYLAKLAEOAERYEEMVENMKAVASSGQELSVEERNLLSVAYKNVIGARRASWRIVSSIEQ
KEEAKNESQVALIRDYRAKLEELSKICEDILSVLSDHLITSAQTGESKVFYVKMGDYHRYLAEPAL
AEKRKEAADLSLEAYKAASDVAVTELEPPTHPIRLGLALNFSVFYVEILNSPDRACHLAKQAFDDAVADL
ETLSEDSYKIDSTLIMQLLRDNLTLWIDLSEAPAATEEQQSSQAPAAQPTGKADQE

YDR099W_homolog 642bp public: 1..642 (SEQ ID NO 603)

ATGCTCTGAATCTGAGAAAATGTACATTTTCGTACAATAATATACACCAGTTATGTCAAGAAATAGCCCT
AAGATCAAAGAATTTAAGCCTGACTTTGATCATTTGCTATTGGTGGCGCTGCTTTTATTCCAGCTAGAAATG
TTGCGTTCTCTTCTGAAAGAACCAGGTCAACCAACGTTAGAATTATGCTATCATATTGTCTTTATAC
GAAGAGATTGAGACTGAAAACGGTATTGAAAAGCCAGCTACCCAAGTTCTGCGGTACTCAATGGATTAT
TATCATCAATCTAAAATTGACTTGGTTGCTAAAATGTGTTAATTATTGATGAGGTTGATGATACCA
ACCCTTTGCATTACCCAGTCAGTGAATTGAAAAAGATGTGGAAGAGCANTCAAAGCCAAAGCTGCA
GATCTTAAAGATACCAAGTTTGGTATTTTTGTGTTGTCACGACAAGCAAAAGCAAAAGCAAGCAAAATG
CCAGATGATATTTATCAACTGCTAATTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
CCATGGGAGTCTACTGACATTGTTTATCATCAATGAAAGCTGAAGAACAAAGGAACCATGTGTTCTCT
CCTTCATCCACTTTAGAGTAA

YDR099W_homolog 213aa (SEQ ID NO 604)

MSESEKMYLSYNNIHQLCQELAPKIKEFKPDLLIAIGGGGFIPARMLRSFLKEPGQPNVRIMAILSLY
ELIESENGIEKPGTQVVRTONIDYHQS KIDLVGKNVLIIDEVLDTRITPLHYAVSELAKUVEEQSKAKGA
DPKDTKFGIFVLHDKQKQKKAELPDDIMKTCNYFAARSVPDSWIAYVWFSTDLVYHQMKAHEQGNDFL
PSTLE

YDR418W_homolog_498bp_public: 1..498(SEQ ID NO 605)
ATGCCTCCAAATTTGATCCAAATGAAGTTAAATTCCCTTACTTAAAGACCTGTTGGTGGTGAAGTTGGT
GTTTCATCTGCTTTAGCTCCAAAGATTGGTCCATTAGGTTTATCCCCAAAGAAGTTGGTGAAGATATT
GCCAAAGCCACCAAGAATACAAAGGTATTAAAGTTACTGTTCAATTGAGAATTCAAAACAGACAAGCT
ACFGCTTCTGTTGTCCATCCGCTTCAATCTTTAGTCATCAACGCTTTTGAAGAACCCAGTCAGAGACAGA
AAGAAGGAAGAAAGACGTCAAACACTCTGGTAACATTCCATTGATGAAATCTTTGAAATTGCCAGAAA
ATGCAACACAAATCATCCGTAACAATTTGGCATCTGTCTCCAAGCAAATCTTGGGTACTGCTCAATCT
TTTGGTTCGAGAGTTGATGGTAAGAACCCTCATGCATCATGACGCCATCAACCGCTGGTGAATTTGAT
GTTCCAGAAAACTAG

YJR418W_homolog_165aa(SEQ ID NO 605)
 NPPKFDPEVEYKPIYLRAVGGEGVASSALAPKICPLGLSPKKVGEDIAKATKEYKGIKVTQVLRIQNRQA
 TASVSPASSLVTALKEPVRDRKKEKNVKHSGNIFLDEIFETARKMQHKSPGKNLASVSKELGTAQS
 VGCPVDGKNPEDIIDAINAGEIDVPEN

YDR513W_homolog 360bp public: 1..360(SEQ ID NO 607)
ATGTTTCGTACATTATTAACCAAAAGACTATTCAATACATCAACAATGGTTTCATCTCAAGTTAAGAAC
AAGGTGGAACAATTGATCAAAACCAAAACAGTTTTCATTGCCTCCAAATCCTATTGTCCATACTGTAAG
CTTACCAAAAGCACAAATTGAAGCTATAACAAGGATGCTTACATTCCTTGAATTACACCAAGTTACACGAC
GGTGTCTGAAATCCAAAGAGCATTTAATGGGAAATCACATGGTCCAAAGAACCGTTCCAAATGTCTTTATTGGT
GGTCAACATATTGGTGGCAATTCCGATGTGCAAGCTTTGAGTCTAGTGACAAATTAGATGACAAATC
AAGCTTCGTTTATAA

YDR513W_homolog_119aa(SEQ ID NO 603)
 NPPTLLTKRLPMTSTMGASSQVKNKVFQLTKTKPVPLASKSYCPYCKATKSTIEAITKDAYTLELDFVDD
 GAEIQRALLLETTTCETVENVFEGGHHIGNSDVAALKSSQSLDDKIKAAAL

YEL009C_homolog 972bp public: 1..972 (SEQ ID NO 609)
ATGCCCTGCTACTACTCCTATTATTTATGAAGATTCTTTATTTGAATCTCAAGATTTATTTGCTTCTCCA
GTTAAACAACAACATCAAAAGGTTGATACTGTTGCTACCAAAAACGAAATTGGTTTGGAATTAAATTTA
GGTTTACCAGAAATGCAAAAGGCTTCAGAAACTGTTTCCACTCCATTTCAAATCCATTCCACTGTATTC
GAGTCGGGTTTACCACCAATTTGGATGGAGTCAATGATATGATCATCACTCCAATGTTTGGATGAATTC
GATTTGATTATGGACGGGACCAAAGTCAATCATCAGAAAGATTGGGTTGCTCTTTTGGAGATGACAA
GATGATGGTGTTCATAGCTGGTGTCTACTAGCAAAGAACCAATGTTATCATTTGAATGAAGATAACGAC
AACCAATGATGACGAGCTGATGACGCTGATGATGATGATGATGCTCTTGTTCCTCAAGAGAAGATACTATT
GAAGCTTTATTATTGGAAAGTACTCAOCAAATCGTACCATTCTCTGCTGCTACTTCTGCTTCTACTCTCATCA
TTAAACAGTCCAGAAAGTACTATTGCTACCAAGTCACTGCTGGTGGTGAAGTGTGTTGTTGCAAGTAAA
AAGCAATTTCAATTTGGTAAACACCAAATCCTTCATCCACTTTACCAACACCAATTATTTGGATTCTAAAAAT
TCTAAAAAAGAGCTTTAAAGTTGATCATTTTGGTTTCTGTTAATCTATTTCGAAAAAACATAGATCTCAACCT
TTACAACCGATTGTTGTTGATGACATTAAAGATGCTGCTGCTTTGAAAAGAGCTAAAAAATCTGAAGCT
GCTAGAAAGATCCAGAGCTCTGTAATAATGGAAGAATGAGTCAATTCGGAAGATAAAGTTGAGAATTTGATT
AATGAAAAGCAAGCTTTACAAGATCAAGTTGAAAGATTACAAGAAATTGTTTAAAGAGTTAATGGTATTCAA
TTTTAA

YEL009C_homolog_323aa(SEQ ID NO 610)
MPATTPIIYEDSLFESQDLFASPVKQQHQKVDTVATKNEIGLE¹NLGLPEMQKASETVSTP²⁰FQTHSSVL
ESGFSTNL³⁰LDGVNDIDHTPMFDEL⁴⁰DLINCGAKVNSS⁵⁰EDWVALFGDDND⁶⁰GVAIAGATSKEPMLS⁷⁰LNEDNE
NNDDADDA⁸⁰ADDDALVPR⁹⁰RTTEAL¹⁰⁰LLEPSN¹¹⁰RTISAATS¹²⁰SSLSN¹³⁰SP¹⁴⁰ESTIATTV¹⁵⁰TAGGEVVVASK
KQFQLVTPNP¹⁶⁰SS¹⁷⁰TLPTLLDSKNSKKRVKVDH¹⁸⁰LGCVTYSKKHRS¹⁹⁰QPLQPIVVD²⁰⁰IKDAAL²¹⁰KRAKNT²²⁰EA
ARRSRARKMERMSGLE²³⁰EDKVEN²⁴⁰LINEKALCD²⁵⁰VERLOELLRVNGIO²⁶⁰F

[illegible]

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YGL123W_homolog 249aa (SEQ ID NO 612)
 MSAPAPKRQFGDRRRGGRGGRRDGEKGGTFVTKLGRLVKAGKJTSVEQIYLHSLPVKEYOIIDLILLP
 DLKDDVMKIRSVQKQTRAGQRTMRKAVVVICDSNGHVGLGIKTAKEVASAIKAAIVIAKLSIIPIRRGY
 WGSNLQGPHELPCKVTKXCGSVAVRLIPAPRGKGTVASPVVKRLMLQACGVEDVVTSSSGSTRTTENTLK
 AAFAAIGNTYSFLLTPNLWAETPLAASPLEVYABEAAAGKKRY

YGR209C_homolog 312bp public: 1..312 (SEQ ID NO 613)
 ATGGTTCACGTTGTCACTGAAGTTAACGAAATCCAAACCCCTTTTAAAGGAAAACAACCTTAGTTATTGTT
 GACTTTTTTTGCCACTTGGTGTCGTCATGTAAATGATTGCTCCATTATTAGAAAAATTCCTAAAATGAA
 TATTCTAATATTAAATTTTTGAAAATTGATGTTGATCAATTCGCTTCTTTAGCACACAATATAATGTT
 AGTTCTATGCCAACTTTGATTTTATTCAAAAATGGTGAAGAAGTCAATCGTGTCTATTGGTGCTAACCCN
 GCTGCTAATAAACAAGCTTTGGCTTCTCTTGGCTTAA

YGR209C_homolog 103aa (SEQ ID NO 614)
 MVHVVEVNEFQTLLENLVIVDFATWCGPCKMIAPLLEKFQNEYSNIKFLKIDVDQLGSLAQEYNV
 SSMFTLLFKNGEEVNRVIGANPAATKQALASIA

YHR039C-B_homolog 342bp public: 1..342 (SEQ ID NO 615)
 ATGTCATCTGGTATCCAATCATTATTGAAAACCGAAAAAGAAGCTCCAGAAATTGTTAATGAAGCTAGA
 AAATATAGAAACCAACGTTTGAACCTCTCCAAAACAAGATGCTCAAGCTGAAATTGATAACTATAAAAAG
 CAAAAGGAAGAAGAATTAAAAAATTTTGAAGAAAGAACACGAGGGTTAAATGAAAGATCGATAAAGAA
 CCTGATGCTGAAGTTGAAAAGGAAATTGACCACTTCCAAATCCACTTTTGAAAAGAAAAAGAGTGCAGTT
 GTTAAATTGTTAGTTGACGCTACTGTCAAGCCAACCACTTTACACATAAATCCATCTCAATAA

YHR039C-B_homolog 113aa (SEQ ID NO 616)
 MSSGIQSLKTEKEAAEIVNEARKVYRTRRLKSAKQDAQAEIDNYKKQKEEELKNPKEHEGUNEKIDKE
 ADAEVEKELTSIKSTFEKKKSAVVKLLVDATVKFTFTLHINASQ

YJL138C_homolog 1194bp public: 1..1194 (SEQ ID NO 617)
 ATGGCATCCGAAGGTATTACTGAAATCGACTCTGGTTTAAITGAACCAATTACGATAACGTCGTCTAC
 AAGTTCGACGATTTAAACTTGAAACCAACATTGTTAGAGGTATTTTGGTTACCGGTATGAAAATCCA
 TCCGCTATTCAACAAAGAGCCATCTTGCCAATCAGCTGAAGGTAGAGATCTTTTCGCTCAAGCTCAATCC
 GGTACTGGTAAACCGCTACCTTTACCATTTCTGCTATTACAAAGAATCAATGAAAAATGAAAAAGCCACT
 CAAGCTTTAATCTTGGCCCCAACACAGACAAATTCGCTTTGCAAAATCAAGAATGTTATCACTGCTATTGGT
 TTGTACTTGAAGGTTACTGTCCATGCTTCTATTGGTGGTACCTCAATGAGTGACGATATTGAAGCTTTC
 AGATCTGCTGTTCAAATTGTGCTTGGTACTCCAGGTAGAGTCTTAGACATGATTGAAAGAAGATATTTC
 AAAACCGATAAAGTCAAGATGTTCACTTTGGATGAAGCTGATGAAATGTTATCAAGTGGATTTAAAGAA
 CAAATTTACAAACATTTTCAGATTATACACAGAAACCAACCAATTTGCTTTATTATCTGCCACCATGCCA
 CAAGACGTTTTGGAAGTCAACCAAAATTCATGAACCAACCCAGTCAGAAATCTTAGTCAAAAAGATGAA
 TTGACTTTGGAAGCTATCAAACAATCTATATTAAATGTTGAATTAGAAGATTCAAATTCGATTGTTTG
 TGTGATTGTACGATTCTATTTCTGTCAACCAAGCCGTCATTTCTGTAACTAGATCCAAGGTTGAA
 TTTTTAAACCAACAAATTCAGAGAAACAACATTTACTGTCTCTGCCATCCACGCTGATTTGCCACAAGCC
 GAAACAGACACCATTTATGAAGAATTCAGATCTGGTCTCTCAAGAATCTTGATCTCTACATGATTTGTTA
 GCTAGAGGTATTGATGTCCAACAAGTTTCTTTAGTTATCAACTACGATTTGCCAGCCNACAACGAAAC
 TACATTATAGAAATTCGTAGAGGTGGTCTGTTTCGGTAGAAAAGGGGGTGGCCATCAACCTTGTCACTGAC
 AGAGATGTTGGTATGATGAGAGAAATTCAAAATTTCTACTCTACTCAAATCGAAGAAATGCCAGCTGAT
 ATTGGTGCTTTATTTGCTTAG

YJL138C_homolog 397aa (SEQ ID NO 618)
 MASEGITELDSGLIETNYDENVVYKFDDLNLKPNIVRGIFGYGYETPSAIQQRAIIPPTTGGEDVIAQAQS
 GTGKTATFTI3ALQRINENEKATQALILAPTRELALQIKNVPTAIGLYLKVTVHASIGGTSMSDDIEAF
 RSGVQIVVGTBGRVLDNIERRYFKTDKVKMFIIDRAQPMISSGFKEOIYNIFRLLPETTQIVLLSATMP
 QDVLEVITTKFMNPNVRILVKKDELTLLEGIKQFYINVELEDYKFDCLCDLYDSISVTQAVTFCNTRSKVE
 FLTNKLRREQHTVSATIAHAPLQAERDTIMKEFRSGSSRILISTDLLARGIDVQQVSLVINYDLPANKEN
 YIHRIGRGRFRGRKGVAINFVTDTRDVGMMREIEKFYSTQTEEMPADIGALFA

YKL060C_homolog 1080bp public: 1..1080 (SEQ ID NO 619)
 ATGGCTCCTCCAGCAGTTTTAAGTAAATCCGGTGTTATCTACGGTAAAGACGTCAAAGACTTGTGTTGAC
 TATGCTCAAGAAAAAGGTTTTGCCATTCCAGCTATCAATGTCACCTTCATCTCACTGTTGTTGCTGCT
 TTAGAAAGCTGCCAGAGACAAACAAGGCTCCAATCATCTTGCAAACCTCTCAAGGTGGTGCTGCCTACTTT
 GCCGGTAAGGTGTCCACAACAAAGATCAAGCTGCTTCCATTGCTGGTTCATTTGCTGCCCTCACTAC
 ATTAGAGCCATTGCTCCAACTTATGCTATCCAGTTGTTTACACACTGATCACTGTGCCAAAAAATTA

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TDECCATNGGTTCCATGGTATGTTGAAAGCCGATGAAGAATTCTTTGCTAAGACCCGGTACTCCATTTGTTC
TCATCCCACACATTTGGATTTATCTGAAGAAACCGATGACGAAAACATTGCTACTTCTGCCAAATATTTTC
GAAAGAATGGCTAAAATGGGTCAATGGTTAGAAATGGAAATGGTATCACTGGTGGTGAAGSAGATGGT
GTCAACAACGAACACGTTCAAAAAGATGCTTTATACACTTCTCCAGAAACTGTTTTTCGCTGTCTACGAA
TCTTTACACAAGATTTCTCCAAACTTTTCTATTGCTGCTGCTTTTGGTAACCTCCACGGTGTTTACAAA
CCAGGTAATGTGCAATTGAGACCAGAAATCTTGGGTGACCACCAAGTTTACGCTAAGAAACAAATTGGT
ACTGATGCTAAACACCCACTTATACTTGGTTTTCACGGTGGTTCCTGGTTCTACTCAAGAGAATTC AAC
ACTGCTATCAAGAAATGGTGTGTCAAGGTCAACTTGGACACTGATTGTCAATATGCTTACTTGACTTGGT
ATCAGAGATTACGTCAACCAACAAGATTGAATACCTTGAAAGCACCACTTGCTAACCCAGAAGGTGCTGAC
AAACCAACAAGAATACTTTGACCCAAAGAGTCTGGGTAGAGAAAGGTGAAAAGACCATGTCCAAAGAGA
ATTGCTGAAGCTTTGGATATTTTCCACACCAAAAGGACAAATTGTAA

YKL060C homolog 359aa (SEQ ID NO 620)

MAPFAVLKSGVIYGKDVKDLFDYAQEKGFALPAINVTSSTVVAALEAARDNKAPIILQTSQGGAAAYF
AGKGVNDKDAQASIAGSIAAAHYIRAIAPTYGI PVVTHFDHCAKKTLPWFQGMKKADEEFPFAKTGTPFLF
SSHMLDLSEETDDENIATCAKYFERMAKMGOWLEMEIGITGGBEDGVNNEHV EKDALYTSFETVFAVYF
SLHKISPNFSIAAAFNGVHGVYKPGNVQLRPEILGDHQVYAKKQIGTDAKHPLYLVPHGGSGSTQEEFN
TAKNGVVKVNLDTDCQYAYLTGIRDYVVKKIEYLKAPVGNPFGADKPNKKYFDPRVWVRGEKTM SKR
LAEALDIFHTKGQL

YKL150W_homolog 906bp public: 1..906 (SEQ ID NO 621)

ATGTTGACTCATCATTTTATCGAATTTGGCTACTCCAAAATTCCTTAGTACCATTTGCTCCTCCCACTGCT
TTGTCATTTGGTTTGGCATTCGCAATATCTACTTCCAAACAATTACATTGCTAACGAAACTGGTAAAACCT
TTCACATGATGCAATGAATGGGTGGACTTGAATTTATCTTACTCAATTGATTTTACTCATTAACACCAAA
CACTTGGTTTTCAAATTAAGAATGAGAATGATGTTTCTGTTTTCATCACTGCTTCATGTTTGTTCACC
AATTTCTTACACCAAAGGGTAACAATGTTTATTCGTCCATATACCCCTGCTCTCTGATGTTAACCAATCT
GGTCAAAATGATTTCTGTGATTAATAAATACGACGGAGGTAAAATGTCAAGTCACATTTTCCGATTTGAAA
GAAGGIGAAACUTTATCATTTCAAAGGACCAATTGTTAAATGCAATTCGGAACCAATCAATTCAAGTCC
ATTGCTTTGATTTGGTGGTGGTACTGGTATTACTCCATTTATACCAATTTGTTGCAATCAATCACTTTCTAAT
CCAAAGGACAACACCAAGTTAATTTGATTTACGGTAACTTGACTCCAGAAGATATCTTGTAAAAGAAA
GAAATCGATGCTATTCCTTCTAAACACAAGGACCAAGTTAAAGTTCATTACTTTGTTGACAAGGCAGAT
GAAAAGAAATGGGAAGGTCAAAATTTGATTTCAATTAACAAAGAAATCTTACAAAAGAAATTAGAAAACCA
GGTCTGATTTCAAGCTTTTGTTTGTGGTCCACCAGGTTTATACAAGGCTATATCAGGTCTCTAAAGTCT
TCCCAACTGATCAAGGTGAATTGACTGGTGGCTTTGAAAGATTTGGGTTTCGAAAAGAACATGTCTTT
AAATTTTAG

YKL150W_homolog 301aa (SEQ ID NO 622)

MTTHHLSKLATPKFLVPTAGATALSIGLALQYSTSNMYLANETGKTFTDSNEWVDLKLKSIDLTHNTK
HLVFKLKDENDVSLITASCLLTKEFVTPKGNVIRPYTPVSDVNQSGEIDFVIKKYDGGKMSSTFDLX
EGETLSFKGPVYKWKWEPNQFKSIALIGGGTGITPLYLHLHQITSNPKDNTKVNLIYGNITPFDILLKK
ETDATASKHKDQVKVHYFVDPKADKKWEGQIGFITKEFLQKELEKPGSDFKVYVCGPFGLYKAISGPKV
SPFDQGELELGALKDLGFEKEHVFKE

YLR029C_homolog 615bp public: 1..615 (SEQ ID NO 623)

ATGGGTGCCTACAAATATTTAGAAGAATTGCAAAGAAAGCAATCTGATGTTATGAGATTTCTTGAT
CGTGTCAGATGTTGGGAATACAGACAAAAGAATGTCTATCTACAGAGCTTCCAGACCATCTAGACCACAC
AAGGCTAGAAGATTAGGTTACAAGCTAAACAAGGTTTCTGTTATCTACAGAAATCAGAGTTAGAAGAGGT
GGTAGAAAGAGACCACTTCCAAAGGGTGCCACTTACGGTAAACCAACCAACCAAGGGGTTAACCAATTG
AAAATACCAAAAATCATTTGAGATCTACTGCTGAAGAAAGAGTTGGTGGTGGTCTTCTAACTTGAGAGTC
CTGAATCTATCTGGGTTAACCAAGATTCACCTACAAATACTTTGAAGTTATTTTAGTCCGACCCATCT
CACAAAGCTATCAGAAGAGATGCTAGATACAACCTGGATCGTTAACCCAGTTTACAAACACAGAGAAAGCC
AGAGGTTTGACTTCTGGCTGGTAAGAAATCCAGAGGTATTAACAACCGTCATTTGTTCAACAAAACCAAA
GCTGGTAGAAGACACACCTGGAAGAGCACAAACACCTTATCTTTATGGAGATACAGATCTTAA

YLR029C_homolog 204aa (SEQ ID NO 624)

MSAYKYLEELQPKKQSLVMRFLYRVHCNEYRQKNVLRASRPSRPDKARRLGKYKAKQGFVIYRIRVRRC
GRKRPVYKGYCKPTNQVNLKYQKSTLSTAEERVGRAGNLRVLNLYWVWQDSYKYFVILVDPSS
HKAIRRDARVNWTVNPFVHKHREARGLTSAKKSRGINKCHLPNRTKAGRRHTWKKHNTLSLWRYRS

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YNL030W_homolog 318bp public: 1..318 (SEQ ID NO 625)
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 ATTTTAAGAGATAACATTCAAGGTATTACAAAACCAGCTATCAGAAGATTGCGCCAGAAGAGGTGGTGT
 AAACGTATTCTCGCTTTGATTTATGAAGAAGTCAGAGTTGTCCTGAAACAATTTTGGAAAAACGTTATC
 AGAGATGCTGTTACTTACACTGAACATGCTAAAAGAAAAACCGTCACTTCATTGGATGTTGTTTACGCT
 TTGAAGAGACAAGSTAGAACCTTGTATGGTTTCGGTGGTTAA

YNL030W_homolog 105aa (SEQ ID NO 626)
 M9GTGRGKGGKSLGKGGAKRHRKILRDNIQGITKPAIRRLAERGGVKRISALIYEEVRVVLKQFLENVZ
 RDAVTYTEHAKRKIVTSLDVVYALKRQGRITLYGFGG

YOR285W_homolog 546bp public: 1..546 (SEQ ID NO 627)
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 GGATTAAGAACTACACCAAGATTTTATAGTGTATTGACTGAATCTCCAGAGGCCAAAAGTATATAAATAT
 GCGATGTTAAGGATGTGGCCGTACACCCCTGAAAACCCCTGATTCGTTTTAGTGGATGTTAGAGAA
 CCAACTGAATTTGCAGATCGTCATATACCAGGACCTTTGAATATTCCATTTAAAAGTAGTCCCGGCGCA
 TTGCATTTGTCAGAAGAAGATTCCCAAGAACATTTTGGATTTCCCTAAACCAAGTACTGAATAAGAATTG
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 AAAAGAGGAAAATTATCTTGAAGTTGGGAAGATTGGGTAAACNTGAAAATAAAAAGAACTAA

YOR285W_homolog 181aa (SEQ ID NO 628)
 MFAFKKSTTSILKTVVAPTSSRYLSTVTLRSIPRTFHNATKVSLENGLRTPRFYSVLTESPEAKVYKY
 ADVKDVAVHPENIIPDSVLVDVKEPTFPGCHI PGALNLPFKSSPGALDLSEEDFQEHFGFKPKPSTDKEL
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YOR327C_homolog 603bp public: 1..603 (SEQ ID NO 629)
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 GTATCCCAAAGAACTCAACCTGGACAGAGACAAAGTGTGAAGAAGGTAATTATATTGGTTCATACATTAT
 ACCAGATCAGAAGGAATTTCTGGTATCATTATAACCCACAAGCATTACCCTCTAAGACCAGCATATACA
 TTAATAAATAAAATCTTGAAGAATATTTATCATTGCATCCTAAATCTGATTGGGAAAACATTGATAAA
 GCAAATGAAACTTTACAATATGGACAATTAGAAGCATATTTGAAAAATATCAAGATCCCACTCAAGCT
 GATTCAATCATGAAAGTTCAACAAGAATTAGATGATACTAAGGTGTGTTTTACACAAAACATTGGAAGGG
 GTTTTACAAAGAGGAGAGAATTAGATTCAATGGTTGACAAATCAGAAGCATTTGCAAGTTCTTCAAGA
 ATGTTTTATAAACAAGCAAAGAAAACCAATTCTTGTTGTGTGATTATGTGA

YOR327C_homolog 200aa (SEQ ID NO 630)
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 DSIWKVQQELDIPKVVV LHKPIEGVLRGEKLDLSLVKSEALSSSSRMFYKQAKKTNSSCCVIM

YFL037C_homolog 474bp public: 1..474 (SEQ ID NO 631)
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 AAAGCTACCAAAATCGAAGGTGTTGAAGAAGCCAACTTCTTCAGAGAAGATGGTAAAGTTTTACATTTT
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 AATATTACTCAATCGATCCCAAAATTTTACCACAAATTGGGTGCTGAAAACCTTGGAAATCTTGAGACAA
 TTGGCTGAACAAAATCCAAAGCTGCTAAAACCTCCAAAACACTTCAACACTGCTTCTGCTAACGCTGCTGCT
 GATGCCGGTGGTGAAGATATTCCAGACTTGGTTGACCAAAAATTTGACGATGTAGATAA

YFL037C_homolog 157aa (SEQ ID NO 632)
 MFVCPPEKLAKLQKSSAKKVGGSRVKAKENIKTEQDDTKLIEALGKLKATKIEGVVEANFFREDGKVLHF
 NRVGVQCAPASNTFAFTGYPPQEKNTQLIPQILPQLGAENLEILRLALQLQAGKTPKLFNTGSANAAA
 DAGGEDIPDLVDQKFLDVE

YFL070W_homolog 330bp public: 1..330 (SEQ ID NO 633)
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 CACTCTGCTTGTCTGTCAGGAATCTTGAACAGAGTTAAATCTAACGCTGCTAAAAAGAGAGAAGCTAAA
 CCTAACCGTGAACCCCTTTACTTGAAGAGACAAGCTTCCAAAGCCAGAGGTTCAAGAATTATCTCCACT
 GAAGGTAAACATTCCTCAAACCTTGGCTCCAGTGGCTTACGAAACCTTCATTTAA

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YPLC79N_homolog 109aa (SEQ ID NO 634)
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YBR089C-A_homolog EMBL_entry 279bp public: 1..279 (SEQ ID NO 635)
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 GGTCAAGTTGGTAAATTATTAGGTGAAAAATGGAAGGCTTTAAACAGTGAAGATAAATTACCTTACGAA
 AACAAAGGCTGAAAGCTCATAAAAAGAGATATGAAAAGAAAAGGCTGAATACGCTAAAAAGAAATTCGGCC
 TAA

YBR089CA_homolog SWISS-PROT_entry 92aa (SEQ ID NO 636)
 MAPGERKKSSRKKNDFDAPKRSLSAYMFFANENRDIRVAENPGISFGQVGNLLGEKWKALNSEDKLPYE
 NKABADKKRYEKEKAEYAKKNSA

YBL092W_homolog EMBL_entry 396bp public: 1..396 (SEQ ID NO 637)
 ATGGCTACTTCTGTTCACACCCAAAAATTTGTTAAGAAATACACCAAGAAATTCAAGAGACACCATTCT
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 TTCAGAGGTACCATCCACACAACCAACATTGGTTACGGTTCCAACAAAAAGACCAAGTTCTTTGAACCCA
 GCTGCTTACAAAAGTTTACTTTGGTTAAAAACGTTAAAGACTTAGATGTCTTGTATTTCACACATAAATCT
 TATGCTGCTGAAAATTGCTCTTTCTGTCTCATCTAGAAAAGAGTTGAAATCGTTGCTAAAGCTAAGAAA
 CTCGGTGTAAAGTCACTAATCCAAAGGGTAAATTGAACTTGGAAAGCTTAA

YBL092W_homolog SWISS-PROT_entry 131aa (SEQ ID NO 638)
 MATSVPHPKIVKKYTKFKRHHSDRYHRVAENWRKQKRGIDSCVRRRFRCTIPQPNIGYCSNKKTKFLNP
 AGYKVYLKQNVKDLQVLLHTRKSYAAELASSVSSRKRVEIVAKAKKLGVKVTNPKGKLNLEA

YEL059C_homolog 2791bp PathoSeq: 1..2791 (SEQ ID NO 639)
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ATATTTGTAGATTTCTGCTGGCCCAAGTTGTTCTCTAAAAGTACCATCTTTCAATACCTAATCGTATTTTCACTACA
ACAAGCCGAGAAATCACTGTTTTCATCTTTTATTTTCCCGTTTGGGTTAAATATACCAATCCCAAAAATTTGTCGGG
GTGACCATTCCTATCCA

YDL059C_homolog_1 67aa PathoSeq: 1..67 (SEQ ID NO 640)
ENKYSALVIVKIELILKDGTFEESGQAEFTNMPYKHCYASARZKAVTEAIKNAIVGLRQLYLEYE

[illegible]

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 AACAAAGTTGCTCACGTCAAGGCATTAGAGCCTCACATGCAAGTATTATTCAAAACATATCAGAAAGAGTGGTGCTA
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ACTGGAGTTTATCAAATGAATCGGATTTAGATGAACATAACAGCAGAGTTGTTATATAACGCAAGTGACTTG
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YGR008C_YLR327C_homolog_1 79aa PathoSeq: 1..79 (SEQ ID NO 644)

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YGR034W_homolog 2004bp PathoSeq: 1..2004 (SEQ ID NO 645)

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YGR034W_homolog 120aa PathoSeq: 1..120 (SEQ ID NO 646)

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YMR273C_homolog 935bp PathoSeq: 1..935 (SEQ ID NO 647)

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YMR273C_homolog 198aa PathoSeq: 1..98 (SEQ ID NO 648)

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YPR028W_homolog 3616bp PathoSeq: 1..3616 (SEQ ID NO 649)

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YFR028W_homolog 149aa PathoSeq: 1..149 (SEQ ID NO 650)

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YFR033C_homolog 24142bp PathoSeq: 1..24142 (SEQ ID NO 651)

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YFR033C_homolog 114aa PathoSeq: 1..114(SEQ ID NO 652)
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[illegible]

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YJL166W_homolog_1 91aa PathoSeq: 1..93 (SEQ ID NO 656)

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YPL271W_homolog 7123bp PathoSeq: 1..7123 (SEQ ID NO 657)

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 T A C T C A A T T C C A T T A A A A T T T C A A C A A A T T G T A A C A T A T C T T C C C G T T C A C T T T T C A A A A T A A A T T T T G A A A T
 T A A T T A A T A C T T G T A A A U C A A A T A G C C T A C C A A A T A A A A C T G C T G G T T G T T C T T T A C C T T T C A T T G A A C T G G T T A
 A T T T T G T A G T T T C A A C A A G T A A A T C T A A A T A T T T C C C A A C A G T T A A A G T T C C C C G A T T A T T A A T I C A T T G A C A A
 C T T C A G T T A A T G C C A T A C T A A A A C C A A A T T T T G C T G A T T G C T A C T A G T T A A A A T C C C T T T A A A C T A T C T A T T C A
 A C G C A T A T G A C C A T T C T T C T T C A T T A T C T C C A G C A A C A A A T T C T G A A A T T A A C A G A G T G G C T G C A T T C A A A C G T T
 C T T T T G G T A A T T C A G A A C C C A A T T T A A A A T A A T G A T C T C T C A G G A C T G C C A T A T G C T C T A T A A C C G T T A G T T T T C
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 P T T C T C T T A C T T C T C G A T G C C T C C A A C A A C C A C G G A C C C A C C A T C G C A G A A A A A A A A T T T A T G T T A T T A C T T
 C T A T A G T T T T T T G A C G C G T T T A A C T C T T A A C A C A C G A A T A T T A C A T T A T G T T G T C T A C A A A A T T C A C T C T A C G G T
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 C G A T A T C A A C A A T T C A T A A T C A T T T A C T A A C C C A T T C T C G A G A T A A T A C C A T T A A G A T A T G G G A C A G A T C G T A T A
 G C T G T G T T T T G A A A T A C C T T C C A A G C A T T C A A T T T T A G T A A T A T T T G T A T T A T A T A T G A T T T A T T A A T T A C T C
 C T G C A G A T A C A A T T C T A A T A A T T T G G A T G T T T A T A A A T C G A T A A A G A T T G G C A A A T T A C A A G A T T A A T A T C G G
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 A T A T C A T T A T C T G C C C T T T G A A A G T G G T G A T A T T G T A G G G C T A C A G T T G A T A T T A C C A C G G G C A A G A A T A T T A T
 C A A C T A C A G G A A A C A C T A A T G A T A A A A C C C T T A T T A T C A A T C A G C G A A A T T T A T T C T T C A A T A T C A T A A T T C A A
 C T C A T G T C C C T A A T C C A G T C A T T T C T C T A C T G A A T C T A G A T T C A G T G T T A G T A T C T G G A T C A A C A C T A A T A A A G
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 C C T A T T G T C T C C C A C T G G G A A T A T T G C C A T G A T T A C T A A T A A A C T G C G S G C T A C T A T G A T T G G G T G G G T G T G T A
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 T C A T T T C T T T T T C G C A A T T T C A G T G A T C A T T A A T T G T T G A A A T A T A T T C A T A A T C T A A A G A C A A C C A G G T T
 G A A T T G T C C A C C A C A A T A A G T A C A A G T A T A G C C A C A A T T G A G G T A T T C T T A A C C G T T A A T T C A T T C A C A C A C T T
 A C C A C A A A G T A C A G C C T T G G T T G T A T T G T C A T T T T A T C G A A T C G G I C T G G T T C A T G G T T A G T T G A T T C T T G A T C
 G C A T T T A A A G C A T G G A T A A T A A T T G T T A C A A C A T T T G A A T C T T A A G C A A T G A T A T C T A G T T T A G T A T G A T A A T G
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[illegible]

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[illegible]

YKL156W_homolog 2002bp PathoSeq: 1..2002 (SEQ ID NO 665)
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[illegible]

224/251

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YLR038C_homolog_1 74aa PathoSeq: 1..74 (SEQ ID NO 668)

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YNL131W_homolog 15251bp PathoSeq: 1..15251 (SEQ ID NO 669)

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TGGTITACCTCTTTTCTTGATGAATCAAACTCTTTACCACTTAGTTAATTTACUATCATAATGAATGGTTACAGT
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 AATTTAATCTAATTTAAGTTAATGAACAATTTGCAAAATAACAGTTATATGTGTCAATTTGAATTTGATCATAAAGTG
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[illegible]

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YNL131W_homolog 150aa PathoSeq: 1..150 (SEQ ID NO 670)
MVKLTQIQDETQQQFENQSVAKNNHIIDEASSEESDDDDSDDDDFENETLLERIVALKDIVPPEQRE
SIYNLSSITIGDLFXSSVQNGGKFLNLTLS\$SLLGVFLALAILSETQLQEWERGMSI,FKSAQDVTAPQSF
AFGNENKK

YHR161C_homolog 4220bp PathoSeq: 1..4220 (SEQ ID NO 671)
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TCCTTAAGTCTCACAGTTAAAGTTGTAGTACCCCTCCCATAGAGCCTGATGATGTCGTGTACGAAAACCTTGTA
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YHR161C_homolog 609aa PathoSeq: 1..609 (SEQ ID NO 672)

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GRRLRLDQDKGLLREVESVQKQIDSLLKNFMENEINADIVLTAFRLLVNDLLALFOELNEGVINILEHYFEMSK
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QQQSQQQAQQQAQQQALQQQVQLQQAQQQALQQQATQQATQQQQQTLFSQLPSISQSQTLQSTFTGVVFGGYGS
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YDR544C_homolog 1700bp GeneSeq: 1..1700 (SEQ ID NO 673)

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NATATCTTTTCAAAACACACACGTACCACTGATAATTCACCAATATCGAAATTTGAACCTCATCAGTCAAGTTT
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YDR544C_homolog 518aa GeneSeq: 1..518 (SEQ ID NO 674)

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FIEDLGQSKYKVNPTSIKTLGLGLKYLXPTQVFI IQQIKWFEPHQSSLMVSIIRSTTFLVLENFVVSVALNQDI
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YHR034C_homolog 1653bp public: 1..1653 (SEQ ID NO 687)

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YHR094C_homolog 550aa (SEQ ID NO 688)

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 TVGTTIVQTASQHAWYQIMIGRTITCLAVGMLSVLCPFLSEVSPKELRGTLVYCFQLMITLIGFLGYCT
 SYGTKKYSDSRQWRIFLGLCFAWALCLLGGMVRMPESPRYLVGKDRIDDAKISLAKTNKVPEDPALYR
 ELQLIQAGVERERLAGKASWGALITGKPRILERVIVGCMQLSQLQLTGDNYYFFYSTTIFKSVGLNDSF
 ETSIILGVINFASTFVGIYAIERLGRRLCLLTGSMVMSCTFLIYSLIGTQHLIYIDQPGGPTRKPDGNAM
 IFITALYVFFFASTWAGGVYSIVSELYPLKVRSKAMGFANACNWLWGFLLSFPTSFITDAIHFYYGFFV
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YBL099W_homolog 1344bp public: 1..1344 (SEQ ID NO 717)

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YBL099W homolog 447aa public: 1..447 (SEQ ID NO 718)

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 YIPINVISITDGOIFLEAEIFYKGRPAINVGLSVSRVGSAAQVKAKQVAGSLKFLAQYREVAAPAFQF
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YF032W_homolog 2637 bp public: 1..2637 (SEQ ID NO 719)

AUGGATGAACGATTTTGTGAATCCACCACCTACAGCTGATCAAGATGATACTAATCAGCCACTTGATGCC
 ATCTTTGGTGATAGAGTCAGAAAGATTTCAAGAGTTTTTAGATAGAATTGATTCTAATACAGGTATAGAT
 TACAGATCTATTATCAAAGATATGTTGATCAACAGCTAAGTTTACATTGAGTGTTCATTGATGAAAATA
 AGAGAGTTTGACAGAGAAATTTGGTTTGGGTTGCTCAACCAGCCAGCTGACTATTTACCAGCTTGTGAA
 AGACCTTTGAGAGACACAGTTTTAGCTTAATTACGACCCACAGGATCCAAGTTTCCACATGACAGTTAT
 GACCCTAACCAGCAATACTATTTATCATTCAAGGGAGCATTTGGGGGACATTCGCTCACTCCTAGATCG
 ATTGATTCAGCTATCTTTCCAAAATGGTTTTCTATTGAAGGTATTGTGACTAGAGCTTCATTAGTTAGA
 CCAAAGGTTATTAGATCGGTTCAATTATGCTGAAAAAACTGGTAGATTTTATGCACGTGAATAACCGAGAC
 CAAACAACATCCTTTGATGCCAATTCCTACTCCCGCTATATATCCAACTGAAGATATGGAAGGTAACTAAA
 TTAACCACAGAGTATGGTTATTCGACATACAGAGATTACCAGAAGATCTCTGTACAAGAAATGCCCTGAA
 ACAGCTCCTTCAGGTTCAATTGCCAAGATGGGTTGACGTTATTTTGGATGATGATTTGGTGGATTGTGACA
 AAAACCGGTGATCGTGATCAAAATGTTGGTGTTTATCGTGCCTTAGGAGGTGCTGCAAACAATAGTTCT
 TCTTTCAAAACGGTTATCTTAAGTAAATCTGTTTACTTGTACATGCCAGATCAACAGGGGTTGCTTCA
 CAGAAAAGTTAACTGATCAAGATATTAGAAATATAAAATAAACTTCCAAACCATAGAAACATTTTTGAT
 ATTTTATCCCGTTCTTTGGCCCTTCAATTTATCGGTTTGACTATATTAAGAAACCTCTTTTACTTATG
 ATGATGGGAGGTGTTGAAAAAAATTTAGATAATGGTACACATTTGAGAGGTGACATTAAACATTTTGAATG
 GTGGCTGACCCATCCACTGCCAAATCTCAAGTATTACGGTTTGTGTTGAACACTGCTTCATTAGCTATT
 GCCACTACTGCTAGAGCATCGTCAAGTGTAGGTTTAAACAGCTGCTGTTACTACCGACAAGGAAACACCGA
 GAAAGAGATTGGAGGCTGGTGCATTCCTATTCGCTGACAGAGGTATTGTTTGATTTGATGAATTTGAT
 AAAATGTCAGATATCGACCCGAGTGGCCATTACGAAAGTTATGGAACAAACAACTGTCACTATTGCTATAA
 GCTGCTATTTCACACCTTCATTGAATGCTCGTTGTTCTGTTATTGCTGCGCAAAATCCGTTTGTGGACAC
 TACGATGTCCATAAAGATCCACATAAAAAATATTCCTTGGCCCGATTCAATTATTGCTCTCGTTTGTATTG
 CTCTTTGTTGTTTACAGATGATGTCAACCCAAACAGAGACAGGGTTATTTCTGAGCATCTTTTAAGAATG
 CACAGGTTTGTTCCTCCTGGATTGATGGAGGGAGAGCCCAATCAGAGAAAAATCAGCAGTTACATTGGCT
 GTCGAGATGATGAAACCAATGAACAAGAAATTATTAGAACAGCCCAATGTTTGAAGAAATTAACACATTA
 TTGCATGCTGCTATTCAAAAACAAAAAGTCAAAATAAATACTTTTCGATTCCATTCTTTGAAAAAATATGTC
 CAGTACGCCCAAGCAAGAGTGCACCCAGTGTTCACCAAGGGTGCATCCGACTACATTGTTACTACATAT
 TCCTCCTTAAGAAACGATTGATACGCCAACCAACCAACAAATACAGCTCCAAATAACTGCTAGAACTTTA
 GAACCTTTGATTTCGTTTACCAACAGCTCATGCAAAAGTCCGTTTATCCAAAACCTCTTCATCTGAAAGAT
 GCAAAAGTTGCCGAAGAGCTATTGAGATATGCATTATTCAAGGAAGTAGCCAAAAAGACAAAAAGAGA
 CAAAAAAGTACAAAGTATAGTGGACTCAGAGAGAGGAGGAAGAGGATGAGTCTGATGCAGAAATGGAAAT
 TCCGATATACGAAATAATGCCCAGAGAAAGTACTAGAAGAAACAGAGCTACAGCAAAACACAGCTCCCA
 CAACAGCAAGCAAGCATCTCTTCACTTAACACCCGAAACCCCACTTTGGACATCGCGAGCATGGAGATGAC
 GATGGAGTTGGTGAAGAATTAGAACAATTCATTGTCATCATCTCAGCAACCAACAGCAACCAACATAT
 TTGCAACCATTCAGTGCAGATCATCAAGTAACTTTGTATCATCTACCGCCACAAATGCAATCAGCGTT
 GAGAGATTGAATAATTTTCAAAAGAACTACTAGCCAGGTGTCAAGTTCTGCATTATTTGCCAATGATCAA
 GCTGCGGCAAACTATCATGACGTTACTGCTGCTATCAATGAACAGATGGAACAAGAGATATTTTCTCA
 GAGCAAGAGTTGAGTGTGGATTTGAAGTGTGAGTTCTGAAAACAAGTTTTACCTAGAAAGTGATAAG
 ATTTGGAAGATTTAA

YEL032W_homolog 878 aa public: 1..878 (SEQ ID NO 720)

MDERFLNPPPTAQDQDTNQPLDAPGCRVRRFQEFLDRIQSNQIDYRSIIKMDLIKSKFRLSVSIDEI
 REFDFEPWLGLLNQPAJYLPACERARCTVLAIYDPQDPSPPHDSYDPNQYYLSFKGAFGGHSLTPRS
 IGSSYLSKMVSIEGIVTRASLVRPKVIRSVHYAEKTGRFYAREYRDQTTSFDAIATPAIYPTEDMEGNK
 LTTEYGVSTYRDYQKISVQEMPRTAFFGQLPRSVGVLEDDDLVDLTKPQDRVQIVGVYRALGGAANNSS
 SFKTVILSNVYLLHARSTGVASQEKLTDDQDIRNINKLAKDRKIFDILSRSLAPSIYGPDIYIKKAVLLM
 MMGGVEKNLUNGTHLRGDINILMVGDPEFAKSKQLRFPVLNTASLAIAATTGRGSGSVGLTAAVTTDKETG
 ERRIEAGAMVLADRGIVCIDFDMSDIDRVAIHEVMEQQTVTIAKAGIHTSLNARCSVIAAANPVPFGQ
 YDVHMDPHXNIALPDSLLSRFDLLFVVTDDVNFTRDRVISEHVLRMHRFPVFPGLMEGEPIREKSAVTLA
 VGDDETNEQELLEQPMFEKFNLLHAGIONKKSNNILSIPFLKKYVOYAKORVOPVLTKGASDIYVTTY
 SSTANDLICNNQRNTAPITARTLETILRLATAHAKVRLSKTVDKDAKVAEELLRYALFKEVAKKTKKA
 QKTTGIVDSEEEDESDAEMENSDNEIMPRESRRRTRATAQTQPFQQQASPSLTPEPLGHRDOGDD
 DGVGEELECFHLSSSQOQOQOQYLOPLTERSSSKIVSSTATNAISVERLNIKFRILAQVRSALFANDQ
 AAANYHDVTRALNEQMEQEDIFSEQELSGAFVMSSENKFYLESDKIWKI

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YHR135C_homolog 1488 bp public: 1..1488 (SEQ ID NO 721)

ATGACAACAAACCCCTGCTTTGGGUGGCTGCTCAAGCAATCATATAAATATTCCCTACAAAGCAAAATGAAT
 CATTTCAACTTCATCTTCAAAACCGTAACGGTAGCAATAATTCATCCCGTGGTTGGACTTCACTACAAGATT
 GGGAAAAAATTTGGTGAAGGTTCTTTTGGTGTCAATTTTGAAGCTACTAATATAAATAAATGGAGTACCC
 GGGGCCATAAAATTTGAACCTAGAAAGACTGAAGCTCCTCAATTACGAGATGAATATAGAACCTATAAA
 CATTTACAAGGATGTGACGGAATTCCTAATGCATATTATTTTGGTCAAGAAGGATTACATAATATTTTA
 GTCAATTGATTTATTTGGGTCTTCTTTAGAAAGATTATTTGATTGGTGTGGTGAAGAATTTACTCTTAAA
 ACCGTGGTACAAGTTGCTATACAAATGTGACTTTAGTAGAAGAAGTTCATCGTCAATGATTTAATCTAT
 AGAGATATCAAACCCGACAAATTTTTTAATGGAAGAAGAGGTGCTACTGATGAAAATAATGTTCATTTG
 ACTGATTTTGGTATGGCCAAGCAATATCCTGATCCCAAGAACAAACCAACATATTCATATAGAGAGAAG
 AAATCTTTGAGTGGGACAGCTAGATATATAGAGTACTAACACTCATTTAGGAAGAGAACAATCAAGAAGA
 GATGATTTTAGAAGCATTTGGGTCAATGATTTTTTTTTATTTTCTTTAGAGGCCAAATTAATTTAGGAAGGTTTA
 AAAGCTCCCAACCAATAAACAAGATATGAGAAAATTTGGTGATAAAAAGAGAACTACACCAGCAGTTTACA
 TATGTGATGGCTTACCTCAACAAATTTGCTGAATATTTAGATTCAAGTTAGATCATTACCATTTGATGCT
 GAACCTCCATATCAAGAATATAGAATGTTATTTATTTGTCAGTGTGGATGATTTGGGTCAAGCTTGTGAT
 GGAGATATGGATTGGATGTCATCTTAATGGTGGTAGAGGTTGGCATCCTACATTTAATAAAAAACCCAAC
 TGGCAGCGTTATGGACATCCTAATCCACCAAAATGAACGTGAAAGAAGACATCGTGATCAAGAAGAACA
 AGACAACATCAACAACACTGCAACAAGTACAACAACAACAATTACAAGCTCAAGCTCAAGCACAACAATTA
 CAACAATTACAACAAGCACAAACAGGCCACAACAACAACAACACTGCAACAACATCAACCACTATCTGCA
 GCCCAGTTACATCAACAAAAATTACAGCAATTTGGTTAATCGACCATTACCACCAATTTAAACAAGATCA
 CAATCAGCAATCAAAAGTGGTAATGGACATCATGAACCTTTTGAATAATAATTTAGGTGATCAGCATGGA
 GGAACAACATGAAGGATACAGTTTACAGACCAATCAATATCAACAACAACAATCGTTTGCUGAAGAAGAA
 GAAAACAAGGGTTCTGGTCTAAATTTGTGTTGTCATTAG

YHR135C_homolog 495 aa public: 1..495 (SEQ ID NO 722)

MTTNPALAAQAASHNNIPTKQMNISTSSSNGNGSNNSSVVGLHYKTKGKTGEGSPGVIFEGTNTITNGVP
 VAIKFEPRKCEAPQLRDEYRTYKHLQGGDGLFNAYYFGQEGLEHNLVLDLLGPSLEDLPDWCGRRFSVK
 TVVQVAIQMLTLVEEVHREDLIYRDIKPDNFLIGRRGATDENNVHLIDFGMAKQYRDPRTKQHLIPYREK
 KSLSGTARYMSINTHLGFEQSRDDLEALGHVFFYFLRGQLPWQGLKAPTNYKQKYEKIGDKERTTPAVT
 LCDCLPQQFAEYLDVSRSLPFDAPPYEEYRMLLLSVLDDLQACDGDMDWMHLNGGRWDATINKPEN
 LHGYGHFNPPNERERRRHRDQKMTTQHQQQSQQVQQQQLQAQAQAQQLQLQAQAQAQQAQQAQQAQQAQQA
 AQLHQQKIQHLVNRPLPPIKQESQSAIQSGNCHHELLNNNLGDCHGGKHEGYSSRPDQVQQCQMVAAEE
 ENKGFWSKLCCH

YJL060W_homolog 1362 bp public: 1..1362 (SEQ ID NO 723)

ATGTTAAGACGGCTCTTTCCAATACGACAATTGTACACAACAACCTAGAGCCATGGCCAGCAAAATCAACA
 GACCCAACTAGTTTTCATATAATCCGTATTTTATCAAAAACCTGGGGCAAAAAGATATCTGGTCTGTTAATC
 AACGAAACTGCGGCCAGGCACAACAAGAAATCCGGCGAGCCAAATTTGTCAAATTGGGACAAGGGTTTTC
 TCCTACAAATCCTCCTCACTTTGCGATTAAAGCTGTTGAGGAAGCATTGACCAAGCCGCAATTCAACCAA
 TATGCACATGCTCGTGGAAACCCAAACTTATTGAAACAAGTGGCAGAGCACTATTGCGGATCGTATGGA
 CGTGCTGTGGGGGTTGACGAGGTCCAAATCACCAACGGGTGCAATGAGGGAATGTTTGCCATTTTCTTT
 GGTTCCTTCACCCCGGCGCATGAAGTCATTGTGTTTTGAACCATTTTTTGACCAATACATCCCCAATGTT
 GAAATGACAGGAGCCAAAGATCAAGTACGTTGAAATCAAGTATCCCAAGAAATTTGACAAACGAGGTTGTC
 ACGGGCCAGGATTGGGAGATTGACTGGGAAGGATTGAAATAATGCCATTACCCACACACCAAGATCATC
 GTGATAAATACCCACACAAACCAATCGGCAAAGTTTTACCGAGAAGGAGTTGTACAAGATTGGCAAG
 CTTCGCCGTGGAACACAATTTAATCCTTGTGAGGCAAGAGGTTTACGAGAAGTTCTATTATACCTGACAAG
 TTCCCTCGTCCAGCTGCATTACCAAGTTGCCCTGAATTTGGCTGAAAGGACGTTGACAGTGGGTTCTGCT
 GGGAAATCATTTTCTGCCACTGGTTGGAGAGTAGGGTATATCCAGGGCCCTGCCAATTTGATTAAATTT
 GTAACACGCGGCCACACCAAGAATTTGTTTTCTCGACCCCAACACCATTCACACACCCAGTATCTCAGCCC
 TTTGAGCAGGCTGAGAAATCAAACTATTTTGGGAACACTCGAAAGGAGTATGAACACAATACAAATA
 TTCACCAAGGTATTTGACGACTGGGGTTACCTACACCGTTGCCGAAGGAGGGTACTTTGTGTTGGTG
 AACTTGCTGAAAGTTAAGATACCCGAGATATGACTTTCCCGGAACCATCAGCGATAGAGGCACTTTA
 GATTTCAAATTTGGCGTATTTGGTTGATCAAAACAATTTGGGGTTGTGGGAATCCCTCCAACAGAGTTTTTA
 ACCGAATCGAATAGAAAGGGGAACCGCTTACAANNCTGTCTCAGATTTGCTGTTTGCAAGATGATTCT
 GTTTTAGAAGACCGCGTTGAGAGATTGAAAAAATTAAAGACTATTTATAA

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YJL060W_homolog 453 aa public: 1..453 (SEQ ID NO 724)

MLKRLFFPIRQLYPTTRAMASKSTGPTSLHNPYFYQKPGQKDIWSLINETAAQAQOQESGEPIVNLGQGFF
 SYNPPEFAINAVEEALTKPQFNQYAMARGNPNLLKQVAEHYSRSYGRAVGVDEVQETTGANEGMFAIFF
 GFLTPEGDEVIVFEPFFDQYITNVEMTGAKYKYVEIKYPKKFDNEVVTGQDWEIDWEGLNNAITDKTKIT
 VINTPHNPICKVFTEKELYKISKLAVEHNLILVSDEVYENLYYTDKFPRAALPQLPELAERTLTVGSA
 CKSPAATGWRVCYIQGPANLIKVFVTAHTRICPSOPAPLQQAVSQGFECAEKSNFYFENTRKEYEHKYKI
 FTKVTFDDLGLPYTVAEGGYFVLVNLKVKIPAUYEFFGTISDRGTLGFKLAYWLIKEIGVVGIPPIKFL
 TESNRKGNGLENCVRFAVCKDDSVLEDAVERLKKLKDYL

YML028W_homolog 591 bp public: 1..591 (SEQ ID NO 725)

ATGGCTCCAGTCGTTCAACAACCACTCCCAAGTTTCAAGAAAACCGCCGTCGTTGATGGTGTCTTTGAA
 GAAGTCACTTTAGCAACAATACAAAGGTAAATGGGCTCTGTTGGUUTTATTCATTGGCUITTCACATTC
 GTCTGCCCATCAGAAATTATTGCTTATTCCGAAGCTGTAAAGAAATTTCCGAARAGGATGCTCAAGTT
 TTGTTTGCTCTACTGACTCCGAATACACCTEGTTGGCTTGGACCAATGTGCCAGAAAAGACGGTGGT
 ATTGGCAAGTCGACTTCCAGTCTTGGCTGACACCAACCACTCCTTGCTCCAGAGACTACGCTCTCTTA
 ATTGAAGAAGAGGTGTTCCTTGAGAGGTATTTTCTTGATTGATCCAAACCCCTCTCTTGAGACAAATC
 ACCATCAATGACTTTGCCAGTCGGTAGATCTGTTGAAGAATCTTGGAGATTGTTGGAGGCTTTCCAATTC
 ACTGAAAAATACGGTGAAGTTTGTCCAGCTAACTGGCACCAGGTGATGAAACCATCAAGCCAAAGCCCA
 GAAGCATCCAAAGCAATACTTCAACAAAGTCAACAAATAA

YML028W_homolog 196 aa public: 1..196 (SEQ ID NO 726)

MAPVVQQPAPSFKKTAVVDCVFEEVTLQYKKGWVLLAFIPLAFTFVCPSEIIAYSEAVKKFAEKDAQV
 LFASTDSEYTWLAWTNVARKDGGIGKVDFFVLADTNHSLSRDYGVLTRREGVALRGTFILIDPKGVLRQI
 TINDLPVGRSVEESLRLLLEAFQFTEKYGEVCPANWHPGDETICKPSFZASKEYFNKVNK

YOL100W_homolog 2835 bp public: 1..2835 (SEQ ID NO 727)

ATGCATAAAATTTAGATATTTCTTTCGCAUCAAACACTATAGCAAAACGCAATTCAGTGCACAAATCCAAAGAC
 AGTCCAAATTAGCCAAAACAGCAATGAAGAAAATGATTGCACTAAATTAAGTTCAAGTAGTCTTCAAGAC
 TTACATGATGATCTCGATGATATTTATAACAACATATACTTTAGCACAGGGTACCAATAACAACTCTTA
 GATACATTTGGAATCTGAAAATAAATCAAGCTATAAATAACTTTATTGATAAACCTCCAGCAATTCATGGT
 ATGGAAACCACAACCTACCGGTGATGCACGTTTCTTCACGATTATCTTCTTAGGTAATACCACCAATGAA
 CATCGTGAAGCATCGCCAAAGATGCACCAAGCAATCGGTATCTTACATTCATTTGATTTCAGACCG
 ACCATCTCTGCGTGCAGTAACCAACTCATCCCTCAATGCTATTGTTAGACACCCCTAATGTCAAGTTCGGAA
 TTCAATCATTTAGTGGATCAAAACACCACCCCAATGAGTCGGTAGAAAGGTTTGACGACAGTAATAATACT
 GTGGACAATACAGAAGAGGAAGAAAATAATGATGATACAGACGAAATACAAAATCCGAAACATTGAAA
 CAAAACCCAGCAGAAATTCGGAAATTAAGGTTGCTTCAGTTAAACTATCAAGACTATGGATGGAGAAATC
 AAAACTATTTCGSCGAAATGTTACTGATTTCAAATTTGGTAAAGAATTGGGTGAAGGTTTCATATTCACG
 GTGATTTTAGCCACTGATAAGATTACTGGTAAACAATATGCTGTAAAAGTACTTCATAAGCGACATATT
 ATAAAAGAAAAGAAAGTCAAGTATGTCAATATAGAAAACATGCATTGAATCGATTAAAGTAATAGATTA
 GGGGTATTTTCATTATATTTACCTTCACAGATAAAGATTCCGCTTATTTTGTTTTGGATTATGCTTCA
 AAUGGTGAATTTATTGACATTTGATCAAGAGATACAACTATTAATGAGCAATGTACTAGACATTTTCGGT
 GCACAAATATTAGATGCTATTAATATATATGATGATAATGGTGTTATACATCGAGACCTAAAAACCAAG
 AATATATTATTAGATGACAAAATGACAATTCAAATTACACATTTTCTTACTGCCACATTTATTAGAGAAA
 AAGAAATGATGAAAGTGAAGAAATACCCAGTCGATGTAACACCAAAAATCATTTCCTTCCAAACCGCTGAATAT
 GTATCCCTTGAAATTAATAGAAAATAAGTATTGTGGTAAACCTGGAGATGTTTGGGCTTTTGGTTGCAATC
 ATATATCAAAATGATTGCTGGGAAACCAACATTTAAGCCAACTAATGAATATTTAACCCTTCAAAAAATT
 ACGAATTTGCAATTTGCGTCTAGTGCAGGATTCCTTACAATATTAGAGATTTAATAAAGAGATTCCTT
 GTGTTGCAACCTTCACGACGTGCAACCAATTCAGAGAAATACAAAAACATTACTTTTCCAAATCCGTTGAC
 TTAAAGATTTTATCTGATTTGCTGCTGATCTCTGAAATAGCACTTTATATTAATGACACGCAAAA
 TCCATGATGAAAGTACCGGAATTGAATAAGGCACCTATAACCACAGTCATTAAAGAAGAAATGTGAAGAAA
 TCCACAAACTCAAAATCAAAATACCAACAATGTCCGCACTGCTGTTGGTGGTAGTAGTAGTAACGGACAT
 AAAGCGCTCTACCCGACTCCTGAGAAAGAGCCGAGCCGAGTACTATTAATAACAGTCCACAGAAATA
 GTTAGTGCCGCTAGTGTAGCTGCATATGTTTAAACAAACCAAGCTACAAACCAAAATTCAGTACATCC
 GAGGATTCATCTAAGCGTAGCAGCACTCCAATGAACTCCCAAACTTTCATATTCACAAAGAGATTAT
 ATTCCGGGAACAAATATTTTACGTCCACAGATTACTACTAGACCGTCAGTAGGATCTTATGTGAAAACC
 ACACCAATCAAAAGGATAGAAAAACATTAACCAAGGTCCCACTGAATATCCATCAACAACAAGAAAAATG

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AAACCGAAAGTAAAGGAAGTGAAGCCAGCAACTACATTGGGAAGCAGCATGGGAAACCATATTTAACCCAT
 CCAGATGAAAGAATACTTCGTATTGGTCCAGTTATTGCTCATAAAGAACCAACAGAACCATTTGAAAAG
 AAGAATAAAGCATCTTTACATATATCACCTTTGGATATAAATAAAGAAACAAAGAGTAGATCCAAATACCT
 AGTTTACTTTACACAAAATTGTAAATGAAGTAAACAATAACACCAGCGAATTGAAAAAGTGGAAAATGCT
 GATGAATCACTTTGCCATTATGAACCACAATATAATATGAAGAGAAGTCCAACTTCTGATAGTAAGAAA
 AGTATGGATAFTTGAAAGATCTGCATCTACTTCTGGAAGTAGAAATTAGTAAGAACCCAATTTTCAAAAAA
 TTGGGGTTTTAGTCATTTAGAAAAAAATGATAGTGAAGAAATCAAAATGGTCCTAGTTTAAACCGAAAAACCA
 CAAACTTGTACATTGGTTGTTACAACCTCATGGTCCGAGCATTACTTTTCATTAGAAATGATATAGAATCC
 AATTATCTTTTAATTGCTGAAATCAAAATGAAATATCCATTATTCATTTCCTCAAGAAATTAGTTATATCA
 UAAACTAAAATTTTCTAAATTAGTACCATCAGTCGGAGTATTTCTCATTAGTTCGAATTGATAATTCATTAA
 ATTTTTGAAGTAGAAAAATTTGAAGTGAATCAATGGACTGAAGCATTAGCTAAATCTAAATATAATGAA
 ATATAA

YOL100W_homolog 944 aa public: 1..944 (SEQ ID NO 726)
 MHKFRYSLHQHYSKRNSDUXSKDSPISQNSNEENDSTKLSSESLQDLHDDLDDIYNNYTLAQGTNNNSV
 DTLDEENWQAINKFIDKPPAIHQMEFQLPVMIIVSSRLSSLGNTTNETGESIAKSAPGTFPLSSHSEDFRP
 HHPRAVTNSSLNVLLDTPNVSEEFNHLVDQTPPNESVERFDSDSNMTVDNTEEEENNDDTDEIPKSETLK
 QNEENWEKKGAAVKTIKTMDEMKTIIRNVTDPKFGKELGEGSYSTVILATDKITGKQYAVKVLDRHI
 _KEKKVKYVNIKKHALNRLSNRLGVISLYPTFQDKDSLFTVLDYASNGELLTLIKRYNTLNEECTRIHG
 AQILDAIKYMHNDNGVIHRDLKPENILLDDKMRIQITDFGTARLLEKKNDESEBYPVDVRAKSEVGTAEY
 VSPFLEENKYCKPGDVAFCCLIIYQMIAGKPPFKATNEYLTQKIKTLQFAFSAGFPTIIRDLIKKII
 VLQPSRRATIPETIQIKIYTFQSEVDFKDFDSIWLSDPPEIGPYKMTAKSMNKVPELNKAPITTVIKKNVKK
 STNSNSNTNNVATAVGGSSSNHGKSSPTPEKEPSPATINNKSTKVSAAASVAAYVLNKPATNQNSSTS
 EDSSKRSSNSNETRKLSSYSQCDYIPGTNLLRPQISTRPSVGSYVKTTPSKDKRKTTLTKVPSNIHQQQEKV
 KTKVNEVWPATTLFAAWRPYLTHPDERILRTGPVIAHKEPTEPFKKKASLHISPLDINKEQSRSEN
 SLTQIVNEVNNNTSELKKVENADESLAIEPQYNMKRSPSTDSSKSMDIERSASTSGSRISKKAIFKK
 LGPSHLEXMDSEESNCPSLTEKPQTCTLVVTTTCRALLFIRNDIESNYLLIAEIKLYPFIFHQELVIS
 QCKPSKLVPVSVGVFVISSIDNSLIFEVEKFEVNQWTEALAKSKYNEI

YJL166W_homolog 288bp PathoSeq: 1..288 (SEQ ID NO 729)
 ATGGCAGGTGCACCATCCACATACTTATATGGGCTGGTGGGGIAGTTTAGGUTCCCCAAGCAAAAA
 TATATTACTCAATATACTATTTCTCCATATGCTGCTAAACCATTAAGGGGGCTGCTTATAATGCTGTT
 TCCAATACTTTTGAAGAAGCAAGAAATCAATTTCTTTATGTTTGGCAATCCATTTTGTGTGTTTGGAGT
 ATTGGAUTAGAGCTAGAGATTATAATGAATACTTTGTACACTAAAGAAGCTAGAGAGAAGATTTGGAAGA
 GTTAATGTTTAA

YJL166W_homolog 95aa PathoSeq: 1..95 (SEQ ID NO 730)
 MAGAPHPHTYMGWNGSLGSPKQKYITQYIISPYAAKPLKGAAYNAVFNTPFRRTKNQFLYVAIPFWVWWS
 IWTRARDYNKYLYTKEGREELKRVNV

YLR038C_homolog 252bp PathoSeq: 1..252 (SEQ ID NO 731)
 ATGCCAGTCCGATCCAGCTACTTTTAAATTGAAACTCCACAATTTGACCCAAGATTCCCAAACCAAAAC
 CAATCCAAACATTGTGCTCAAGCCTACGTTGATTACCACAAATGTGTCAATGTCAAAGGTGAAGAATT
 GAACCATGCAAAATCTTTTTCAAACTTTCACTTCATTATGTCCTTTGGATTGGGTGAAAAATGGGAT
 GATCAAGACCTGCTCCTAAATTCCCACTCAACATGGACGCTTAE

YLR038C_homolog 83aa PathoSeq: 1..83 (SEQ ID NO 732)
 MPVDPATFKFETPQFDPFRFPNQNSKHCAQAYVDYHKCVNVKGEEFEPCKIFFKTFTSLCPLDWVEKWD
 DQRAAGKFPVNMMA

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Human homologues

>YGL080W_homolog, CDS: 1-330 bp (SEQ ID NO 575)

ATGGCGGCGCGGTTGGTGCGGAAAGCGGCGGACTATGTCCGAAGCAAGGATTTCCGGGACTACCTCATG
ACTACGCACTTCTGGGGCCCAGTAGCCAACTGGGGTCTTCCCAATTGCTGCCATCAATGATATGAAAAAG
TCTCCAGAGATTATCAGTGGGCGGATGACATTTGCCCTCTGTTGCTATTCTTTGACATTTCATGAGATTT
GCCTACAAGGTACAGCCTCGGAAGTGGCTTCTGTTTGCATGCCACGCCAACAAATGAAGTAGCCCGCTC
ATCCAGGCGCGGCGGCTTATCAACACGAGATGACTAAAACGGCATCTGCATAA

>YGL080W_homolog, 109 aa (SEQ ID NO 576)

MAGALVRKAADYVRSKDFRDYLMSTHFVGPVANWGLPIAAINDMKKSPEIISGRMTFALCCYSLTFMRF
AYKVQPRVWLTAFCHATNFAQLTQGGRIKHEMTKTASA

>YGR243W_homolog, CDS: 1-384 bp (SEQ ID NO 577)

ATGTCCGCGCGCGGTTGGCGGAGGCGCTGCGGGCCACCTACCACCGGCTCCTCGATAAAGTGGAGCTGATG
CTGCCCCGAGAAATTGAGGCGGCTGTACAAACCATCCAGCAGGTCGCCAGAACAGTTTTCTTCTGGGCTCCA
ATTATGAAATGGGGGTTGGTGCTGTGCTGGATTGGCTGATATGCCAGACCTGCAGAAAACTTAGCACA
CCTCAATCTGCTGTTTTGATCCCTACAGGCTTTATTTGGTCAAGATACTCAGCTGTAATTATTCCAAAA
AATPGAGTCTGTTTTGCTGTTAATTTCTTTGTGGGGGCAGCAGGAGCCTCTCAGCTTTTTCGTATTTGG
AGATATAACCAAGAACTAAAAGCTAAAGCACACAAATAA

>YGR243W_homolog, 127 aa (SEQ ID NO 578)

MSAAGARSLRATYHRLLDKVELMLPEKLRPLYNHPAGERTVFFWAPIMKWGLVCAGLADMARPAEKLST
AQSAVLMATGFIWSRYSLVLIIPQWWSLFAVNFVGAAGASQLFRIWRYNQELKAKAHK

>YGR183C_homolog, CDS: 1-399 bp (SEQ ID NO 579)

ATGCGCGCGCGCACCTTGACTTCGAATTTCTACTCCCTGCTCTTCCGCGAGACCTCCACCTTCGCGCTCA
CCATCATCTTGGCGCTCATGTTCTTCCAGCGCGCCTTTCATCAAGGCGCGGACGCTATCTACGACCACA
TCAACGAGGCTAAGCTGTGCAAAACACATCAAGCACAAAGATGAGAACAAGTAGTTCTTGGAGGCCCCC
ATCCAGGCGCAGAAAGGACCGGTCACCCAGCAGCTGTTTTGCCAGAGCTGGAGCCTCAGCTTGAAGATG
ATGCTCAAGGTACTCTTCATGGACCACCATTCGCTGTTGGCAAGAAACGGCTTTACTTACAAAACAGAC
TCTTTACCTTCTGCTGTGTTGAAGTATGTTTAGTCAGCATGCTCAGGAATAA

>YGR183C_homolog, 132 aa (SEQ ID NO 580)

MAAATLTSKLYSLLFRRPSPSPSSWASCSSEAPSIKARTLSTTTSTRGSCGNTSSTSMRTSSSLEAP
TQARRTRSTQQLFAQSWSLSLKMLKVLPMDHSLLARNGFTYKTDSLPSAVFEVCLVSMRLK

>YBR009C_homolog, CDS: 1-312 bp (SEQ ID NO 581)

ATGTCCTGGCCGCGGCAAGGCGGCAAGGCTCTTGGCAAGCGCGGCTAAGCCCCACCTAAAGTACTG
CGCGACAATATCCAGGSCATCACCAAGCGCGCATTCGGCGGCTTGGCTCGCGCGCGGCGGTGAAGCGC
ATCTCCGGCTTCTTACGAGGAGACTCGCGGGGTGCTGAAGGTGTTCTCGAGAAAGTGATCCGGGAC
GCGGTGACCTATACAGAGCAGCGCAAGCGCAAGACGGTACCGGCTATGGATGTGGTCTACCGGCTCAAG
CGCAAGGKXGACUUTCTACGGTTTCGGTGGTTGA

>YBR009C_homolog, 103 aa (SEQ ID NO 582)

MSGRGKGKGLGKGGAKRHRKVLRDNTQGTTRPATRRLARFGGVKRTSGLIYEETRQVLKVFLENVTRD
AVTYTEHAKRKTVTAMDVVYALKRQGRITLYGFGG

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>YGR209C_homolog, CDS: 1-318 bp (SEQ ID NO 683)
ATCGTGAAGCAGATCCACAGCAAGACTGCTTTTCAGGAAGCCTTGGACGCTGCAGGTGATAAACTTGTA
GTAGTTGACTTCTCAGCCACCTCCTGTGGGCCTTGCAAAATGATCAACCCCTTCCTTTCATTCCTCTCT
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>YGR209C_homolog, 105 aa (SEQ ID NO 684)
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>YPR028W_homolog, CDS: 1-594 bp (SEQ ID NO 685)
CCGAGCGGCGAGACGCTCCCCCCCATCTCTCCGCCATGAGGGAGAGGTTTCGACCGGTTCTTCGACGAG
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ASTGTGGTCAAGGACCTTAAAGACAACCCCAAGACACTCCACATCCCATCACTAAAGAAGCGACGAAA
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>YPR028W_homolog, 197 aa (SEQ ID NO 686)
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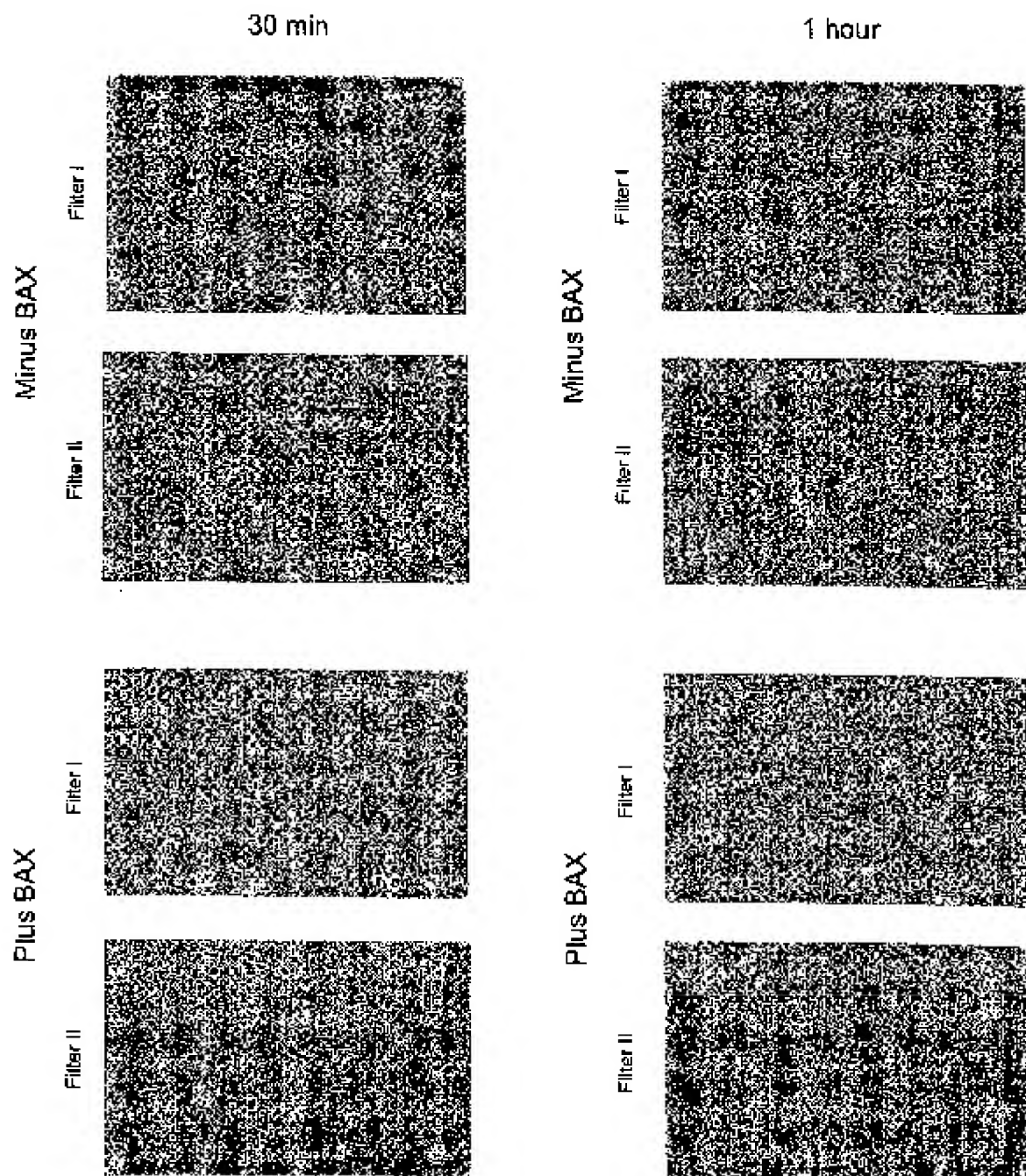


Figure 3 1

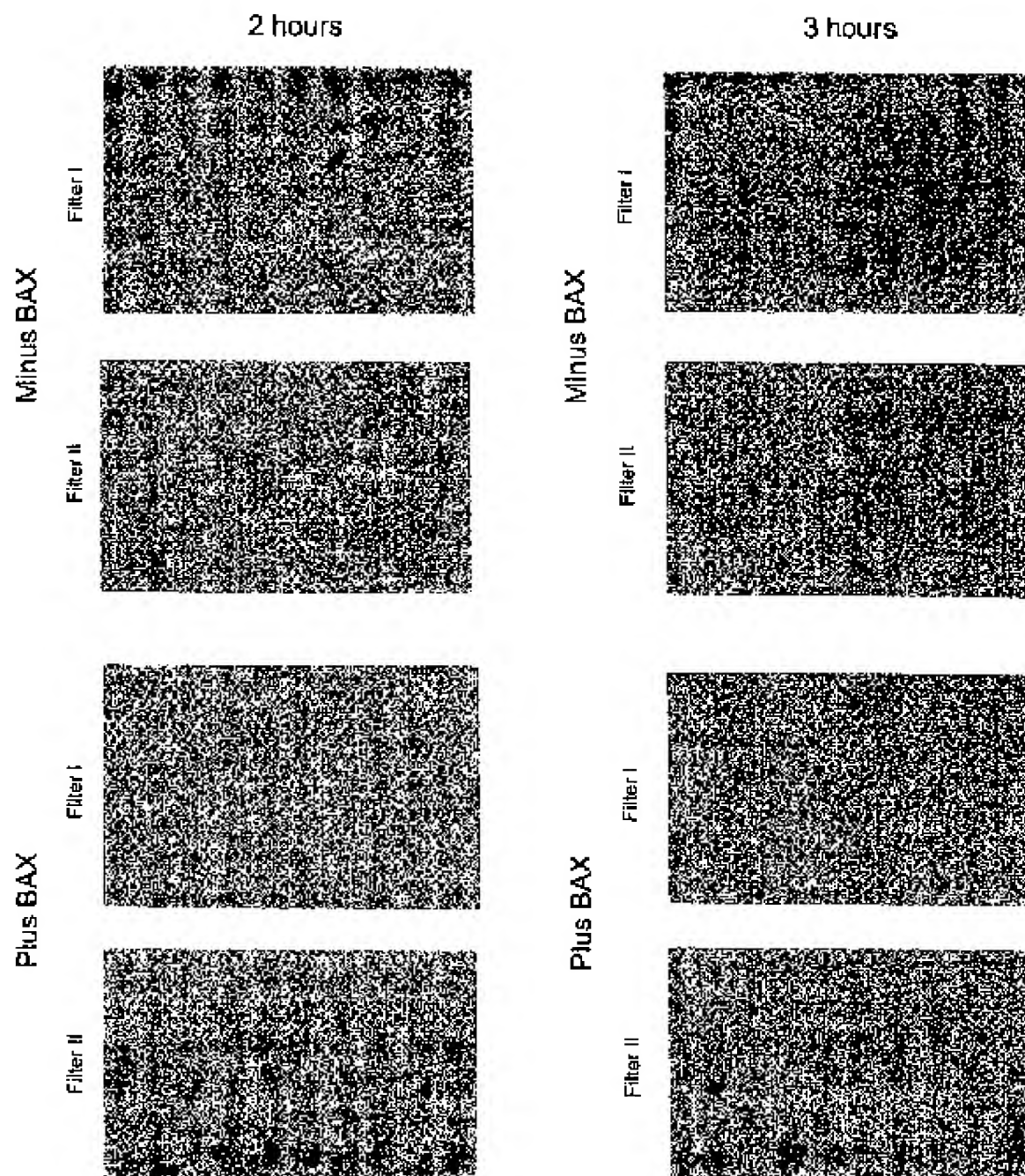


Figure 3 - 2

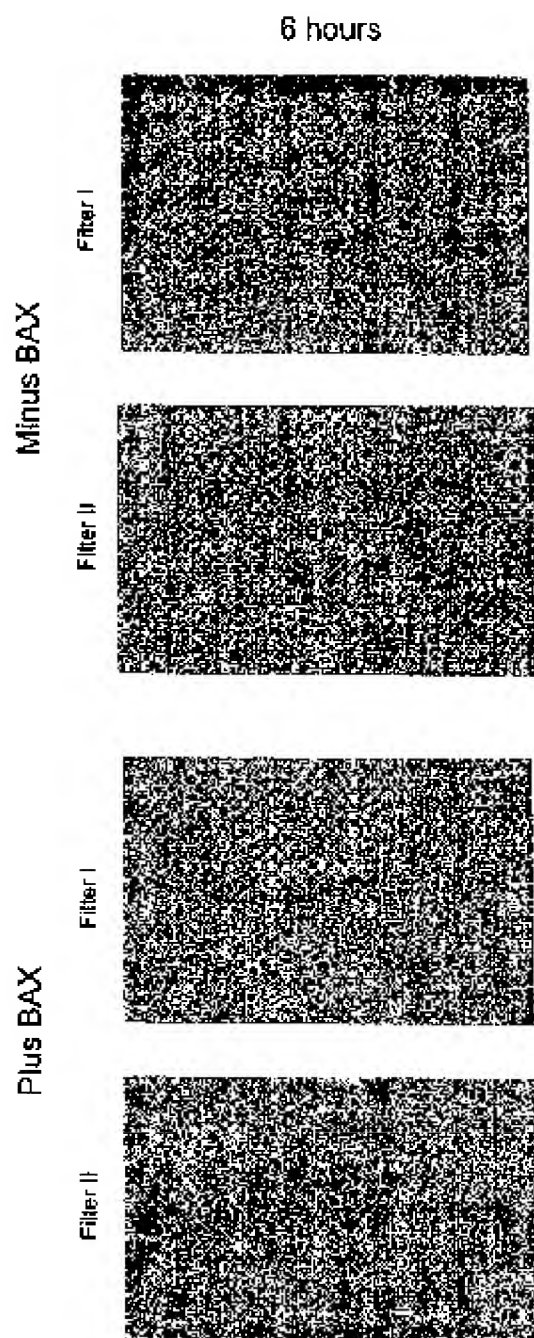
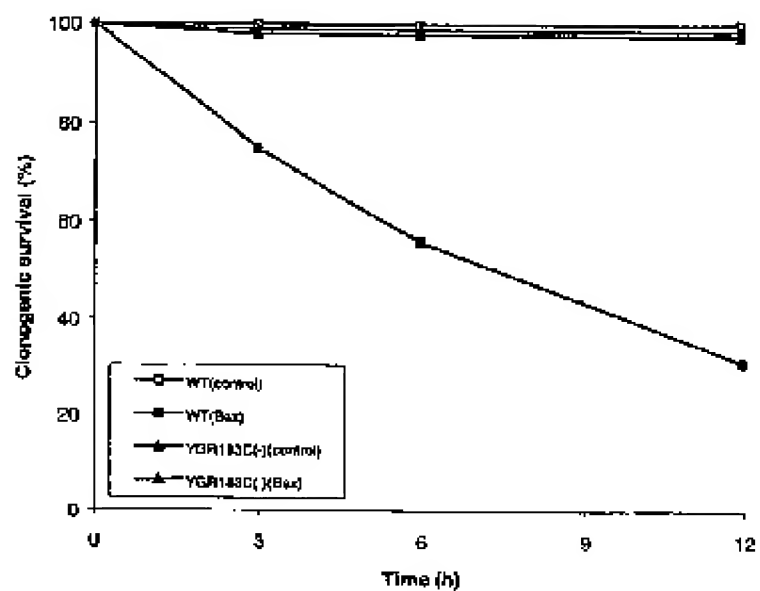
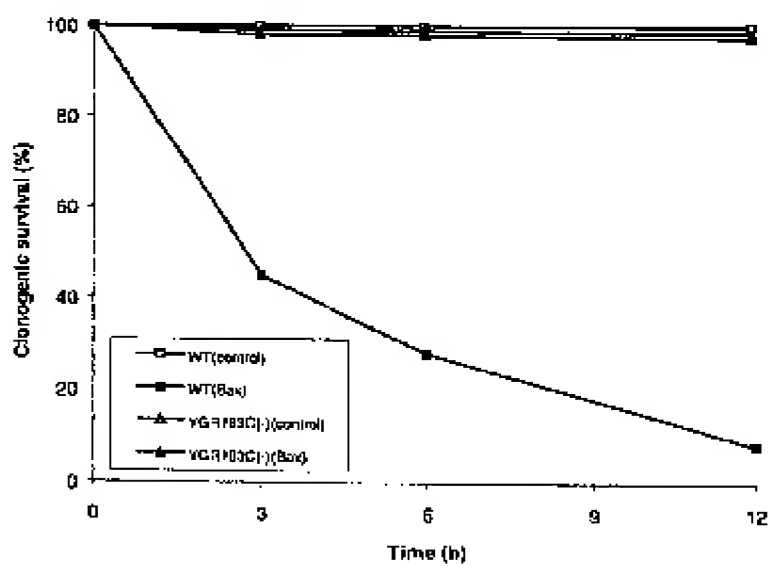


Figure 3 - 3



(A)



(B)

Figure 4

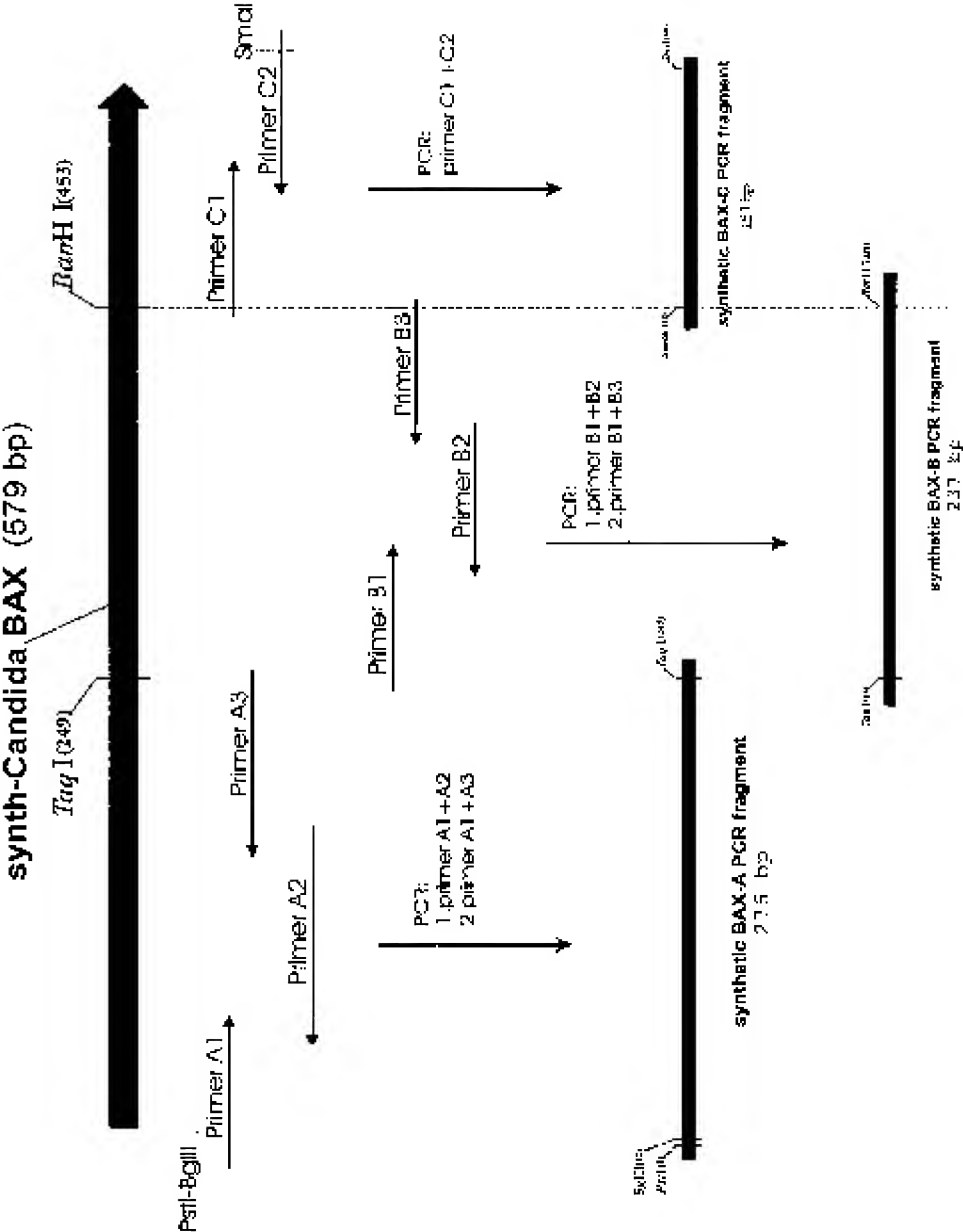


Fig. 5

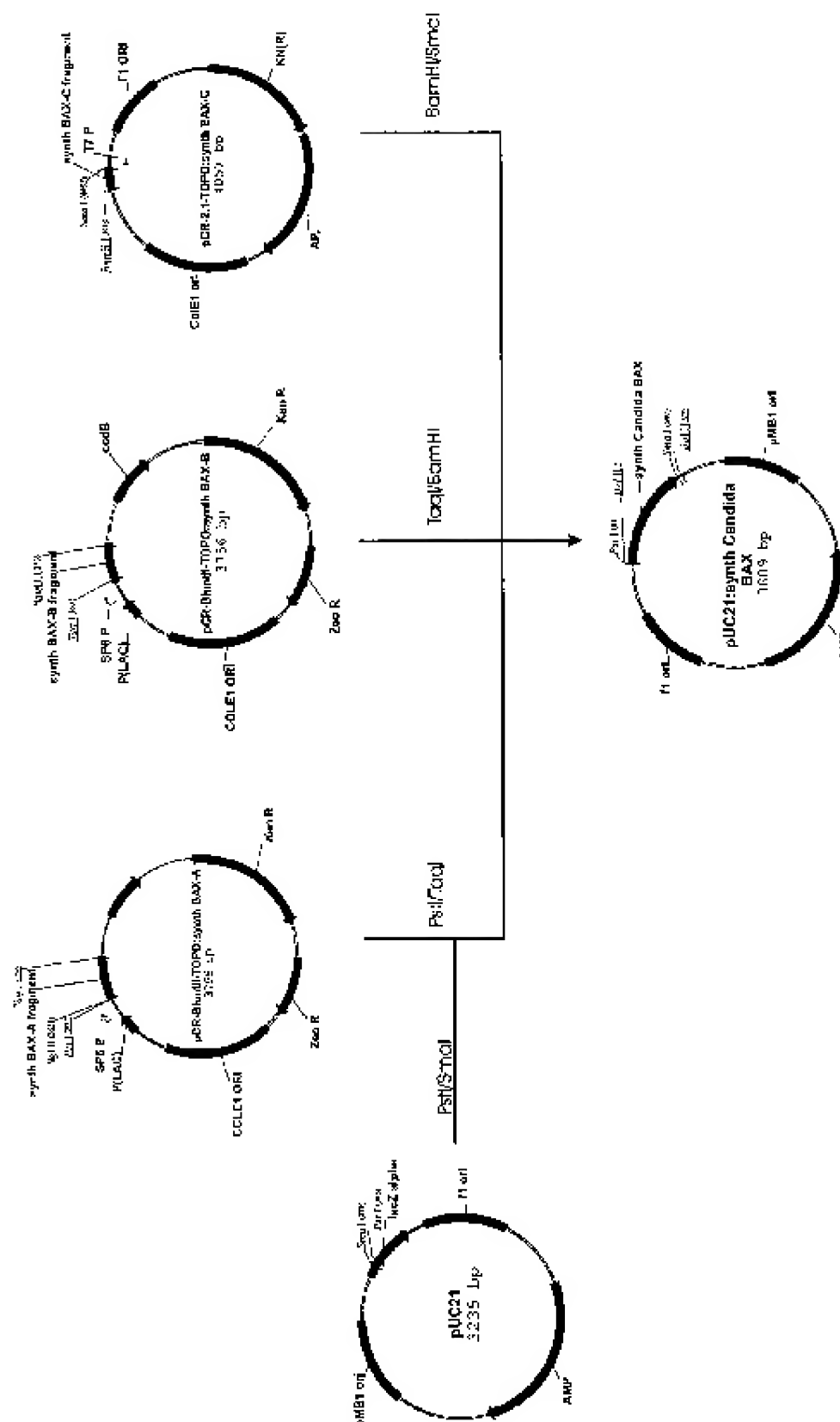


Fig. 5. Continued

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Lys Thr Gly Ala Phe Leu Leu Gln Gly Phe Ile Gln Asp Arg Ala Gly Arg Met Ala Gly
61  AAA ACC GGT GGT TTC TTG TTG GAA GGT TTC ATC CAA GAT AGA GCT GGT AGA ATG GCT GGT

Glu Thr Pro Glu Leu Thr Leu Gln Glu Pro Pro Gln Asp Ala Ser Thr Lys Lys Leu Ser
121  CAA ACC CCA CAA GAG AAC TTG GAA CAA CCG CCG CAA GAT GCT TCT ACC AAA AAA TTG TCT

Glu Cys Ser Arg Arg Ile Gly Asp Glu Leu Asp Ser Asn Met Met Glu Leu Gln Arg Met Ile
181  GAA TGT TTG ACA AGA ATC GGT GAT GAA TTG GAT TCT AAC ATG GAA TTG CAA AGA ATG ATC

Ala Asp Val Asp Thr Asp Ser Pro Arg Glu Val Phe Phe Arg Val Ala Ala Asp Met Phe
241  GCT GAT GTC GAA ACC CAG TCT CCA AGA GAA CTC TTC TTC AGA GTC GCT GCT GAT ATG TTG

Ala Asp Gly Asn Phe Gln Trp Gly Arg Val Val Ala Leu Phe Tyr Phe Ala Ser Lys Leu
301  GCT GAT GGT AAC TTC AAC TGG GGT AGA GTC CTC GCT TTC TTC TAC TTC GCT TCT AAA TTA

Val Leu Lys Ala Leu Cys Thr Lys Val Pro Glu Leu Ile Arg Thr Ile Met Gly Trp Thr
361  GTC TTG AAA GCT TTG GGT ACU AAA GTC CUA GAA TTC ATC AAA ACC ATC ATC ATC GGT TGG ACC

Leu Asp Phe Leu Arg Glu Arg Leu Leu Val Trp Ile Gln Asp Gln Gly Gly Trp Glu Gly
421  TTC GAT TTC TTG AGA GAA AGA TTG TTG GTC TGG ATC CAA GAT CAA GGT GCT TGG GAA GGT

Leu Leu Ser Tyr Phe Gly Thr Pro Thr Trp Cln Thr Val Thr Phe Phe Val Ala Gly Val
481  TTG TTG TCT TAC TTC GGT ACC CCA AGA TCT CCA ACC CCA ACC ATC ACC CTA CCA CCA GGT CTC

Leu Thr Ala Ser Leu Thr Ile Trp Lys Lys Met Gly (SEQ ID NO 2)
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Fig. 6

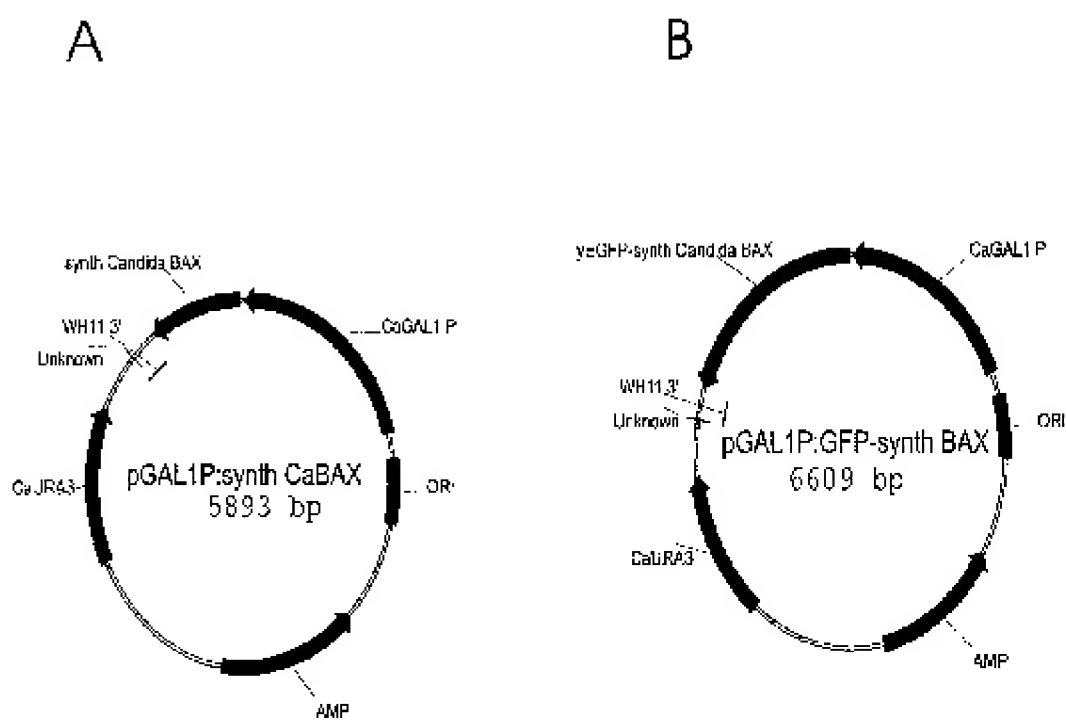


Fig. 7.

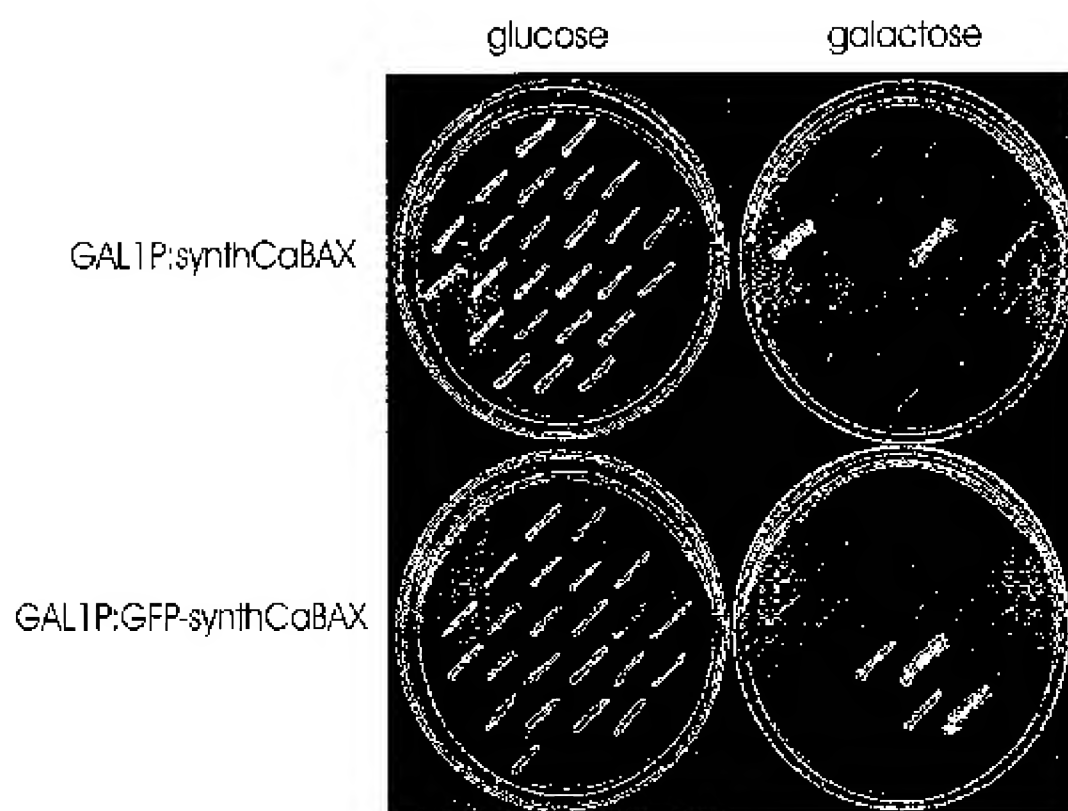


Fig. 8.

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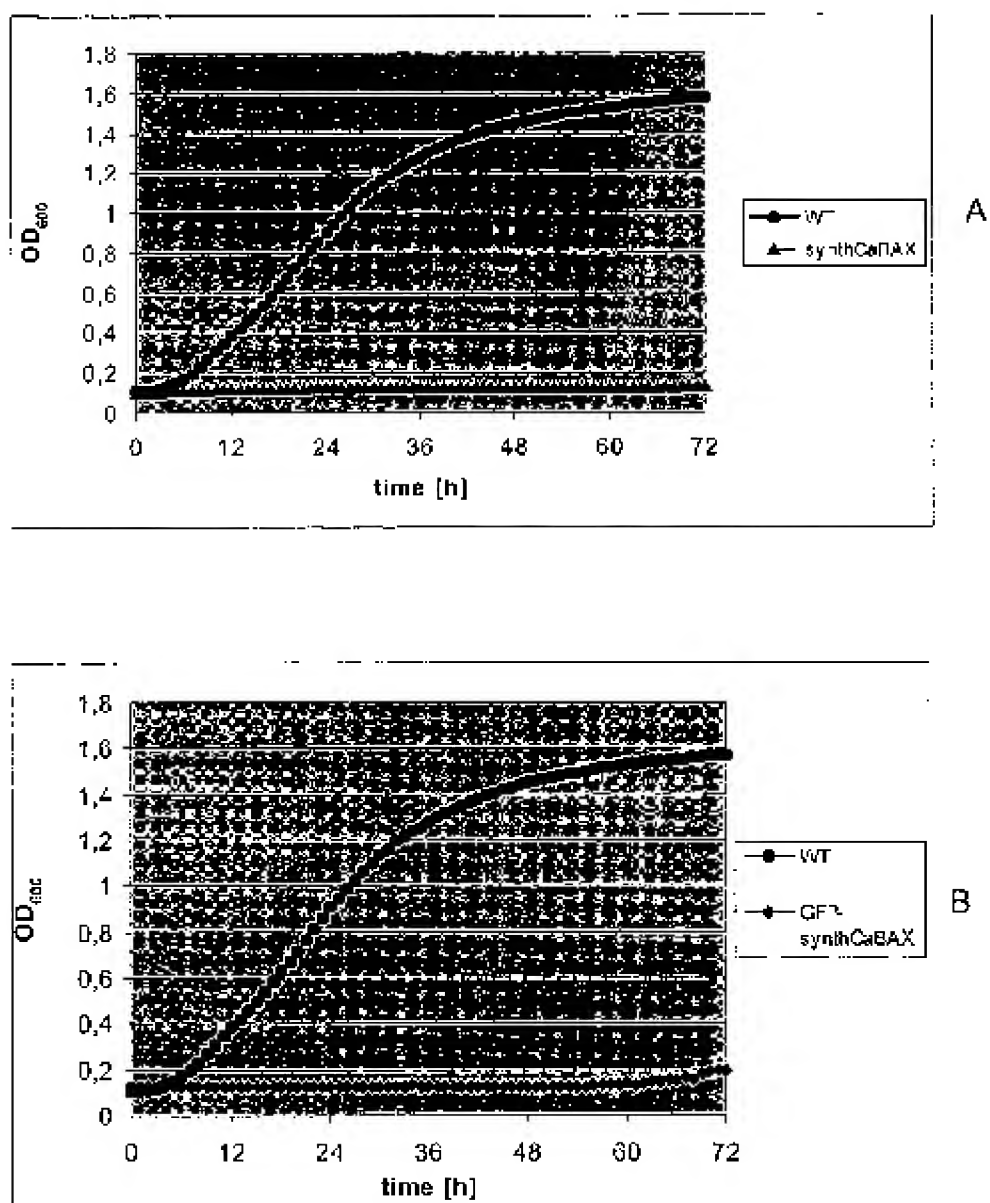


Fig. 9.

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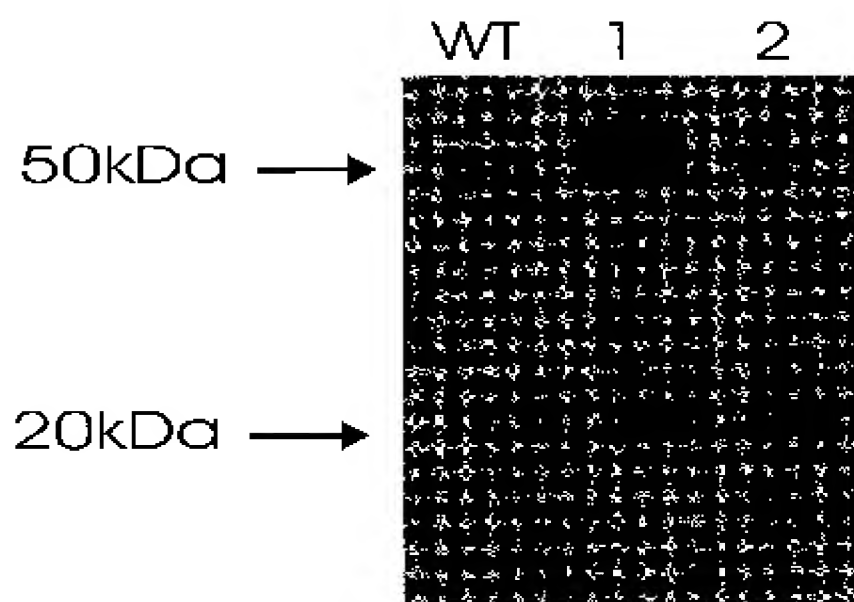


Fig. 10.

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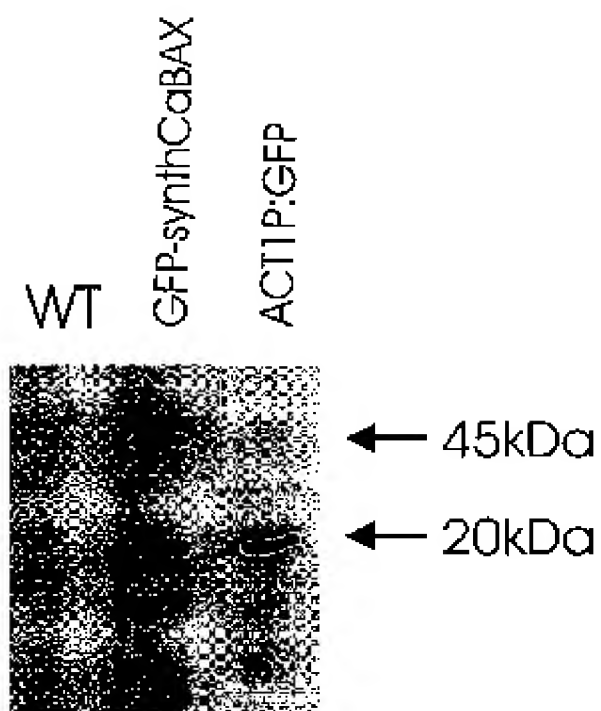


Fig. 11.

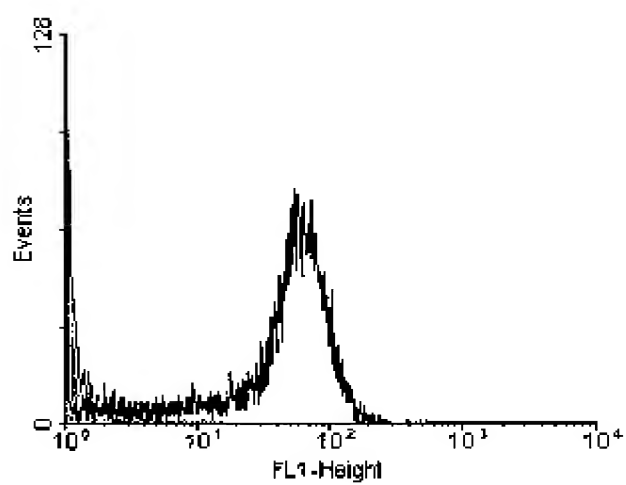
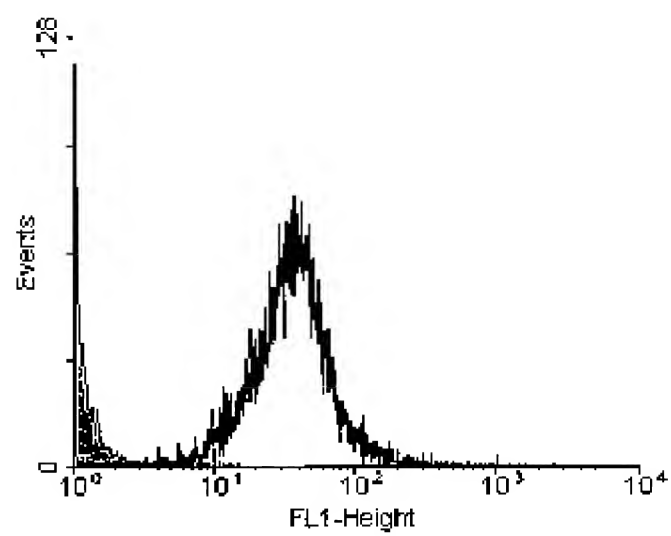


Fig.12.

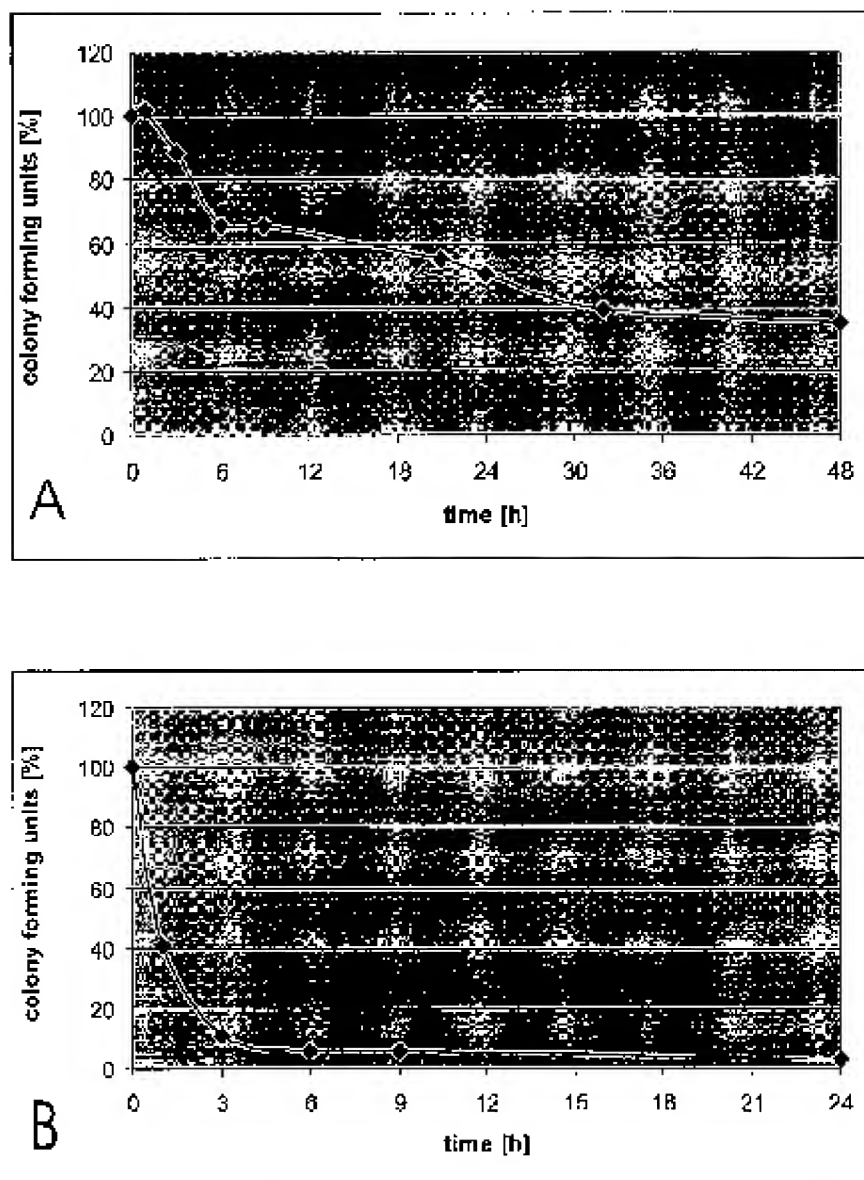


Fig. 13.